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## INTERNATIONAL APPLICATION PUBLISHED UNDER THE PATENT COOPERATION TREATY (PCT)

(51) International Patent Classification <sup>6</sup> : <b>C12N 15/31, C07K 14/315, 16/12, C12Q 1/68</b>	<b>A2</b>	(11) International Publication Number: <b>WO 98/18931</b>
		(43) International Publication Date: 7 May 1998 (07.05.98)

(21) International Application Number: PCT/US97/19588

(22) International Filing Date: 30 October 1997 (30.10.97)

(30) Priority Data:  
60/029,960 31 October 1996 (31.10.96) US

(71) Applicant (for all designated States except US): HUMAN GENOME SCIENCES, INC. [US/US]; 9410 Key West Avenue, Rockville, MD 20850 (US).

(72) Inventors; and

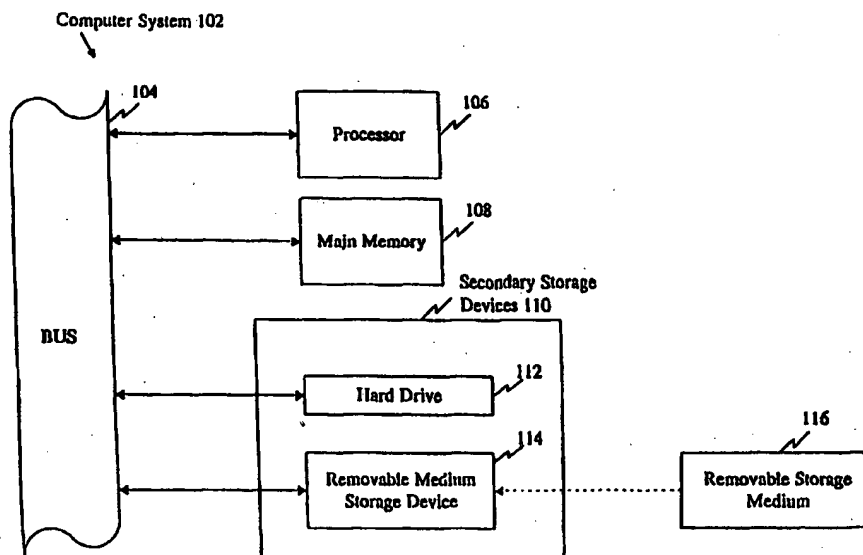
(75) Inventors/Applicants (for US only): KUNSCH, Charles, A. [US/US]; 2398B Dunwoody Crossing, Atlanta, GA 30338 (US). CHOI, Gil, H. [KR/US]; 11429 Potomac Oaks Drive, Rockville, MD 20850 (US). DILLON, Patrick, J. [US/US]; 1055 Snipe Court, Carlsbad, CA 92009 (US). ROSEN, Craig, A. [US/US]; 22400 Rolling Hill Road, Laytonsville, MD 20882 (US). BARASH, Steven, C. [US/US]; 582 College Parkway #303, Rockville, MD 20850 (US). FANNON, Michael [US/US]; 13501 Rippling Brook Drive, Silver Spring, MD 20850 (US). DOUGHERTY, Brian, A. [US/US]; 708 Meadow Field Court, Mount Airy, MD 21771 (US).

(74) Agents: BROOKES, A., Anders et al.; Human Genome Sciences, Inc., 9410 Key West Avenue, Rockville, MD 20850 (US).

(81) Designated States: AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, CA, CH, CN, CU, CZ, DE, DK, EE, ES, FI, GB, GE, GH, HU, ID, IL, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, UA, UG, US, UZ, VN, YU, ZW, ARIPO patent (GH, KE, LS, MW, SD, SZ, UG, ZW), Eurasian patent (AM, AZ, BY, KG, KZ, MD, RU, TJ, TM), European patent (AT, BE, CH, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE), OAPI patent (BF, BJ, CF, CG, CI, CM, GA, GN, ML, MR, NE, SN, TD, TG).

Published

Without international search report and to be republished upon receipt of that report.

(54) Title: *STREPTOCOCCUS PNEUMONIAE* POLYNUCLEOTIDES AND SEQUENCES

## (57) Abstract

The present invention provides polynucleotide sequences of the genome of *Streptococcus pneumoniae*, polypeptide sequences encoded by the polynucleotide sequences, corresponding polynucleotides and polypeptides, vectors and hosts comprising the polynucleotides, and assays and other uses thereof. The present invention further provides polynucleotide and polypeptide sequence information stored on computer readable media, and computer-based systems and methods which facilitate its use.

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## *Streptococcus pneumoniae* Polynucleotides and Sequences

### FIELD OF THE INVENTION

5       The present invention relates to the field of molecular biology. In particular, it relates to, among other things, nucleotide sequences of *Streptococcus pneumoniae*, contigs, ORFs, fragments, probes, primers and related polynucleotides thereof, peptides and polypeptides encoded by the sequences, and uses of the polynucleotides and sequences thereof, such as in fermentation,  
10       polypeptide production, assays and pharmaceutical development, among others.

### BACKGROUND OF THE INVENTION

15       *Streptococcus pneumoniae* has been one of the most extensively studied microorganisms since its first isolation in 1881. It was the object of many investigations that led to important scientific discoveries. In 1928, Griffith observed that when heat-killed encapsulated pneumococci and live strains constitutively lacking any capsule were concomitantly injected into mice, the nonencapsulated could be converted into encapsulated pneumococci with the same  
20       capsular type as the heat-killed strain. Years later, the nature of this "transforming principle," or carrier of genetic information, was shown to be DNA. (Avery, O.T., et al., *J. Exp. Med.*, 79:137-157 (1944)).

      In spite of the vast number of publications on *S. pneumoniae* many questions about its virulence are still unanswered, and this pathogen remains a  
25       major causative agent of serious human disease, especially community-acquired pneumonia. (Johnston, R.B., et al., *Rev. Infect. Dis.* 13(Suppl. 6):S509-517 (1991)). In addition, in developing countries, the pneumococcus is responsible for the death of a large number of children under the age of 5 years from pneumococcal pneumonia. The incidence of pneumococcal disease is highest in infants under 2  
30       years of age and in people over 60 years of age. Pneumococci are the second most frequent cause (after *Haemophilus influenzae* type b) of bacterial meningitis and otitis media in children. With the recent introduction of conjugate vaccines for *H. influenzae* type b, pneumococcal meningitis is likely to become increasingly prominent. *S. pneumoniae* is the most important etiologic agent of community-

acquired pneumonia in adults and is the second most common cause of bacterial meningitis behind *Neisseria meningitidis*.

The antibiotic generally prescribed to treat *S. pneumoniae* is benzylpenicillin, although resistance to this and to other antibiotics is found occasionally. Pneumococcal resistance to penicillin results from mutations in its penicillin-binding proteins. In uncomplicated pneumococcal pneumonia caused by a sensitive strain, treatment with penicillin is usually successful unless started too late. Erythromycin or clindamycin can be used to treat pneumonia in patients hypersensitive to penicillin, but resistant strains to these drugs exist. Broad spectrum antibiotics (e.g., the tetracyclines) may also be effective, although tetracycline-resistant strains are not rare. In spite of the availability of antibiotics, the mortality of pneumococcal bacteremia in the last four decades has remained stable between 25 and 29%. (Gillespie, S.H., et al., *J. Med. Microbiol.* 28:237-248 (1989).

*S. pneumoniae* is carried in the upper respiratory tract by many healthy individuals. It has been suggested that attachment of pneumococci is mediated by a disaccharide receptor on fibronectin, present on human pharyngeal epithelial cells. (Anderson, B.J., et al., *J. Immunol.* 142:2464-2468 (1989). The mechanisms by which pneumococci translocate from the nasopharynx to the lung, thereby causing pneumonia, or migrate to the blood, giving rise to bacteremia or septicemia, are poorly understood. (Johnston, R.B., et al., *Rev. Infect. Dis.* 13(Suppl. 6):S509-517 (1991).

Various proteins have been suggested to be involved in the pathogenicity of *S. pneumoniae*, however, only a few of them have actually been confirmed as virulence factors. Pneumococci produce an IgA1 protease that might interfere with host defense at mucosal surfaces. (Kornfield, S.J., et al., *Rev. Inf. Dis.* 3:521-534 (1981). *S. pneumoniae* also produces neuraminidase, an enzyme that may facilitate attachment to epithelial cells by cleaving sialic acid from the host glycolipids and gangliosides. Partially purified neuraminidase was observed to induce meningitis-like symptoms in mice; however, the reliability of this finding has been questioned because the neuraminidase preparations used were probably contaminated with cell wall products. Other pneumococcal proteins besides neuraminidase are involved in the adhesion of pneumococci to epithelial and endothelial cells. These pneumococcal proteins have as yet not been identified. Recently, Cundell et al., reported that peptide permeases can modulate



pneumococcal adherence to epithelial and endothelial cells. It was, however, unclear whether these permeases function directly, as adhesions or whether they enhance adherence by modulating the expression of pneumococcal adhesions. (DeVelasco, E.A., *et al.*, *Micro. Rev.* 59:591-603 (1995). A better understanding of the virulence factors determining its pathogenicity will need to be developed to cope with the devastating effects of pneumococcal disease in humans.

Ironically, despite the prominent role of *S. pneumoniae* in the discovery of DNA, little is known about the molecular genetics of the organism. The *S. pneumoniae* genome consists of one circular, covalently closed, double-stranded DNA and a collection of so-called variable accessory elements, such as prophages, plasmids, transposons and the like. Most physical characteristics and almost all of the genes of *S. pneumoniae* are unknown. Among the few that have been identified, most have not been physically mapped or characterized in detail. Only a few genes of this organism have been sequenced. (See, for instance current versions of GENBANK and other nucleic acid databases, and references that relate to the genome of *S. pneumoniae* such as those set out elsewhere herein.)

It is clear that the etiology of diseases mediated or exacerbated by *S. pneumoniae*, infection involves the programmed expression of *S. pneumoniae* genes, and that characterizing the genes and their patterns of expression would add dramatically to our understanding of the organism and its host interactions. Knowledge of *S. pneumoniae* genes and genomic organization would improve our understanding of disease etiology and lead to improved and new ways of preventing, ameliorating, arresting and reversing diseases. Moreover, characterized genes and genomic fragments of *S. pneumoniae* would provide reagents for, among other things, detecting, characterizing and controlling *S. pneumoniae* infections. There is a need to characterize the genome of *S. pneumoniae* and for polynucleotides of this organism.

### SUMMARY OF THE INVENTION

5 The present invention is based on the sequencing of fragments of the *Streptococcus pneumoniae* genome. The primary nucleotide sequences which were generated are provided in SEQ ID NOS:1-391.

10 The present invention provides the nucleotide sequence of several hundred contigs of the *Streptococcus pneumoniae* genome, which are listed in tables below and set out in the Sequence Listing submitted herewith, and representative fragments thereof, in a form which can be readily used, analyzed, and interpreted by a skilled artisan. In one embodiment, the present invention is provided as contiguous strings of primary sequence information corresponding to the nucleotide sequences depicted in SEQ ID NOS:1-391.

15 The present invention further provides nucleotide sequences which are at least 95% identical to the nucleotide sequences of SEQ ID NOS:1-391.

20 The nucleotide sequence of SEQ ID NOS:1-391, a representative fragment thereof, or a nucleotide sequence which is at least 95% identical to the nucleotide sequence of SEQ ID NOS:1-391 may be provided in a variety of mediums to facilitate its use. In one application of this embodiment, the sequences of the present invention are recorded on computer readable media. Such media includes, but is not limited to: magnetic storage media, such as floppy discs, hard disc storage medium, and magnetic tape; optical storage media such as CD-ROM; electrical storage media such as RAM and ROM; and hybrids of these categories such as magnetic/optical storage media.

25 The present invention further provides systems, particularly computer-based systems which contain the sequence information herein described stored in a data storage means. Such systems are designed to identify commercially important fragments of the *Streptococcus pneumoniae* genome.

30 Another embodiment of the present invention is directed to fragments of the *Streptococcus pneumoniae* genome having particular structural or functional attributes. Such fragments of the *Streptococcus pneumoniae* genome of the present invention include, but are not limited to, fragments which encode peptides, hereinafter referred to as open reading frames or ORFs, fragments which modulate the expression of an operably linked ORF, hereinafter referred to as expression  
35 modulating fragments or EMFs, and fragments which can be used to diagnose the

presence of *Streptococcus pneumoniae* in a sample, hereinafter referred to as diagnostic fragments or DFs.

Each of the ORFs in fragments of the *Streptococcus pneumoniae* genome disclosed in Tables 1-3, and the EMFs found 5' to the ORFs, can be used in numerous ways as polynucleotide reagents. For instance, the sequences can be used as diagnostic probes or amplification primers for detecting or determining the presence of a specific microbe in a sample, to selectively control gene expression in a host and in the production of polypeptides, such as polypeptides encoded by ORFs of the present invention, particular those polypeptides that have a pharmacological activity.

The present invention further includes recombinant constructs comprising one or more fragments of the *Streptococcus pneumoniae* genome of the present invention. The recombinant constructs of the present invention comprise vectors, such as a plasmid or viral vector, into which a fragment of the *Streptococcus pneumoniae* has been inserted.

The present invention further provides host cells containing any of the isolated fragments of the *Streptococcus pneumoniae* genome of the present invention. The host cells can be a higher eukaryotic host cell, such as a mammalian cell, a lower eukaryotic cell, such as a yeast cell, or a procaryotic cell such as a bacterial cell.

The present invention is further directed to isolated polypeptides and proteins encoded by ORFs of the present invention. A variety of methods, well known to those of skill in the art, routinely may be utilized to obtain any of the polypeptides and proteins of the present invention. For instance, polypeptides and proteins of the present invention having relatively short, simple amino acid sequences readily can be synthesized using commercially available automated peptide synthesizers. Polypeptides and proteins of the present invention also may be purified from bacterial cells which naturally produce the protein. Yet another alternative is to purify polypeptide and proteins of the present invention from cells which have been altered to express them.

The invention further provides methods of obtaining homologs of the fragments of the *Streptococcus pneumoniae* genome of the present invention and homologs of the proteins encoded by the ORFs of the present invention. Specifically, by using the nucleotide and amino acid sequences disclosed herein as

a probe or as primers, and techniques such as PCR cloning and colony/plaque hybridization, one skilled in the art can obtain homologs.

The invention further provides antibodies which selectively bind polypeptides and proteins of the present invention. Such antibodies include both  
5 monoclonal and polyclonal antibodies.

The invention further provides hybridomas which produce the above-described antibodies. A hybridoma is an immortalized cell line which is capable of secreting a specific monoclonal antibody.

The present invention further provides methods of identifying test samples  
10 derived from cells which express one of the ORFs of the present invention, or a homolog thereof. Such methods comprise incubating a test sample with one or more of the antibodies of the present invention, or one or more of the DFs of the present invention, under conditions which allow a skilled artisan to determine if the sample contains the ORF or product produced therefrom.

15 In another embodiment of the present invention, kits are provided which contain the necessary reagents to carry out the above-described assays.

Specifically, the invention provides a compartmentalized kit to receive, in close confinement, one or more containers which comprises: (a) a first container comprising one of the antibodies, or one of the DFs of the present invention; and  
20 (b) one or more other containers comprising one or more of the following: wash reagents, reagents capable of detecting presence of bound antibodies or hybridized DFs.

Using the isolated proteins of the present invention, the present invention further provides methods of obtaining and identifying agents capable of binding to  
25 a polypeptide or protein encoded by one of the ORFs of the present invention. Specifically, such agents include, as further described below, antibodies, peptides, carbohydrates, pharmaceutical agents and the like. Such methods comprise steps of: (a) contacting an agent with an isolated protein encoded by one of the ORFs of the present invention; and (b) determining whether the agent binds to said protein.

30 The present genomic sequences of *Streptococcus pneumoniae* will be of great value to all laboratories working with this organism and for a variety of commercial purposes. Many fragments of the *Streptococcus pneumoniae* genome will be immediately identified by similarity searches against GenBank or protein databases and will be of immediate value to *Streptococcus pneumoniae* researchers

and for immediate commercial value for the production of proteins or to control gene expression.

The methodology and technology for elucidating extensive genomic sequences of bacterial and other genomes has and will greatly enhance the ability to  
5 analyze and understand chromosomal organization. In particular, sequenced contigs and genomes will provide the models for developing tools for the analysis of chromosome structure and function, including the ability to identify genes within large segments of genomic DNA, the structure, position, and spacing of regulatory elements, the identification of genes with potential industrial applications, and the  
10 ability to do comparative genomic and molecular phylogeny.

### DESCRIPTION OF THE FIGURES

**FIGURE 1** is a block diagram of a computer system (102) that can be  
15 used to implement computer-based systems of present invention.

**FIGURE 2** is a schematic diagram depicting the data flow and computer programs used to collect, assemble, edit and annotate the contigs of the *Streptococcus pneumoniae* genome of the present invention. Both Macintosh and  
20 Unix platforms are used to handle the AB 373 and 377 sequence data files, largely as described in Kerlavage *et al.*, *Proceedings of the Twenty-Sixth Annual Hawaii International Conference on System Sciences*, 585, IEEE Computer Society Press, Washington D.C. (1993). Factura (AB) is a Macintosh program designed for automatic vector sequence removal and end-trimming of sequence files. The  
25 program Loadis runs on a Macintosh platform and parses the feature data extracted from the sequence files by Factura to the Unix based *Streptococcus pneumoniae* relational database. Assembly of contigs (and whole genome sequences) is accomplished by retrieving a specific set of sequence files and their associated features using Extrseq, a Unix utility for retrieving sequences from an SQL  
30 database. The resulting sequence file is processed by seq\_filter to trim portions of the sequences with more than 2% ambiguous nucleotides. The sequence files were assembled using TIGR Assembler, an assembly engine designed at The Institute for Genomic Research ( TIGR ) for rapid and accurate assembly of thousands of sequence fragments. The collection of contigs generated by the assembly step is  
35 loaded into the database with the lassie program. Identification of open reading

frames (ORFs) is accomplished by processing contigs with zorf or GenMark. The ORFs are searched against *S. pneumoniae* sequences from GenBank and against all protein sequences using the BLASTN and BLASTP programs, described in Altschul *et al.*, *J. Mol. Biol.* 215: 403-410 (1990)). Results of the ORF  
5 determination and similarity searching steps were loaded into the database. As described below, some results of the determination and the searches are set out in Tables 1-3.

### DETAILED DESCRIPTION OF ILLUSTRATIVE EMBODIMENTS

10

The present invention is based on the sequencing of fragments of the *Streptococcus pneumoniae* genome and analysis of the sequences. The primary nucleotide sequences generated by sequencing the fragments are provided in SEQ ID NOS:1-391. (As used herein, the "primary sequence" refers to the nucleotide  
15 sequence represented by the IUPAC nomenclature system.)

In addition to the aforementioned *Streptococcus pneumoniae* polynucleotide and polynucleotide sequences, the present invention provides the nucleotide sequences of SEQ ID NOS:1-391, or representative fragments thereof, in a form which can be readily used, analyzed, and interpreted by a skilled artisan.

20 As used herein, a "representative fragment of the nucleotide sequence depicted in SEQ ID NOS:1-391" refers to any portion of the SEQ ID NOS:1-391 which is not presently represented within a publicly available database. Preferred representative fragments of the present invention are *Streptococcus pneumoniae* open reading frames ( ORFs ), expression modulating fragment ( EMFs ) and  
25 fragments which can be used to diagnose the presence of *Streptococcus pneumoniae* in sample ( DFs ). A non-limiting identification of preferred representative fragments is provided in Tables 1-3. As discussed in detail below, the information provided in SEQ ID NOS:1-391 and in Tables 1-3 together with routine cloning, synthesis, sequencing and assay methods will enable those skilled  
30 in the art to clone and sequence all "representative fragments" of interest, including open reading frames encoding a large variety of *Streptococcus pneumoniae* proteins.

While the presently disclosed sequences of SEQ ID NOS:1-391 are highly accurate, sequencing techniques are not perfect and, in relatively rare instances,  
35 further investigation of a fragment or sequence of the invention may reveal a

nucleotide sequence error present in a nucleotide sequence disclosed in SEQ ID NOS:1-391. However, once the present invention is made available (*i.e.*, once the information in SEQ ID NOS:1-391 and Tables 1-3 has been made available), resolving a rare sequencing error in SEQ ID NOS:1-391 will be well within the skill of the art. The present disclosure makes available sufficient sequence information to allow any of the described contigs or portions thereof to be obtained readily by straightforward application of routine techniques. Further sequencing of such polynucleotide may proceed in like manner using manual and automated sequencing methods which are employed ubiquitous in the art. Nucleotide sequence editing software is publicly available. For example, Applied Biosystem's (AB) AutoAssembler can be used as an aid during visual inspection of nucleotide sequences. By employing such routine techniques potential errors readily may be identified and the correct sequence then may be ascertained by targeting further sequencing effort, also of a routine nature, to the region containing the potential error.

Even if all of the very rare sequencing errors in SEQ ID NOS:1-391 were corrected, the resulting nucleotide sequences would still be at least 95% identical, nearly all would be at least 99% identical, and the great majority would be at least 99.9% identical to the nucleotide sequences of SEQ ID NOS:1-391.

As discussed elsewhere herein, polynucleotides of the present invention readily may be obtained by routine application of well known and standard procedures for cloning and sequencing DNA. Detailed methods for obtaining libraries and for sequencing are provided below, for instance. A wide variety of *Streptococcus pneumoniae* strains that can be used to prepare *S. pneumoniae* genomic DNA for cloning and for obtaining polynucleotides of the present invention are available to the public from recognized depository institutions, such as the American Type Culture Collection (ATCC). While the present invention is enabled by the sequences and other information herein disclosed, the *S. pneumoniae* strain that provided the DNA of the present Sequence Listing, Strain 7/87 14.8.91, has been deposited in the ATCC, as a convenience to those of skill in the art. As a further convenience, a library of *S. pneumoniae* genomic DNA, derived from the same strain, also has been deposited in the ATCC. The *S. pneumoniae* strain was deposited on October 10, 1996, and was given Deposit No. 55840, and the cDNA library was deposited on October 11, 1996 and was given Deposit No. 97755. The genomic fragments in the library are 15 to 20 kb

fragments generated by partial Sau3A1 digestion and they are inserted into the BamHI site in the well-known lambda-derived vector lambda DASH II (Stratagene, La Jolla, CA). The provision of the deposits is not a waiver of any rights of the inventors or their assignees in the present subject matter.

5       The nucleotide sequences of the genomes from different strains of *Streptococcus pneumoniae* differ somewhat. However, the nucleotide sequences of the genomes of all *Streptococcus pneumoniae* strains will be at least 95% identical, in corresponding part, to the nucleotide sequences provided in SEQ ID NOS:1-391. Nearly all will be at least 99% identical and the great majority will be  
10   99.9% identical.

Thus, the present invention further provides nucleotide sequences which are at least 95%, preferably 99% and most preferably 99.9% identical to the nucleotide sequences of SEQ ID NOS:1-391, in a form which can be readily used, analyzed and interpreted by the skilled artisan.

15       Methods for determining whether a nucleotide sequence is at least 95%, at least 99% or at least 99.9% identical to the nucleotide sequences of SEQ ID NOS:1-391 are routine and readily available to the skilled artisan. For example, the well known fasta algorithm described in Pearson and Lipman, *Proc. Natl. Acad. Sci. USA* 85: 2444 (1988) can be used to generate the percent identity of nucleotide  
20   sequences. The BLASTN program also can be used to generate an identity score of polynucleotides compared to one another.

### COMPUTER RELATED EMBODIMENTS

25       The nucleotide sequences provided in SEQ ID NOS:1-391, a representative fragment thereof, or a nucleotide sequence at least 95%, preferably at least 99% and most preferably at least 99.9% identical to a polynucleotide sequence of SEQ ID NOS:1-391 may be "provided" in a variety of mediums to facilitate use thereof. As used herein, provided refers to a manufacture, other than an isolated nucleic acid molecule, which contains a nucleotide sequence of the present invention; *i.e.*,  
30   a nucleotide sequence provided in SEQ ID NOS:1-391, a representative fragment thereof, or a nucleotide sequence at least 95%, preferably at least 99% and most preferably at least 99.9% identical to a polynucleotide of SEQ ID NOS:1-391. Such a manufacture provides a large portion of the *Streptococcus pneumoniae* genome and parts thereof (*e.g.*, a *Streptococcus pneumoniae* open reading frame  
35   (ORF)) in a form which allows a skilled artisan to examine the manufacture using



means not directly applicable to examining the *Streptococcus pneumoniae* genome or a subset thereof as it exists in nature or in purified form.

In one application of this embodiment, a nucleotide sequence of the present invention can be recorded on computer readable media. As used herein, "computer readable media" refers to any medium which can be read and accessed directly by a computer. Such media include, but are not limited to: magnetic storage media, such as floppy discs, hard disc storage medium, and magnetic tape; optical storage media such as CD-ROM; electrical storage media such as RAM and ROM; and hybrids of these categories, such as magnetic/optical storage media. A skilled artisan can readily appreciate how any of the presently known computer readable mediums can be used to create a manufacture comprising computer readable medium having recorded thereon a nucleotide sequence of the present invention. Likewise, it will be clear to those of skill how additional computer readable media that may be developed also can be used to create analogous manufactures having recorded thereon a nucleotide sequence of the present invention.

As used herein, "recorded" refers to a process for storing information on computer readable medium. A skilled artisan can readily adopt any of the presently know methods for recording information on computer readable medium to generate manufactures comprising the nucleotide sequence information of the present invention. A variety of data storage structures are available to a skilled artisan for creating a computer readable medium having recorded thereon a nucleotide sequence of the present invention. The choice of the data storage structure will generally be based on the means chosen to access the stored information. In addition, a variety of data processor programs and formats can be used to store the nucleotide sequence information of the present invention on computer readable medium. The sequence information can be represented in a word processing text file, formatted in commercially-available software such as WordPerfect and MicroSoft Word, or represented in the form of an ASCII file, stored in a database application, such as DB2, Sybase, Oracle, or the like. A skilled artisan can readily adapt any number of data-processor structuring formats (e.g., text file or database) in order to obtain computer readable medium having recorded thereon the nucleotide sequence information of the present invention.

Computer software is publicly available which allows a skilled artisan to access sequence information provided in a computer readable medium. Thus, by providing in computer readable form the nucleotide sequences of SEQ ID NOS:1-

391, a representative fragment thereof, or a nucleotide sequence at least 95%, preferably at least 99% and most preferably at least 99.9% identical to a sequence of SEQ ID NOS:1-391 the present invention enables the skilled artisan routinely to access the provided sequence information for a wide variety of purposes.

5       The examples which follow demonstrate how software which implements the BLAST (Altschul *et al.*, *J. Mol. Biol.* 215:403-410 (1990)) and BLAZE (Brutlag *et al.*, *Comp. Chem.* 17:203-207 (1993)) search algorithms on a Sybase system was used to identify open reading frames (ORFs) within the *Streptococcus pneumoniae* genome which contain homology to ORFs or proteins from both  
10 *Streptococcus pneumoniae* and from other organisms. Among the ORFs discussed herein are protein encoding fragments of the *Streptococcus pneumoniae* genome useful in producing commercially important proteins, such as enzymes used in fermentation reactions and in the production of commercially useful metabolites.

15       The present invention further provides systems, particularly computer-based systems, which contain the sequence information described herein. Such systems are designed to identify, among other things, commercially important fragments of the *Streptococcus pneumoniae* genome.

20       As used herein, "a computer-based system" refers to the hardware means, software means, and data storage means used to analyze the nucleotide sequence information of the present invention. The minimum hardware means of the computer-based systems of the present invention comprises a central processing unit (CPU), input means, output means, and data storage means. A skilled artisan can readily appreciate that any one of the currently available computer-based systems are suitable for use in the present invention.

25       As stated above, the computer-based systems of the present invention comprise a data storage means having stored therein a nucleotide sequence of the present invention and the necessary hardware means and software means for supporting and implementing a search means.

30       As used herein, "data storage means" refers to memory which can store nucleotide sequence information of the present invention, or a memory access means which can access manufactures having recorded thereon the nucleotide sequence information of the present invention.

35       As used herein, "search means" refers to one or more programs which are implemented on the computer-based system to compare a target sequence or target structural motif with the sequence information stored within the data storage

means. Search means are used to identify fragments or regions of the present genomic sequences which match a particular target sequence or target motif. A variety of known algorithms are disclosed publicly and a variety of commercially available software for conducting search means are and can be used in the computer-based systems of the present invention. Examples of such software includes, but is not limited to, MacPattern (EMBL), BLASTN and BLASTX (NCBIA). A skilled artisan can readily recognize that any one of the available algorithms or implementing software packages for conducting homology searches can be adapted for use in the present computer-based systems.

As used herein, a "target sequence" can be any DNA or amino acid sequence of six or more nucleotides or two or more amino acids. A skilled artisan can readily recognize that the longer a target sequence is, the less likely a target sequence will be present as a random occurrence in the database. The most preferred sequence length of a target sequence is from about 10 to 100 amino acids or from about 30 to 300 nucleotide residues. However, it is well recognized that searches for commercially important fragments, such as sequence fragments involved in gene expression and protein processing, may be of shorter length.

As used herein, "a target structural motif," or "target motif," refers to any rationally selected sequence or combination of sequences in which the sequence(s) are chosen based on a three-dimensional configuration which is formed upon the folding of the target motif. There are a variety of target motifs known in the art. Protein target motifs include, but are not limited to, enzymic active sites and signal sequences. Nucleic acid target motifs include, but are not limited to, promoter sequences, hairpin structures and inducible expression elements (protein binding sequences).

A variety of structural formats for the input and output means can be used to input and output the information in the computer-based systems of the present invention. A preferred format for an output means ranks fragments of the *Streptococcus pneumoniae* genomic sequences possessing varying degrees of homology to the target sequence or target motif. Such presentation provides a skilled artisan with a ranking of sequences which contain various amounts of the target sequence or target motif and identifies the degree of homology contained in the identified fragment.

A variety of comparing means can be used to compare a target sequence or target motif with the data storage means to identify sequence fragments of the

*Streptococcus pneumoniae* genome. In the present examples, implementing software which implement the BLAST and BLAZE algorithms, described in Altschul *et al.*, *J. Mol. Biol.* 215: 403-410 (1990), is used to identify open reading frames within the *Streptococcus pneumoniae* genome. A skilled artisan can readily  
5 recognize that any one of the publicly available homology search programs can be used as the search means for the computer-based systems of the present invention. Of course, suitable proprietary systems that may be known to those of skill also may be employed in this regard.

Figure 1 provides a block diagram of a computer system illustrative of  
10 embodiments of this aspect of present invention. The computer system 102 includes a processor 106 connected to a bus 104. Also connected to the bus 104 are a main memory 108 (preferably implemented as random access memory, RAM) and a variety of secondary storage devices 110, such as a hard drive 112 and a removable medium storage device 114. The removable medium storage device 114  
15 may represent, for example, a floppy disk drive, a CD-ROM drive, a magnetic tape drive, *etc.* A removable storage medium 116 (such as a floppy disk, a compact disk, a magnetic tape, *etc.*) containing control logic and/or data recorded therein may be inserted into the removable medium storage device 114. The computer system 102 includes appropriate software for reading the control logic and/or the  
20 data from the removable medium storage device 114, once it is inserted into the removable medium storage device 114.

A nucleotide sequence of the present invention may be stored in a well known manner in the main memory 108, any of the secondary storage devices 110, and/or a removable storage medium 116. During execution, software for accessing  
25 and processing the genomic sequence (such as search tools, comparing tools, *etc.*) reside in main memory 108, in accordance with the requirements and operating parameters of the operating system, the hardware system and the software program or programs.

## BIOCHEMICAL EMBODIMENTS

Other embodiments of the present invention are directed to isolated fragments of the *Streptococcus pneumoniae* genome. The fragments of the  
5 *Streptococcus pneumoniae* genome of the present invention include, but are not limited to fragments which encode peptides and polypeptides, hereinafter open reading frames (ORFs), fragments which modulate the expression of an operably linked ORF, hereinafter expression modulating fragments (EMFs) and fragments which can be used to diagnose the presence of *Streptococcus pneumoniae* in a  
10 sample, hereinafter diagnostic fragments (DFs).

As used herein, an "isolated nucleic acid molecule" or an "isolated fragment of the *Streptococcus pneumoniae* genome" refers to a nucleic acid molecule possessing a specific nucleotide sequence which has been subjected to purification means to reduce, from the composition, the number of compounds which are  
15 normally associated with the composition. Particularly, the term refers to the nucleic acid molecules having the sequences set out in SEQ ID NOS:1-391, to representative fragments thereof as described above, to polynucleotides at least 95%, preferably at least 99% and especially preferably at least 99.9% identical in sequence thereto, also as set out above.

20 A variety of purification means can be used to generate the isolated fragments of the present invention. These include, but are not limited to methods which separate constituents of a solution based on charge, solubility, or size.

In one embodiment, *Streptococcus pneumoniae* DNA can be enzymatically sheared to produce fragments of 15-20 kb in length. These fragments can then be  
25 used to generate a *Streptococcus pneumoniae* library by inserting them into lambda clones as described in the Examples below. Primers flanking, for example, an ORF, such as those enumerated in Tables 1-3 can then be generated using nucleotide sequence information provided in SEQ ID NOS:1-391. Well known and routine techniques of PCR cloning then can be used to isolate the ORF from  
30 the lambda DNA library or *Streptococcus pneumoniae* genomic DNA. Thus, given the availability of SEQ ID NOS:1-391, the information in Tables 1, 2 and 3, and the information that may be obtained readily by analysis of the sequences of SEQ ID NOS:1-391 using methods set out above, those of skill will be enabled by the present disclosure to isolate any ORF-containing or other nucleic acid fragment of  
35 the present invention.

The isolated nucleic acid molecules of the present invention include, but are not limited to single stranded and double stranded DNA, and single stranded RNA.

As used herein, an "open reading frame," ORF, means a series of triplets coding for amino acids without any termination codons and is a sequence translatable into protein.

Tables 1, 2, and 3 list ORFs in the *Streptococcus pneumoniae* genomic contigs of the present invention that were identified as putative coding regions by the GeneMark software using organism-specific second-order Markov probability transition matrices. It will be appreciated that other criteria can be used, in accordance with well known analytical methods, such as those discussed herein, to generate more inclusive, more restrictive, or more selective lists.

Table 1 sets out ORFs in the *Streptococcus pneumoniae* contigs of the present invention that over a continuous region of at least 50 bases are 95% or more identical (by BLAST analysis) to a nucleotide sequence available through GenBank in October, 1997.

Table 2 sets out ORFs in the *Streptococcus pneumoniae* contigs of the present invention that are not in Table 1 and match, with a BLASTP probability score of 0.01 or less, a polypeptide sequence available through GenBank in October, 1997.

Table 3 sets out ORFs in the *Streptococcus pneumoniae* contigs of the present invention that do not match significantly, by BLASTP analysis, a polypeptide sequence available through GenBank in October, 1997.

In each table, the first and second columns identify the ORF by, respectively, contig number and ORF number within the contig; the third column indicates the first nucleotide of the ORF (actually the first nucleotide of the stop codon immediately preceeding the ORF), counting from the 5' end of the contig strand; and the fourth column, "stop (nt)" indicates the last nucleotide of the stop codon defining the 3' end of the ORF.

In Tables 1 and 2, column five, lists the Reference for the closest matching sequence available through GenBank. These reference numbers are the databases entry numbers commonly used by those of skill in the art, who will be familiar with their denominators. Descriptions of the nomenclature are available from the National Center for Biotechnology Information. Column six in Tables 1 and 2 provides the gene name of the matching sequence; column seven provides the BLAST identity score and column eight the BLAST similarity score from the

comparison of the ORF and the homologous gene; and column nine indicates the length in nucleotides of the highest scoring segment pair identified by the BLAST identity analysis.

Each ORF described in the tables is defined by "start (nt)" (5') and "stop (nt)" (3') nucleotide position numbers. These position numbers refer to the boundaries of each ORF and provide orientation with respect to whether the forward or reverse strand is the coding strand and which reading frame the coding sequence is contained. The "start" position is the first nucleotide of the triplet encoding a stop codon just 5' to the ORF and the "stop" position is the last nucleotide of the triplet encoding the next in-frame stop codon (i.e., the stop codon at the 3' end of the ORF). Those of ordinary skill in the art appreciate that preferred fragments within each ORF described in the table include fragments of each ORF which include the entire sequence from the delineated "start" and "stop" positions excepting the first and last three nucleotides since these encode stop codons. Thus, polynucleotides set out as ORFs in the tables but lacking the three (3) 5' nucleotides and the three (3) 3' nucleotides are encompassed by the present invention. Those of skill also appreciate that particularly preferred are fragments within each ORF that are polynucleotide fragments comprising polypeptide coding sequence. As defined herein, "coding sequence" includes the fragment within an ORF beginning at the first in-frame ATG (triplet encoding methionine) and ending with the last nucleotide prior to the triplet encoding the 3' stop codon. Preferred are fragments comprising the entire coding sequence and fragments comprising the entire coding sequence, excepting the coding sequence for the N-terminal methionine. Those of skill appreciate that the N-terminal methionine is often removed during post-translational processing and that polynucleotides lacking the ATG can be used to facilitate production of N-terminal fusion proteins which may be beneficial in the production or use of genetically engineered proteins. Of course, due to the degeneracy of the genetic code many polynucleotides can encode a given polypeptide. Thus, the invention further includes polynucleotides comprising a nucleotide sequence encoding a polypeptide sequence itself encoded by the coding sequence within an ORF described in Tables 1-3 herein. Further, polynucleotides at least 95%, preferably at least 99% and especially preferably at least 99.9% identical in sequence to the foregoing polynucleotides, are contemplated by the present invention.

Polypeptides encoded by polynucleotides described above and elsewhere herein are also provided by the present invention as are polypeptide comprising a an amino acid sequence at least about 95%, preferably at least 97% and even more preferably 99% identical to the amino acid sequence of a polypeptide encoded by an ORF shown in Tables 1-3. These polypeptides may or may not comprise an N-terminal methionine.

The concepts of percent identity and percent similarity of two polypeptide sequences is well understood in the art. For example, two polypeptides 10 amino acids in length which differ at three amino acid positions (*e.g.*, at positions 1, 3 and 5) are said to have a percent identity of 70%. However, the same two polypeptides would be deemed to have a percent similarity of 80% if, for example at position 5, the amino acids moieties, although not identical, were "similar" (*i.e.*, possessed similar biochemical characteristics). Many programs for analysis of nucleotide or amino acid sequence similarity, such as *fasta* and *BLAST* specifically list percent identity of a matching region as an output parameter. Thus, for instance, Tables 1 and 2 herein enumerate the percent identity of the highest scoring segment pair in each ORF and its listed relative. Further details concerning the algorithms and criteria used for homology searches are provided below and are described in the pertinent literature highlighted by the citations provided below.

It will be appreciated that other criteria can be used to generate more inclusive and more exclusive listings of the types set out in the tables. As those of skill will appreciate, narrow and broad searches both are useful. Thus, a skilled artisan can readily identify ORFs in contigs of the *Streptococcus pneumoniae* genome other than those listed in Tables 1-3, such as ORFs which are overlapping or encoded by the opposite strand of an identified ORF in addition to those ascertainable using the computer-based systems of the present invention.

As used herein, an "expression modulating fragment," EMF, means a series of nucleotide molecules which modulates the expression of an operably linked ORF or EMF.



As used herein, a sequence is said to "modulate the expression of an operably linked sequence" when the expression of the sequence is altered by the presence of the EMF. EMFs include, but are not limited to, promoters, and promoter modulating sequences (inducible elements). One class of EMFs are  
5 fragments which induce the expression of an operably linked ORF in response to a specific regulatory factor or physiological event.

EMF sequences can be identified within the contigs of the *Streptococcus pneumoniae* genome by their proximity to the ORFs provided in Tables 1-3. An intergenic segment, or a fragment of the intergenic segment, from about 10 to 200  
10 nucleotides in length, taken from any one of the ORFs of Tables 1-3 will modulate the expression of an operably linked ORF in a fashion similar to that found with the naturally linked ORF sequence. As used herein, an "intergenic segment" refers to fragments of the *Streptococcus pneumoniae* genome which are between two ORF(s) herein described. EMFs also can be identified using known EMFs as a  
15 target sequence or target motif in the computer-based systems of the present invention. Further, the two methods can be combined and used together.

The presence and activity of an EMF can be confirmed using an EMF trap vector. An EMF trap vector contains a cloning site linked to a marker sequence. A marker sequence encodes an identifiable phenotype, such as antibiotic resistance or a complementing nutrition auxotrophic factor, which can be identified or assayed  
20 when the EMF trap vector is placed within an appropriate host under appropriate conditions. As described above, a EMF will modulate the expression of an operably linked marker sequence. A more detailed discussion of various marker sequences is provided below. A sequence which is suspected as being an EMF is  
25 cloned in all three reading frames in one or more restriction sites upstream from the marker sequence in the EMF trap vector. The vector is then transformed into an appropriate host using known procedures and the phenotype of the transformed host is examined under appropriate conditions. As described above, an EMF will modulate the expression of an operably linked marker sequence.

30 As used herein, a "diagnostic fragment," DF, means a series of nucleotide molecules which selectively hybridize to *Streptococcus pneumoniae* sequences. DFs can be readily identified by identifying unique sequences within contigs of the *Streptococcus pneumoniae* genome, such as by using well-known computer analysis software, and by generating and testing probes or amplification primers

consisting of the DF sequence in an appropriate diagnostic format which determines amplification or hybridization selectivity.

The sequences falling within the scope of the present invention are not limited to the specific sequences herein described, but also include allelic and species variations thereof. Allelic and species variations can be routinely determined by comparing the sequences provided in SEQ ID NOS:1-391, a representative fragment thereof, or a nucleotide sequence at least 95%, preferably at least 99% and most at least preferably 99.9% identical to SEQ ID NOS:1-391, with a sequence from another isolate of the same species. Furthermore, to accommodate codon variability, the invention includes nucleic acid molecules coding for the same amino acid sequences as do the specific ORFs disclosed herein. In other words, in the coding region of an ORF, substitution of one codon for another which encodes the same amino acid is expressly contemplated. Any specific sequence disclosed herein can be readily screened for errors by resequencing a particular fragment, such as an ORF, in both directions (*i.e.*, sequence both strands). Alternatively, error screening can be performed by sequencing corresponding polynucleotides of *Streptococcus pneumoniae* origin isolated by using part or all of the fragments in question as a probe or primer.

Preferred DFs of the present invention comprise at least about 17, preferably at least about 20, and more preferably at least about 50 contiguous nucleotides within an ORF set out in Tables 1-3. Most highly preferred DFs specifically hybridize to a polynucleotide containing the sequence of the ORF from which they are derived. Specific hybridization occurs even under stringent conditions defined elsewhere herein.

Each of the ORFs of the *Streptococcus pneumoniae* genome disclosed in Tables 1, 2 and 3, and the EMFs found 5' to the ORFs, can be used as polynucleotide reagents in numerous ways. For example, the sequences can be used as diagnostic probes or diagnostic amplification primers to detect the presence of a specific microbe in a sample, particularly *Streptococcus pneumoniae*. Especially preferred in this regard are ORFs such as those of Table 3, which do not match previously characterized sequences from other organisms and thus are most likely to be highly selective for *Streptococcus pneumoniae*. Also particularly preferred are ORFs that can be used to distinguish between strains of *Streptococcus pneumoniae*, particularly those that distinguish medically important strain, such as drug-resistant strains.

In addition, the fragments of the present invention, as broadly described, can be used to control gene expression through triple helix formation or antisense DNA or RNA, both of which methods are based on the binding of a polynucleotide sequence to DNA or RNA. Triple helix-formation optimally results in a shut-off of RNA transcription from DNA, while antisense RNA hybridization blocks translation of an mRNA molecule into polypeptide. Information from the sequences of the present invention can be used to design antisense and triple helix-forming oligonucleotides. Polynucleotides suitable for use in these methods are usually 20 to 40 bases in length and are designed to be complementary to a region of the gene involved in transcription, for triple-helix formation, or to the mRNA itself, for antisense inhibition. Both techniques have been demonstrated to be effective in model systems, and the requisite techniques are well known and involve routine procedures. Triple helix techniques are discussed in, for example, Lee *et al.*, *Nucl. Acids Res.* 6:3073 (1979); Cooney *et al.*, *Science* 241:456 (1988); and Dervan *et al.*, *Science* 251:1360 (1991). Antisense techniques in general are discussed in, for instance, Okano, *J. Neurochem.* 56:560 (1991) and *Oligodeoxynucleotides as Antisense Inhibitors of Gene Expression*, CRC Press, Boca Raton, FL (1988)).

The present invention further provides recombinant constructs comprising one or more fragments of the *Streptococcus pneumoniae* genomic fragments and contigs of the present invention. Certain preferred recombinant constructs of the present invention comprise a vector, such as a plasmid or viral vector, into which a fragment of the *Streptococcus pneumoniae* genome has been inserted, in a forward or reverse orientation. In the case of a vector comprising one of the ORFs of the present invention, the vector may further comprise regulatory sequences, including for example, a promoter, operably linked to the ORF. For vectors comprising the EMFs of the present invention, the vector may further comprise a marker sequence or heterologous ORF operably linked to the EMF.

Large numbers of suitable vectors and promoters are known to those of skill in the art and are commercially available for generating the recombinant constructs of the present invention. The following vectors are provided by way of example. Useful bacterial vectors include phagescript, PsiX174, pBluescript SK, pBS KS, pNH8a, pNH16a, pNH18a, pNH46a (available from Stratagene); pTrc99A, pKK223-3, pKK233-3, pDR540, pRIT5 (available from Pharmacia). Useful eukaryotic vectors include pWLneo, pSV2cat, pOG44, pXT1, pSG

(available from Stratagene) pSVK3, pBPV, pMSG, pSVL (available from Pharmacia).

Promoter regions can be selected from any desired gene using CAT (chloramphenicol transferase) vectors or other vectors with selectable markers.

- 5 Two appropriate vectors are pKK232-8 and pCM7. Particular named bacterial promoters include lacI, lacZ, T3, T7, gpt, lambda PR, and trc. Eukaryotic promoters include CMV immediate early, HSV thymidine kinase, early and late SV40, LTRs from retrovirus, and mouse metallothionein- I. Selection of the appropriate vector and promoter is well within the level of ordinary skill in the art.

- 10 The present invention further provides host cells containing any one of the isolated fragments of the *Streptococcus pneumoniae* genomic fragments and contigs of the present invention, wherein the fragment has been introduced into the host cell using known methods. The host cell can be a higher eukaryotic host cell, such as a mammalian cell, a lower eukaryotic host cell, such as a yeast cell, or  
15 a procaryotic cell, such as a bacterial cell.

- A polynucleotide of the present invention, such as a recombinant construct comprising an ORF of the present invention, may be introduced into the host by a variety of well established techniques that are standard in the art, such as calcium phosphate transfection, DEAE, dextran mediated transfection and electroporation,  
20 which are described in, for instance, Davis, L. *et al.*, BASIC METHODS IN MOLECULAR BIOLOGY (1986).

- A host cell containing one of the fragments of the *Streptococcus pneumoniae* genomic fragments and contigs of the present invention, can be used in conventional manners to produce the gene product encoded by the isolated  
25 fragment (in the case of an ORF) or can be used to produce a heterologous protein under the control of the EMF. The present invention further provides isolated polypeptides encoded by the nucleic acid fragments of the present invention or by degenerate variants of the nucleic acid fragments of the present invention. By "degenerate variant" is intended nucleotide fragments which differ  
30 from a nucleic acid fragment of the present invention (*e.g.*, an ORF) by nucleotide sequence but, due to the degeneracy of the Genetic Code, encode an identical polypeptide sequence.

Preferred nucleic acid fragments of the present invention are the ORFs and subfragments thereof depicted in Tables 2 and 3 which encode proteins.

A variety of methodologies known in the art can be utilized to obtain any one of the isolated polypeptides or proteins of the present invention. At the simplest level, the amino acid sequence can be synthesized using commercially available peptide synthesizers. This is particularly useful in producing small peptides and fragments of larger polypeptides. Such short fragments as may be obtained most readily by synthesis are useful, for example, in generating antibodies against the native polypeptide, as discussed further below.

In an alternative method, the polypeptide or protein is purified from bacterial cells which naturally produce the polypeptide or protein. One skilled in the art can readily employ well-known methods for isolating polypeptides and proteins to isolate and purify polypeptides or proteins of the present invention produced naturally by a bacterial strain, or by other methods. Methods for isolation and purification that can be employed in this regard include, but are not limited to, immunochromatography, HPLC, size-exclusion chromatography, ion-exchange chromatography, and immuno-affinity chromatography.

The polypeptides and proteins of the present invention also can be purified from cells which have been altered to express the desired polypeptide or protein. As used herein, a cell is said to be altered to express a desired polypeptide or protein when the cell, through genetic manipulation, is made to produce a polypeptide or protein which it normally does not produce or which the cell normally produces at a lower level. Those skilled in the art can readily adapt procedures for introducing and expressing either recombinant or synthetic sequences into eukaryotic or prokaryotic cells in order to generate a cell which produces one of the polypeptides or proteins of the present invention.

Any host/vector system can be used to express one or more of the ORFs of the present invention. These include, but are not limited to, eukaryotic hosts such as HeLa cells, CV-1 cell, COS cells, and Sf9 cells, as well as prokaryotic host such as *E. coli* and *B. subtilis*. The most preferred cells are those which do not normally express the particular polypeptide or protein or which expresses the polypeptide or protein at low natural level.

"Recombinant," as used herein, means that a polypeptide or protein is derived from recombinant (*e.g.*, microbial or mammalian) expression systems. "Microbial" refers to recombinant polypeptides or proteins made in bacterial or fungal (*e.g.*, yeast) expression systems. As a product, "recombinant microbial" defines a polypeptide or protein essentially free of native endogenous substances and unaccompanied by associated native glycosylation. Polypeptides or proteins expressed in most bacterial cultures, *e.g.*, *E. coli*, will be free of glycosylation modifications; polypeptides or proteins expressed in yeast will have a glycosylation pattern different from that expressed in mammalian cells.

"Nucleotide sequence" refers to a heteropolymer of deoxyribonucleotides. Generally, DNA segments encoding the polypeptides and proteins provided by this invention are assembled from fragments of the *Streptococcus pneumoniae* genome and short oligonucleotide linkers, or from a series of oligonucleotides, to provide a synthetic gene which is capable of being expressed in a recombinant transcriptional unit comprising regulatory elements derived from a microbial or viral operon.

Recombinant expression vehicle or vector" refers to a plasmid or phage or virus or vector, for expressing a polypeptide from a DNA (RNA) sequence. The expression vehicle can comprise a transcriptional unit comprising an assembly of (1) a genetic regulatory elements necessary for gene expression in the host, including elements required to initiate and maintain transcription at a level sufficient for suitable expression of the desired polypeptide, including, for example, promoters and, where necessary, an enhancer and a polyadenylation signal; (2) a structural or coding sequence which is transcribed into mRNA and translated into protein, and (3) appropriate signals to initiate translation at the beginning of the desired coding region and terminate translation at its end. Structural units intended for use in yeast or eukaryotic expression systems preferably include a leader sequence enabling extracellular secretion of translated protein by a host cell. Alternatively, where recombinant protein is expressed without a leader or transport sequence, it may include an N-terminal methionine residue. This residue may or may not be subsequently cleaved from the expressed recombinant protein to provide a final product.

"Recombinant expression system" means host cells which have stably integrated a recombinant transcriptional unit into chromosomal DNA or carry the recombinant transcriptional unit extra chromosomally. The cells can be prokaryotic or eukaryotic. Recombinant expression systems as defined herein will express

heterologous polypeptides or proteins upon induction of the regulatory elements linked to the DNA segment or synthetic gene to be expressed.

Mature proteins can be expressed in mammalian cells, yeast, bacteria, or other cells under the control of appropriate promoters. Cell-free translation systems can also be employed to produce such proteins using RNAs derived from the DNA constructs of the present invention. Appropriate cloning and expression vectors for use with prokaryotic and eukaryotic hosts are described in Sambrook *et al.*, *Molecular Cloning: A Laboratory Manual*, 2<sup>nd</sup> Edition, Cold Spring Harbor Laboratory Press, Cold Spring Harbor, New York (1989), the disclosure of which is hereby incorporated by reference in its entirety.

Generally, recombinant expression vectors will include origins of replication and selectable markers permitting transformation of the host cell, *e.g.*, the ampicillin resistance gene of *E. coli* and *S. cerevisiae* TRP1 gene, and a promoter derived from a highly expressed gene to direct transcription of a downstream structural sequence. Such promoters can be derived from operons encoding glycolytic enzymes such as 3- phosphoglycerate kinase (PGK), alpha-factor, acid phosphatase, or heat shock proteins, among others. The heterologous structural sequence is assembled in appropriate phase with translation initiation and termination sequences, and preferably, a leader sequence capable of directing secretion of translated protein into the periplasmic space or extracellular medium. Optionally, the heterologous sequence can encode a fusion protein including an N-terminal identification peptide imparting desired characteristics, *e.g.*, stabilization or simplified purification of expressed recombinant product.

Useful expression vectors for bacterial use are constructed by inserting a structural DNA sequence encoding a desired protein together with suitable translation initiation and termination signals in operable reading phase with a functional promoter. The vector will comprise one or more phenotypic selectable markers and an origin of replication to ensure maintenance of the vector and, when desirable, provide amplification within the host.

Suitable prokaryotic hosts for transformation include strains of *E. coli*, *B. subtilis*, *Salmonella typhimurium* and various species within the genera *Pseudomonas* and *Streptomyces*. Others may, also be employed as a matter of choice.

As a representative but non-limiting example, useful expression vectors for bacterial use can comprise a selectable marker and bacterial origin of replication

derived from commercially available plasmids comprising genetic elements of the well known cloning vector pBR322 (ATCC 37017). Such commercial vectors include, for example, pKK223-3 (available from Pharmacia Fine Chemicals, Uppsala, Sweden) and GEM 1 (available from Promega Biotec, Madison, WI, USA). These pBR322 "backbone" sections are combined with an appropriate promoter and the structural sequence to be expressed.

Following transformation of a suitable host strain and growth of the host strain to an appropriate cell density, the selected promoter, where it is inducible, is derepressed or induced by appropriate means (*e.g.*, temperature shift or chemical induction) and cells are cultured for an additional period to provide for expression of the induced gene product. Thereafter cells are typically harvested, generally by centrifugation, disrupted to release expressed protein, generally by physical or chemical means, and the resulting crude extract is retained for further purification.

Various mammalian cell culture systems can also be employed to express recombinant protein. Examples of mammalian expression systems include the COS-7 lines of monkey kidney fibroblasts, described in Gluzman, *Cell* 23:175 (1981), and other cell lines capable of expressing a compatible vector, for example, the C127, 3T3, CHO, HeLa and BHK cell lines.

Mammalian expression vectors will comprise an origin of replication, a suitable promoter and enhancer, and also any necessary ribosome binding sites, polyadenylation site, splice donor and acceptor sites, transcriptional termination sequences, and 5' flanking nontranscribed sequences. DNA sequences derived from the SV40 viral genome, for example, SV40 origin, early promoter, enhancer, splice, and polyadenylation sites may be used to provide the required nontranscribed genetic elements.

Recombinant polypeptides and proteins produced in bacterial culture is usually isolated by initial extraction from cell pellets, followed by one or more salting-out, aqueous ion exchange or size exclusion chromatography steps. Microbial cells employed in expression of proteins can be disrupted by any convenient method, including freeze-thaw cycling, sonication, mechanical disruption, or use of cell lysing agents. Protein refolding steps can be used, as necessary, in completing configuration of the mature protein. Finally, high performance liquid chromatography (HPLC) can be employed for final purification steps.



The present invention further includes isolated polypeptides, proteins and nucleic acid molecules which are substantially equivalent to those herein described. As used herein, substantially equivalent can refer both to nucleic acid and amino acid sequences, for example a mutant sequence, that varies from a reference sequence by one or more substitutions, deletions, or additions, the net effect of which does not result in an adverse functional dissimilarity between reference and subject sequences. For purposes of the present invention, sequences having equivalent biological activity, and equivalent expression characteristics are considered substantially equivalent. For purposes of determining equivalence, truncation of the mature sequence should be disregarded.

The invention further provides methods of obtaining homologs from other strains of *Streptococcus pneumoniae*, of the fragments of the *Streptococcus pneumoniae* genome of the present invention and homologs of the proteins encoded by the ORFs of the present invention. As used herein, a sequence or protein of *Streptococcus pneumoniae* is defined as a homolog of a fragment of the *Streptococcus pneumoniae* fragments or contigs or a protein encoded by one of the ORFs of the present invention, if it shares significant homology to one of the fragments of the *Streptococcus pneumoniae* genome of the present invention or a protein encoded by one of the ORFs of the present invention. Specifically, by using the sequence disclosed herein as a probe or as primers, and techniques such as PCR cloning and colony/plaque hybridization, one skilled in the art can obtain homologs.

As used herein, two nucleic acid molecules or proteins are said to "share significant homology" if the two contain regions which possess greater than 85% sequence (amino acid or nucleic acid) homology. Preferred homologs in this regard are those with more than 90% homology. Especially preferred are those with 93% or more homology. Among especially preferred homologs those with 95% or more homology are particularly preferred. Very particularly preferred among these are those with 97% and even more particularly preferred among those are homologs with 99% or more homology. The most preferred homologs among these are those with 99.9% homology or more. It will be understood that, among measures of homology, identity is particularly preferred in this regard.

Region specific primers or probes derived from the nucleotide sequence provided in SEQ ID NOS:1-391 or from a nucleotide sequence at least 95%, particularly at least 99%, especially at least 99.5% identical to a sequence of SEQ

ID NOS:1-391 can be used to prime DNA synthesis and PCR amplification, as well as to identify colonies containing cloned DNA encoding a homolog. Methods suitable to this aspect of the present invention are well known and have been described in great detail in many publications such as, for example, Innis *et al.*,  
5 *PCR Protocols*, Academic Press, San Diego, CA (1990)).

When using primers derived from SEQ ID NOS:1-391 or from a nucleotide sequence having an aforementioned identity to a sequence of SEQ ID NOS:1-391, one skilled in the art will recognize that by employing high stringency conditions (*e.g.*, annealing at 50-60°C in 6X SSPC and 50% formamide, and washing at 50-  
10 65°C in 0.5X SSPC) only sequences which are greater than 75% homologous to the primer will be amplified. By employing lower stringency conditions (*e.g.*, hybridizing at 35-37°C in 5X SSPC and 40-45% formamide, and washing at 42°C in 0.5X SSPC), sequences which are greater than 40-50% homologous to the primer will also be amplified.

15 When using DNA probes derived from SEQ ID NOS:1-391, or from a nucleotide sequence having an aforementioned identity to a sequence of SEQ ID NOS:1-391, for colony/plaque hybridization, one skilled in the art will recognize that by employing high stringency conditions (*e.g.*, hybridizing at 50- 65°C in 5X SSPC and 50% formamide, and washing at 50- 65°C in 0.5X SSPC), sequences  
20 having regions which are greater than 90% homologous to the probe can be obtained, and that by employing lower stringency conditions (*e.g.*, hybridizing at 35-37°C in 5X SSPC and 40-45% formamide, and washing at 42°C in 0.5X SSPC), sequences having regions which are greater than 35-45% homologous to the probe will be obtained.

25 Any organism can be used as the source for homologs of the present invention so long as the organism naturally expresses such a protein or contains genes encoding the same. The most preferred organism for isolating homologs are bacteria which are closely related to *Streptococcus pneumoniae*.

### 30 ILLUSTRATIVE USES OF COMPOSITIONS OF THE INVENTION

Each ORF provided in Tables 1 and 2 is identified with a function by homology to a known gene or polypeptide. As a result, one skilled in the art can use the polypeptides of the present invention for commercial, therapeutic and  
35 industrial purposes consistent with the type of putative identification of the

polypeptide. Such identifications permit one skilled in the art to use the *Streptococcus pneumoniae* ORFs in a manner similar to the known type of sequences for which the identification is made; for example, to ferment a particular sugar source or to produce a particular metabolite. A variety of reviews illustrative of this aspect of the invention are available, including the following reviews on the industrial use of enzymes, for example, BIOCHEMICAL ENGINEERING AND BIOTECHNOLOGY HANDBOOK, 2nd Ed., MacMillan Publications, Ltd. NY (1991) and BIOCATALYSTS IN ORGANIC SYNTHESSES, Tramper *et al.*, Eds., Elsevier Science Publishers, Amsterdam, The Netherlands (1985). A variety of exemplary uses that illustrate this and similar aspects of the present invention are discussed below.

### 1. Biosynthetic Enzymes

Open reading frames encoding proteins involved in mediating the catalytic reactions involved in intermediary and macromolecular metabolism, the biosynthesis of small molecules, cellular processes and other functions includes enzymes involved in the degradation of the intermediary products of metabolism, enzymes involved in central intermediary metabolism, enzymes involved in respiration, both aerobic and anaerobic, enzymes involved in fermentation, enzymes involved in ATP proton motor force conversion, enzymes involved in broad regulatory function, enzymes involved in amino acid synthesis, enzymes involved in nucleotide synthesis, enzymes involved in cofactor and vitamin synthesis, can be used for industrial biosynthesis.

The various metabolic pathways present in *Streptococcus pneumoniae* can be identified based on absolute nutritional requirements as well as by examining the various enzymes identified in Table 1-3 and SEQ ID NOS:1-391.

Of particular interest are polypeptides involved in the degradation of intermediary metabolites as well as non-macromolecular metabolism. Such enzymes include amylases, glucose oxidases, and catalase.

Proteolytic enzymes are another class of commercially important enzymes. Proteolytic enzymes find use in a number of industrial processes including the processing of flax and other vegetable fibers, in the extraction, clarification and depectinization of fruit juices, in the extraction of vegetables' oil and in the maceration of fruits and vegetables to give unicellular fruits. A detailed review of the proteolytic enzymes used in the food industry is provided in Rombouts *et al.*,

*Symbiosis* 21:79 (1986) and Voragen *et al.* in *Biocatalysts In Agricultural Biotechnology*, Whitaker *et al.*, Eds., *American Chemical Society Symposium Series* 389:93 (1989).

5 The metabolism of sugars is an important aspect of the primary metabolism of *Streptococcus pneumoniae*. Enzymes involved in the degradation of sugars, such as, particularly, glucose, galactose, fructose and xylose, can be used in industrial fermentation. Some of the important sugar transforming enzymes, from a commercial viewpoint, include sugar isomerases such as glucose isomerase. Other metabolic enzymes have found commercial use such as glucose oxidases  
10 which produces ketogulonic acid (KGA). KGA is an intermediate in the commercial production of ascorbic acid using the Reichstein's procedure, as described in Krueger *et al.*, *Biotechnology* 6(A), Rhine *et al.*, Eds., Verlag Press, Weinheim, Germany (1984).

15 Glucose oxidase (GOD) is commercially available and has been used in purified form as well as in an immobilized form for the deoxygenation of beer. See, for instance, Hartmeir *et al.*, *Biotechnology Letters* 1:21 (1979). The most important application of GOD is the industrial scale fermentation of gluconic acid. Market for gluconic acids which are used in the detergent, textile, leather, photographic, pharmaceutical, food, feed and concrete industry, as described, for  
20 example, in Bigelis *et al.*, beginning on page 357 in *GENE MANIPULATIONS AND FUNGI*; Benett *et al.*, Eds., Academic Press, New York (1985). In addition to industrial applications, GOD has found applications in medicine for quantitative determination of glucose in body fluids recently in biotechnology for analyzing syrups from starch and cellulose hydrosylates. This application is described in  
25 Owusu *et al.*, *Biochem. et Biophysica. Acta.* 872:83 (1986), for instance.

The main sweetener used in the world today is sugar which comes from sugar beets and sugar cane. In the field of industrial enzymes, the glucose isomerase process shows the largest expansion in the market today. Initially, soluble enzymes were used and later immobilized enzymes were developed  
30 (Krueger *et al.*, *Biotechnology, The Textbook of Industrial Microbiology*, Sinauer Associated Incorporated, Sunderland, Massachusetts (1990)). Today, the use of glucose- produced high fructose syrups is by far the largest industrial business using immobilized enzymes. A review of the industrial use of these enzymes is provided by Jorgensen, *Starch* 40:307 (1988).

Proteinases, such as alkaline serine proteinases, are used as detergent additives and thus represent one of the largest volumes of microbial enzymes used in the industrial sector. Because of their industrial importance, there is a large body of published and unpublished information regarding the use of these enzymes in industrial processes. (See Faultman *et al.*, *Acid Proteases Structure Function and Biology*, Tang, J., ed., Plenum Press, New York (1977) and Godfrey *et al.*, *Industrial Enzymes*, MacMillan Publishers, Surrey, UK (1983) and Hepner *et al.*, *Report Industrial Enzymes by 1990*, Hel Hepner & Associates, London (1986)).

Another class of commercially usable proteins of the present invention are the microbial lipases, described by, for instance, Macrae *et al.*, *Philosophical Transactions of the Chiral Society of London* 310:227 (1985) and Poserke, *Journal of the American Oil Chemist Society* 61:1758 (1984). A major use of lipases is in the fat and oil industry for the production of neutral glycerides using lipase catalyzed inter-esterification of readily available triglycerides. Application of lipases include the use as a detergent additive to facilitate the removal of fats from fabrics in the course of the washing procedures.

The use of enzymes, and in particular microbial enzymes, as catalyst for key steps in the synthesis of complex organic molecules is gaining popularity at a great rate. One area of great interest is the preparation of chiral intermediates. Preparation of chiral intermediates is of interest to a wide range of synthetic chemists particularly those scientists involved with the preparation of new pharmaceuticals, agrochemicals, fragrances and flavors. (See Davies *et al.*, *Recent Advances in the Generation of Chiral Intermediates Using Enzymes*, CRC Press, Boca Raton, Florida (1990)). The following reactions catalyzed by enzymes are of interest to organic chemists: hydrolysis of carboxylic acid esters, phosphate esters, amides and nitriles, esterification reactions, trans-esterification reactions, synthesis of amides, reduction of alkanones and oxoalkanates, oxidation of alcohols to carbonyl compounds, oxidation of sulfides to sulfoxides, and carbon bond forming reactions such as the aldol reaction.

When considering the use of an enzyme encoded by one of the ORFs of the present invention for biotransformation and organic synthesis it is sometimes necessary to consider the respective advantages and disadvantages of using a microorganism as opposed to an isolated enzyme. Pros and cons of using a whole cell system on the one hand or an isolated partially purified enzyme on the other

hand, has been described in detail by Bud *et al.*, Chemistry in Britain (1987), p. 127.

5 Amino transferases, enzymes involved in the biosynthesis and metabolism of amino acids, are useful in the catalytic production of amino acids. The advantages of using microbial based enzyme systems is that the amino transferase enzymes catalyze the stereo- selective synthesis of only L-amino acids and generally possess uniformly high catalytic rates. A description of the use of amino transferases for amino acid production is provided by Roselle-David, *Methods of Enzymology* 136:479 (1987).

10 Another category of useful proteins encoded by the ORFs of the present invention include enzymes involved in nucleic acid synthesis, repair, and recombination.

## 2. Generation of Antibodies

15 As described here, the proteins of the present invention, as well as homologs thereof, can be used in a variety of procedures and methods known in the art which are currently applied to other proteins. The proteins of the present invention can further be used to generate an antibody which selectively binds the protein. Such antibodies can be either monoclonal or polyclonal antibodies, as well  
20 fragments of these antibodies, and humanized forms.

The invention further provides antibodies which selectively bind to one of the proteins of the present invention and hybridomas which produce these antibodies. A hybridoma is an immortalized cell line which is capable of secreting a specific monoclonal antibody.

25 In general, techniques for preparing polyclonal and monoclonal antibodies as well as hybridomas capable of producing the desired antibody are well known in the art (Campbell, A. M., *Monoclonal Antibody Technology: Laboratory Techniques In Biochemistry And Molecular Biology*, Elsevier Science Publishers, Amsterdam, The Netherlands (1984); St. Groth *et al.*, *J. Immunol. Methods* 35: 1-21 (1980), Kohler and Milstein, *Nature* 256:495-497 (1975)), the trioma  
30 technique, the human B-cell hybridoma technique (Kozbor *et al.*, *Immunology Today* 4:72 (1983), pgs. 77-96 of Cole *et al.*, in *Monoclonal Antibodies And Cancer Therapy*, Alan R. Liss, Inc. (1985)). Any animal (mouse, rabbit, etc.) which is known to produce antibodies can be immunized with the pseudogene polypeptide. Methods for immunization are well known in the art. Such methods  
35

include subcutaneous or interperitoneal injection of the polypeptide. One skilled in the art will recognize that the amount of the protein encoded by the ORF of the present invention used for immunization will vary based on the animal which is immunized, the antigenicity of the peptide and the site of injection.

5       The protein which is used as an immunogen may be modified or administered in an adjuvant in order to increase the protein's antigenicity. Methods of increasing the antigenicity of a protein are well known in the art and include, but are not limited to coupling the antigen with a heterologous protein (such as globulin or galactosidase) or through the inclusion of an adjuvant during immunization.

10       For monoclonal antibodies, spleen cells from the immunized animals are removed, fused with myeloma cells, such as SP2/0-Ag14 myeloma cells, and allowed to become monoclonal antibody producing hybridoma cells.

      Any one of a number of methods well known in the art can be used to identify the hybridoma cell which produces an antibody with the desired characteristics. These include screening the hybridomas with an ELISA assay, western blot analysis, or radioimmunoassay (Lutz *et al.*, *Exp. Cell Res.* 175:109-124 (1988)).

      Hybridomas secreting the desired antibodies are cloned and the class and subclass is determined using procedures known in the art (Campbell, A. M., 20 *Monoclonal Antibody Technology: Laboratory Techniques in Biochemistry and Molecular Biology*, Elsevier Science Publishers, Amsterdam, The Netherlands (1984)).

      Techniques described for the production of single chain antibodies (U. S. Patent 4,946,778) can be adapted to produce single chain antibodies to proteins of 25 the present invention.

      For polyclonal antibodies, antibody containing antisera is isolated from the immunized animal and is screened for the presence of antibodies with the desired specificity using one of the above-described procedures.

      The present invention further provides the above-described antibodies in 30 detectably labelled form. Antibodies can be detectably labelled through the use of radioisotopes, affinity labels (such as biotin, avidin, *etc.*), enzymatic labels (such as horseradish peroxidase, alkaline phosphatase, *etc.*) fluorescent labels (such as FITC or rhodamine, *etc.*), paramagnetic atoms, *etc.* Procedures for accomplishing such labeling are well-known in the art, for example see Sternberger *et al.*, *J. Histochem. Cytochem.* 18:315 (1970); Bayer, E. A. *et al.*, *Meth. Enzym.* 62:308 35

(1979); Engval, E. *et al.*, *Immunol.* 109:129 (1972); Goding, J. W., *J. Immunol. Meth.* 13:215 (1976)).

The labeled antibodies of the present invention can be used for *in vitro*, *in vivo*, and in situ assays to identify cells or tissues in which a fragment of the  
5 *Streptococcus pneumoniae* genome is expressed.

The present invention further provides the above-described antibodies immobilized on a solid support. Examples of such solid supports include plastics such as polycarbonate, complex carbohydrates such as agarose and sepharose, acrylic resins and such as polyacrylamide and latex beads. Techniques for  
10 coupling antibodies to such solid supports are well known in the art (Weir, D. M. *et al.*, "Handbook of Experimental Immunology" 4th Ed., Blackwell Scientific Publications, Oxford, England, Chapter 10 (1986); Jacoby, W. D. *et al.*, *Meth. Enzym.* 34 Academic Press, N. Y. (1974)). The immobilized antibodies of the present invention can be used for *in vitro*, *in vivo*, and in situ assays as well as for  
15 immunoaffinity purification of the proteins of the present invention.

### 3. Diagnostic Assays and Kits

The present invention further provides methods to identify the expression of one of the ORFs of the present invention, or homolog thereof, in a test sample,  
20 using one of the DFs or antibodies of the present invention.

In detail, such methods comprise incubating a test sample with one or more of the antibodies or one or more of the DFs of the present invention and assaying for binding of the DFs or antibodies to components within the test sample.

Conditions for incubating a DF or antibody with a test sample vary.  
25 Incubation conditions depend on the format employed in the assay, the detection methods employed, and the type and nature of the DF or antibody used in the assay. One skilled in the art will recognize that any one of the commonly available hybridization, amplification or immunological assay formats can readily be adapted to employ the DFs or antibodies of the present invention. Examples of such assays  
30 can be found in Chard, T., *An Introduction to Radioimmunoassay and Related Techniques*, Elsevier Science Publishers, Amsterdam, The Netherlands (1986); Bullock, G. R. *et al.*, *Techniques in Immunocytochemistry*, Academic Press, Orlando, FL Vol. 1 (1982), Vol. 2 (1983), Vol. 3 (1985); Tijssen, P., *Practice and Theory of Enzyme Immunoassays: Laboratory Techniques in Biochemistry and*



*Molecular Biology*, Elsevier Science Publishers, Amsterdam, The Netherlands (1985).

5 The test samples of the present invention include cells, protein or membrane extracts of cells, or biological fluids such as sputum, blood, serum, plasma, or urine. The test sample used in the above-described method will vary based on the assay format, nature of the detection method and the tissues, cells or extracts used as the sample to be assayed. Methods for preparing protein extracts or membrane extracts of cells are well known in the art and can be readily be adapted in order to obtain a sample which is compatible with the system utilized.

10 In another embodiment of the present invention, kits are provided which contain the necessary reagents to carry out the assays of the present invention.

Specifically, the invention provides a compartmentalized kit to receive, in close confinement, one or more containers which comprises: (a) a first container comprising one of the DFs or antibodies of the present invention; and (b) one or more other containers comprising one or more of the following: wash reagents, reagents capable of detecting presence of a bound DF or antibody.

In detail, a compartmentalized kit includes any kit in which reagents are contained in separate containers. Such containers include small glass containers, plastic containers or strips of plastic or paper. Such containers allows one to efficiently transfer reagents from one compartment to another compartment such that the samples and reagents are not cross-contaminated, and the agents or solutions of each container can be added in a quantitative fashion from one compartment to another. Such containers will include a container which will accept the test sample, a container which contains the antibodies used in the assay, containers which contain wash reagents (such as phosphate buffered saline, Tris-buffers, *etc.*), and containers which contain the reagents used to detect the bound antibody or DF.

20 Types of detection reagents include labelled nucleic acid probes, labelled secondary antibodies, or in the alternative, if the primary antibody is labelled, the enzymatic, or antibody binding reagents which are capable of reacting with the labelled antibody. One skilled in the art will readily recognize that the disclosed DFs and antibodies of the present invention can be readily incorporated into one of the established kit formats which are well known in the art.

#### 35 4. Screening Assay for Binding Agents

Using the isolated proteins of the present invention, the present invention further provides methods of obtaining and identifying agents which bind to a protein encoded by one of the ORFs of the present invention or to one of the fragments and the *Streptococcus pneumoniae* fragment and contigs herein  
5 described.

In general, such methods comprise steps of:

- (a) contacting an agent with an isolated protein encoded by one of the ORFs of the present invention, or an isolated fragment of the *Streptococcus pneumoniae* genome; and
- 10 (b) determining whether the agent binds to said protein or said fragment.

The agents screened in the above assay can be, but are not limited to, peptides, carbohydrates, vitamin derivatives, or other pharmaceutical agents. The agents can be selected and screened at random or rationally selected or designed using protein modeling techniques.

15 For random screening, agents such as peptides, carbohydrates, pharmaceutical agents and the like are selected at random and are assayed for their ability to bind to the protein encoded by the ORF of the present invention.

Alternatively, agents may be rationally selected or designed. As used herein, an agent is said to be "rationally selected or designed" when the agent is  
20 chosen based on the configuration of the particular protein. For example, one skilled in the art can readily adapt currently available procedures to generate peptides, pharmaceutical agents and the like capable of binding to a specific peptide sequence in order to generate rationally designed antipeptide peptides, for example see Hurby *et al.*, "Application of Synthetic Peptides: Antisense Peptides," in  
25 *Synthetic Peptides, A User's Guide*, W. H. Freeman, NY (1992), pp. 289-307, and Kaspczak *et al.*, *Biochemistry* 28:9230-8 (1989), or pharmaceutical agents, or the like.

In addition to the foregoing, one class of agents of the present invention, as broadly described, can be used to control gene expression through binding to one  
30 of the ORFs or EMFs of the present invention. As described above, such agents can be randomly screened or rationally designed/selected. Targeting the ORF or EMF allows a skilled artisan to design sequence specific or element specific agents, modulating the expression of either a single ORF or multiple ORFs which rely on the same EMF for expression control.

One class of DNA binding agents are agents which contain base residues which hybridize or form a triple helix by binding to DNA or RNA. Such agents can be based on the classic phosphodiester, ribonucleic acid backbone, or can be a variety of sulfhydryl or polymeric derivatives which have base attachment capacity.

5 Agents suitable for use in these methods usually contain 20 to 40 bases and are designed to be complementary to a region of the gene involved in transcription (triple helix - see Lee *et al.*, *Nucl. Acids Res.* 6:3073 (1979); Cooney *et al.*, *Science* 241:456 (1988); and Dervan *et al.*, *Science* 251:1360 (1991)) or to the mRNA itself (antisense - Okano, *J. Neurochem.* 56:560 (1991);  
10 *Oligodeoxynucleotides as Antisense Inhibitors of Gene Expression*, CRC Press, Boca Raton, FL (1988)). Triple helix- formation optimally results in a shut-off of RNA transcription from DNA, while antisense RNA hybridization blocks translation of an mRNA molecule into polypeptide. Both techniques have been demonstrated to be effective in model systems. Information contained in the  
15 sequences of the present invention can be used to design antisense and triple helix-forming oligonucleotides, and other DNA binding agents.

### 5. Pharmaceutical Compositions and Vaccines

The present invention further provides pharmaceutical agents which can be  
20 used to modulate the growth or pathogenicity of *Streptococcus pneumoniae*, or another related organism, *in vivo* or *in vitro*. As used herein, a "pharmaceutical agent" is defined as a composition of matter which can be formulated using known techniques to provide a pharmaceutical compositions. As used herein, the "pharmaceutical agents of the present invention" refers the pharmaceutical agents  
25 which are derived from the proteins encoded by the ORFs of the present invention or are agents which are identified using the herein described assays.

As used herein, a pharmaceutical agent is said to "modulate the growth pathogenicity of *Streptococcus pneumoniae* or a related organism, *in vivo* or *in vitro*," when the agent reduces the rate of growth, rate of division, or viability of  
30 the organism in question. The pharmaceutical agents of the present invention can modulate the growth or pathogenicity of an organism in many fashions, although an understanding of the underlying mechanism of action is not needed to practice the use of the pharmaceutical agents of the present invention. Some agents will modulate the growth by binding to an important protein thus blocking the biological  
35 activity of the protein, while other agents may bind to a component of the outer

surface of the organism blocking attachment or rendering the organism more prone to act the bodies nature immune system. Alternatively, the agent may comprise a protein encoded by one of the ORFs of the present invention and serve as a vaccine. The development and use of a vaccine based on outer membrane components are well known in the art.

As used herein, a "related organism" is a broad term which refers to any organism whose growth can be modulated by one of the pharmaceutical agents of the present invention. In general, such an organism will contain a homolog of the protein which is the target of the pharmaceutical agent or the protein used as a vaccine. As such, related organisms do not need to be bacterial but may be fungal or viral pathogens.

The pharmaceutical agents and compositions of the present invention may be administered in a convenient manner, such as by the oral, topical, intravenous, intraperitoneal, intramuscular, subcutaneous, intranasal or intradermal routes. The pharmaceutical compositions are administered in an amount which is effective for treating and/or prophylaxis of the specific indication. In general, they are administered in an amount of at least about 1 mg/kg body weight and in most cases they will be administered in an amount not in excess of about 1 g/kg body weight per day. In most cases, the dosage is from about 0.1 mg/kg to about 10 g/kg body weight daily, taking into account the routes of administration, symptoms, *etc.*

The agents of the present invention can be used in native form or can be modified to form a chemical derivative. As used herein, a molecule is said to be a "chemical derivative" of another molecule when it contains additional chemical moieties not normally a part of the molecule. Such moieties may improve the molecule's solubility, absorption, biological half life, *etc.* The moieties may alternatively decrease the toxicity of the molecule, eliminate or attenuate any undesirable side effect of the molecule, *etc.* Moieties capable of mediating such effects are disclosed in, among other sources, REMINGTON'S PHARMACEUTICAL SCIENCES (1980) cited elsewhere herein.

For example, such moieties may change an immunological character of the functional derivative, such as affinity for a given antibody. Such changes in immunomodulation activity are measured by the appropriate assay, such as a competitive type immunoassay. Modifications of such protein properties as redox or thermal stability, biological half-life, hydrophobicity, susceptibility to proteolytic degradation or the tendency to aggregate with carriers or into multimers also may

be effected in this way and can be assayed by methods well known to the skilled artisan.

The therapeutic effects of the agents of the present invention may be obtained by providing the agent to a patient by any suitable means (*e.g.*, inhalation, intravenously, intramuscularly, subcutaneously, enterally, or parenterally). It is preferred to administer the agent of the present invention so as to achieve an effective concentration within the blood or tissue in which the growth of the organism is to be controlled. To achieve an effective blood concentration, the preferred method is to administer the agent by injection. The administration may be by continuous infusion, or by single or multiple injections.

In providing a patient with one of the agents of the present invention, the dosage of the administered agent will vary depending upon such factors as the patient's age, weight, height, sex, general medical condition, previous medical history, *etc.* In general, it is desirable to provide the recipient with a dosage of agent which is in the range of from about 1 pg/kg to 10 mg/kg (body weight of patient), although a lower or higher dosage may be administered. The therapeutically effective dose can be lowered by using combinations of the agents of the present invention or another agent.

As used herein, two or more compounds or agents are said to be administered "in combination" with each other when either (1) the physiological effects of each compound, or (2) the serum concentrations of each compound can be measured at the same time. The composition of the present invention can be administered concurrently with, prior to, or following the administration of the other agent.

The agents of the present invention are intended to be provided to recipient subjects in an amount sufficient to decrease the rate of growth (as defined above) of the target organism.

The administration of the agent(s) of the invention may be for either a "prophylactic" or "therapeutic" purpose. When provided prophylactically, the agent(s) are provided in advance of any symptoms indicative of the organisms growth. The prophylactic administration of the agent(s) serves to prevent, attenuate, or decrease the rate of onset of any subsequent infection. When provided therapeutically, the agent(s) are provided at (or shortly after) the onset of an indication of infection. The therapeutic administration of the compound(s)

serves to attenuate the pathological symptoms of the infection and to increase the rate of recovery.

The agents of the present invention are administered to a subject, such as a mammal, or a patient, in a pharmaceutically acceptable form and in a therapeutically effective concentration. A composition is said to be "pharmacologically acceptable" if its administration can be tolerated by a recipient patient. Such an agent is said to be administered in a "therapeutically effective amount" if the amount administered is physiologically significant. An agent is physiologically significant if its presence results in a detectable change in the physiology of a recipient patient.

The agents of the present invention can be formulated according to known methods to prepare pharmaceutically useful compositions, whereby these materials, or their functional derivatives, are combined in a mixture with a pharmaceutically acceptable carrier vehicle. Suitable vehicles and their formulation, inclusive of other human proteins, *e.g.*, human serum albumin, are described, for example, in REMINGTON'S PHARMACEUTICAL SCIENCES, 16<sup>th</sup> Ed., Osol, A., Ed., Mack Publishing, Easton PA (1980). In order to form a pharmaceutically acceptable composition suitable for effective administration, such compositions will contain an effective amount of one or more of the agents of the present invention, together with a suitable amount of carrier vehicle.

Additional pharmaceutical methods may be employed to control the duration of action. Control release preparations may be achieved through the use of polymers to complex or absorb one or more of the agents of the present invention. The controlled delivery may be effectuated by a variety of well known techniques, including formulation with macromolecules such as, for example, polyesters, polyamino acids, polyvinyl, pyrrolidone, ethylenevinylacetate, methylcellulose, carboxymethylcellulose, or protamine, sulfate, adjusting the concentration of the macromolecules and the agent in the formulation, and by appropriate use of methods of incorporation, which can be manipulated to effectuate a desired time course of release. Another possible method to control the duration of action by controlled release preparations is to incorporate agents of the present invention into particles of a polymeric material such as polyesters, polyamino acids, hydrogels, poly(lactic acid) or ethylene vinylacetate copolymers. Alternatively, instead of incorporating these agents into polymeric particles, it is possible to entrap these materials in microcapsules prepared, for example, by coacervation techniques or by interfacial polymerization with, for example, hydroxymethylcellulose or gelatine-

microcapsules and poly(methylmethacrylate) microcapsules, respectively, or in colloidal drug delivery systems, for example, liposomes, albumin microspheres, microemulsions, nanoparticles, and nanocapsules or in macroemulsions. Such techniques are disclosed in REMINGTON'S PHARMACEUTICAL SCIENCES  
5 (1980).

The invention further provides a pharmaceutical pack or kit comprising one or more containers filled with one or more of the ingredients of the pharmaceutical compositions of the invention. Associated with such container(s) can be a notice in the form prescribed by a governmental agency regulating the manufacture, use or  
10 sale of pharmaceuticals or biological products, which notice reflects approval by the agency of manufacture, use or sale for human administration.

In addition, the agents of the present invention may be employed in conjunction with other therapeutic compounds.

## 15 6. Shot-Gun Approach to Megabase DNA Sequencing

The present invention further demonstrates that a large sequence can be sequenced using a random shotgun approach. This procedure, described in detail in the examples that follow, has eliminated the up front cost of isolating and ordering overlapping or contiguous subclones prior to the start of the sequencing  
20 protocols.

Certain aspects of the present invention are described in greater detail in the examples that follow. The examples are provided by way of illustration. Other aspects and embodiments of the present invention are contemplated by the inventors, as will be clear to those of skill in the art from reading the present  
25 disclosure.

## ILLUSTRATIVE EXAMPLES

### LIBRARIES AND SEQUENCING

#### 30 1. Shotgun Sequencing Probability Analysis

The overall strategy for a shotgun approach to whole genome sequencing follows from the Lander and Waterman (Landerman and Waterman, *Genomics* 2:231 (1988)) application of the equation for the Poisson distribution. According to this treatment, the probability,  $P$ , that any given base in a sequence of size  $L$ , in  
35 nucleotides, is not sequenced after a certain amount,  $n$ , in nucleotides, of random  
0

sequence has been determined can be calculated by the equation  $P = e^{-m}$ , where  $m$  is  $L/n$ , the fold coverage. For instance, for a genome of 2.8 Mb,  $m=1$  when 2.8 Mb of sequence has been randomly generated (1X coverage). At that point,  $P = e^{-1} = 0.37$ . The probability that any given base has not been sequenced is the same as the probability that any region of the whole sequence  $L$  has not been determined and, therefore, is equivalent to the fraction of the whole sequence that has yet to be determined. Thus, at one-fold coverage, approximately 37% of a polynucleotide of size  $L$ , in nucleotides has not been sequenced. When 14 Mb of sequence has been generated, coverage is 5X for a 2.8 Mb and the unsequenced fraction drops to .0067 or 0.67%. 5X coverage of a 2.8 Mb sequence can be attained by sequencing approximately 17,000 random clones from both insert ends with an average sequence read length of 410 bp.

Similarly, the total gap length,  $G$ , is determined by the equation  $G = Le^{-m}$ , and the average gap size,  $g$ , follows the equation,  $g = L/n$ . Thus, 5X coverage leaves about 240 gaps averaging about 82 bp in size in a sequence of a polynucleotide 2.8 Mb long.

The treatment above is essentially that of Lander and Waterman, *Genomics* 2: 231 (1988).

## 2. Random Library Construction

In order to approximate the random model described above during actual sequencing, a nearly ideal library of cloned genomic fragments is required. The following library construction procedure was developed to achieve this end.

*Streptococcus pneumoniae* DNA is prepared by phenol extraction. A mixture containing 200 µg DNA in 1.0 ml of 300 mM sodium acetate, 10 mM Tris-HCl, 1 mM Na-EDTA, 50% glycerol is processed through a nebulizer (IPI Medical Products) with a stream of nitrogen adjusted to 35 Kpa for 2 minutes. The sonicated DNA is ethanol precipitated and redissolved in 500 µl TE buffer.

To create blunt-ends, a 100 µl aliquot of the resuspended DNA is digested with 5 units of BAL31 nuclease (New England BioLabs) for 10 min at 30°C in 200 µl BAL31 buffer. The digested DNA is phenol-extracted, ethanol-precipitated, redissolved in 100 µl TE buffer, and then size-fractionated by electrophoresis through a 1.0% low melting temperature agarose gel. The section containing DNA fragments 1.6-2.0 kb in size is excised from the gel, and the LGT agarose is melted and the resulting solution is extracted with phenol to separate the agarose from the



DNA. DNA is ethanol precipitated and redissolved in 20  $\mu$ l of TE buffer for ligation to vector.

5 A two-step ligation procedure is used to produce a plasmid library with 97% inserts, of which >99% were single inserts. The first ligation mixture (50  $\mu$ l) contains 2  $\mu$ g of DNA fragments, 2  $\mu$ g pUC18 DNA (Pharmacia) cut with SmaI and dephosphorylated with bacterial alkaline phosphatase, and 10 units of T4 ligase (GIBCO/BRL) and is incubated at 14°C for 4 hr. The ligation mixture then is phenol extracted and ethanol precipitated, and the precipitated DNA is dissolved in 20  $\mu$ l TE buffer and electrophoresed on a 1.0% low melting agarose gel. Discrete  
10 bands in a ladder are visualized by ethidium bromide-staining and UV illumination and identified by size as insert (I), vector (v), v+I, v+2i, v+3i, etc. The portion of the gel containing v+I DNA is excised and the v+I DNA is recovered and resuspended into 20  $\mu$ l TE. The v+I DNA then is blunt-ended by T4 polymerase treatment for 5 min. at 37°C in a reaction mixture (50  $\mu$ l) containing the v+I linears,  
15 500  $\mu$ M each of the 4 dNTPs, and 9 units of T4 polymerase (New England BioLabs), under recommended buffer conditions. After phenol extraction and ethanol precipitation the repaired v+I linears are dissolved in 20  $\mu$ l TE. The final ligation to produce circles is carried out in a 50  $\mu$ l reaction containing 5  $\mu$ l of v+I linears and 5 units of T4 ligase at 14°C overnight. After 10 min. at 70°C the  
20 following day, the reaction mixture is stored at -20°C.

This two-stage procedure results in a molecularly random collection of single-insert plasmid recombinants with minimal contamination from double-insert chimeras (<1%) or free vector (<3%).

25 Since deviation from randomness can arise from propagation the DNA in the host, *E. coli* host cells deficient in all recombination and restriction functions (A. Greener, *Strategies* 3 (1):5 (1990)) are used to prevent rearrangements, deletions, and loss of clones by restriction. Furthermore, transformed cells are plated directly on antibiotic diffusion plates to avoid the usual broth recovery phase which allows multiplication and selection of the most rapidly growing cells.

30 Plating is carried out as follows. A 100  $\mu$ l aliquot of Epicurian Coli SURE II Supercompetent Cells (Stratagene 200152) is thawed on ice and transferred to a chilled Falcon 2059 tube on ice. A 1.7  $\mu$ l aliquot of 1.42 M beta-mercaptoethanol is added to the aliquot of cells to a final concentration of 25 mM. Cells are incubated on ice for 10 min. A 1  $\mu$ l aliquot of the final ligation is added to the cells  
35 and incubated on ice for 30 min. The cells are heat pulsed for 30 sec. at 42°C and

placed back on ice for 2 min. The outgrowth period in liquid culture is eliminated from this protocol in order to minimize the preferential growth of any given transformed cell. Instead the transformation mixture is plated directly on a nutrient rich SOB plate containing a 5 ml bottom layer of SOB agar (5% SOB agar: 20 g tryptone, 5 g yeast extract, 0.5 g NaCl, 1.5% Difco Agar per liter of media). The 5 ml bottom layer is supplemented with 0.4 ml of 50 mg/ml ampicillin per 100 ml SOB agar. The 15 ml top layer of SOB agar is supplemented with 1 ml X-Gal (2%), 1 ml MgCl<sub>2</sub> (1 M), and 1 ml MgSO<sub>4</sub> /100 ml SOB agar. The 15 ml top layer is poured just prior to plating. Our titer is approximately 100 colonies/10  $\mu$ l aliquot of transformation.<sup>2</sup>

All colonies are picked for template preparation regardless of size. Thus, only clones lost due to "poison" DNA or deleterious gene products are deleted from the library, resulting in a slight increase in gap number over that expected.

### 3. Random DNA Sequencing

High quality double stranded DNA plasmid templates are prepared using a "boiling bead" method developed in collaboration with Advanced Genetic Technology Corp. (Gaithersburg, MD) (Adams *et al.*, *Science* 252:1651 (1991); Adams *et al.*, *Nature* 355:632 (1992)). Plasmid preparation is performed in a 96-well format for all stages of DNA preparation from bacterial growth through final DNA purification. Template concentration is determined using Hoechst Dye and a Millipore Cytofluor. DNA concentrations are not adjusted, but low-yielding templates are identified where possible and not sequenced.

Templates are also prepared from two *Streptococcus pneumoniae* lambda genomic libraries. An amplified library is constructed in the vector Lambda GEM-12 (Promega) and an unamplified library is constructed in Lambda DASH II (Stratagene). In particular, for the unamplified lambda library, *Streptococcus pneumoniae* DNA (> 100 kb) is partially digested in a reaction mixture (200  $\mu$ l) containing 50  $\mu$ g DNA, 1X Sau3AI buffer, 20 units Sau3AI for 6 min. at 23°C. The digested DNA was phenol-extracted and electrophoresed on a 0.5% low melting agarose gel at 2V/cm for 7 hours. Fragments from 15 to 25 kb are excised and recovered in a final volume of 6  $\mu$ l. One  $\mu$ l of fragments is used with 1  $\mu$ l of DASHII vector (Stratagene) in the recommended ligation reaction. One  $\mu$ l of the ligation mixture is used per packaging reaction following the recommended protocol with the Gigapack II XL Packaging Extract (Stratagene, #227711). Phage

are plated directly without amplification from the packaging mixture (after dilution with 500  $\mu$ l of recommended SM buffer and chloroform treatment). Yield is about  $2.5 \times 10^3$  pfu/ $\mu$ l. The amplified library is prepared essentially as above except the lambda GEM-12 vector is used. After packaging, about  $3.5 \times 10^4$  pfu are plated on the restrictive NM539 host. The lysate is harvested in 2 ml of SM buffer and stored frozen in 7% dimethylsulfoxide. The phage titer is approximately  $1 \times 10^9$  pfu/ml.

Liquid lysates (100  $\mu$ l) are prepared from randomly selected plaques (from the unamplified library) and template is prepared by long-range PCR using T7 and T3 vector-specific primers.

Sequencing reactions are carried out on plasmid and/or PCR templates using the AB Catalyst LabStation with Applied Biosystems PRISM Ready Reaction Dye Primer Cycle Sequencing Kits for the M13 forward (M13-21) and the M13 reverse (M13RP1) primers (Adams *et al.*, *Nature* 368:474 (1994)). Dye terminator sequencing reactions are carried out on the lambda templates on a Perkin-Elmer 9600 Thermocycler using the Applied Biosystems Ready Reaction Dye Terminator Cycle Sequencing kits. T7 and SP6 primers are used to sequence the ends of the inserts from the Lambda GEM-12 library and T7 and T3 primers are used to sequence the ends of the inserts from the Lambda DASH II library. Sequencing reactions are performed by eight individuals using an average of fourteen AB 373 DNA Sequencers per day. All sequencing reactions are analyzed using the Stretch modification of the AB 373, primarily using a 34 cm well-to-read distance. The overall sequencing success rate very approximately is about 85% for M13-21 and M13RP1 sequences and 65% for dye-terminator reactions. The average usable read length is 485 bp for M13-21 sequences, 445bp for M13RP1 sequences, and 375 bp for dye-terminator reactions.

Richards *et al.*, Chapter 28 in AUTOMATED DNA SEQUENCING AND ANALYSIS, M. D. Adams, C. Fields, J. C. Venter, Eds., Academic Press, London, (1994) described the value of using sequence from both ends of sequencing templates to facilitate ordering of contigs in shotgun assembly projects of lambda and cosmid clones. We balance the desirability of both-end sequencing (including the reduced cost of lower total number of templates) against shorter read-lengths for sequencing reactions performed with the M13RP1 (reverse) primer compared to the M13-21 (forward) primer. Approximately one-half of the templates are sequenced from both ends. Random reverse sequencing reactions are

done based on successful forward sequencing reactions. Some M13RP1 sequences are obtained in a semi-directed fashion: M13-21: sequences pointing outward at the ends of contigs are chosen for M13RP1 sequencing in an effort to specifically order contigs.

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#### 4. Protocol for Automated Cycle Sequencing

The sequencing is carried out using ABI Catalyst robots and AB 373 Automated DNA Sequencers. The Catalyst robot is a publicly available sophisticated pipetting and temperature control robot which has been developed specifically for DNA sequencing reactions. The Catalyst combines pre-aliquoted templates and reaction mixes consisting of deoxy- and dideoxynucleotides, the thermostable Taq DNA polymerase, fluorescently-labelled sequencing primers, and reaction buffer. Reaction mixes and templates are combined in the wells of an aluminum 96-well thermocycling plate. Thirty consecutive cycles of linear amplification (*i.e.*, one primer synthesis) steps are performed including denaturation, annealing of primer and template, and extension; *i.e.*, DNA synthesis. A heated lid with rubber gaskets on the thermocycling plate prevents evaporation without the need for an oil overlay.

Two sequencing protocols are used: one for dye-labelled primers and a second for dye-labelled dideoxy chain terminators. The shotgun sequencing involves use of four dye-labelled sequencing primers, one for each of the four terminator nucleotide. Each dye-primer is labelled with a different fluorescent dye, permitting the four individual reactions to be combined into one lane of the 373 DNA Sequencer for electrophoresis, detection, and base-calling. ABI currently supplies pre-mixed reaction mixes in bulk packages containing all the necessary non-template reagents for sequencing. Sequencing can be done with both plasmid and PCR- generated templates with both dye-primers and dye- terminators with approximately equal fidelity, although plasmid templates generally give longer usable sequences.

Thirty-two reactions are loaded per AB373 Sequencer each day, for a total of 960 samples. Electrophoresis is run overnight following the manufacturer's protocols, and the data is collected for twelve hours. Following electrophoresis and fluorescence detection, the ABI 373 performs automatic lane tracking and base-calling. The lane-tracking is confirmed visually. Each sequence electropherogram (or fluorescence lane trace) is inspected visually and assessed for quality. Trailing

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sequences of low quality are removed and the sequence itself is loaded via software to a Sybase database (archived daily to 8mm tape). Leading vector polylinker sequence is removed automatically by a software program. Average edited lengths of sequences from the standard ABI 373 are around 400 bp and depend mostly on the quality of the template used for the sequencing reaction. ABI 373 Sequencers converted to Stretch Liners provide a longer electrophoresis path prior to fluorescence detection and increase the average number of usable bases to 500-600 bp.

## 10        **INFORMATICS**

### **1. Data Management**

A number of information management systems for a large-scale sequencing lab have been developed. (For review see, for instance, Kerlavage *et al.*, *Proceedings of the Twenty-Sixth Annual Hawaii International Conference on System Sciences*, IEEE Computer Society Press, Washington D. C., 585 (1993)) The system used to collect and assemble the sequence data was developed using the Sybase relational database management system and was designed to automate data flow wherever possible and to reduce user error. The database stores and correlates all information collected during the entire operation from template preparation to final analysis of the genome. Because the raw output of the ABI 373 Sequencers was based on a Macintosh platform and the data management system chosen was based on a Unix platform, it was necessary to design and implement a variety of multi-user, client-server applications which allow the raw data as well as analysis results to flow seamlessly into the database with a minimum of user effort.

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### **2. Assembly**

An assembly engine (TIGR Assembler) developed for the rapid and accurate assembly of thousands of sequence fragments was employed to generate contigs. The TIGR assembler simultaneously clusters and assembles fragments of the genome. In order to obtain the speed necessary to assemble more than  $10^4$  fragments, the algorithm builds a hash table of 12 bp oligonucleotide subsequences to generate a list of potential sequence fragment overlaps. The number of potential overlaps for each fragment determines which fragments are likely to fall into repetitive elements. Beginning with a single seed sequence fragment, TIGR Assembler extends the current contig by attempting to add the best matching

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fragment based on oligonucleotide content. The contig and candidate fragment are aligned using a modified version of the Smith-Waterman algorithm which provides for optimal gapped alignments (Waterman, M. S., *Methods in Enzymology* 164:765 (1988)). The contig is extended by the fragment only if strict criteria for the quality of the match are met. The match criteria include the minimum length of overlap, the maximum length of an unmatched end, and the minimum percentage match. These criteria are automatically lowered by the algorithm in regions of minimal coverage and raised in regions with a possible repetitive element. The number of potential overlaps for each fragment determines which fragments are likely to fall into repetitive elements. Fragments representing the boundaries of repetitive elements and potentially chimeric fragments are often rejected based on partial mismatches at the ends of alignments and excluded from the current contig. TIGR Assembler is designed to take advantage of clone size information coupled with sequencing from both ends of each template. It enforces the constraint that sequence fragments from two ends of the same template point toward one another in the contig and are located within a certain range of base pairs (definable for each clone based on the known clone size range for a given library).

The process resulted in 391 contigs as represented by SEQ ID NOs:1-391.

### 3. Identifying Genes

The predicted coding regions of the *Streptococcus pneumoniae* genome were initially defined with the program GeneMark, which finds ORFs using a probabilistic classification technique. The predicted coding region sequences were used in searches against a database of all nucleotide sequences from GenBank (October, 1997), using the BLASTN search method to identify overlaps of 50 or more nucleotides with at least a 95% identity. Those ORFs with nucleotide sequence matches are shown in Table 1. The ORFs without such matches were translated to protein sequences and compared to a non-redundant database of known proteins generated by combining the Swiss-prot, PIR and GenPept databases. ORFs that matched a database protein with BLASTP probability less than or equal to 0.01 are shown in Table 2. The table also lists assigned functions based on the closest match in the databases. ORFs that did not match protein or nucleotide sequences in the databases at these levels are shown in Table 3.

## ILLUSTRATIVE APPLICATIONS

### 1. Production of an Antibody to a *Streptococcus pneumoniae* Protein

Substantially pure protein or polypeptide is isolated from the transfected or transformed cells using any one of the methods known in the art. The protein can also be produced in a recombinant prokaryotic expression system, such as *E. coli*, or can be chemically synthesized. Concentration of protein in the final preparation is adjusted, for example, by concentration on an Amicon filter device, to the level of a few micrograms/ml. Monoclonal or polyclonal antibody to the protein can then be prepared as follows.

### 2. Monoclonal Antibody Production by Hybridoma Fusion

Monoclonal antibody to epitopes of any of the peptides identified and isolated as described can be prepared from murine hybridomas according to the classical method of Kohler, G. and Milstein, C., *Nature* 256:495 (1975) or modifications of the methods thereof. Briefly, a mouse is repetitively inoculated with a few micrograms of the selected protein over a period of a few weeks. The mouse is then sacrificed, and the antibody producing cells of the spleen isolated. The spleen cells are fused by means of polyethylene glycol with mouse myeloma cells, and the excess unfused cells destroyed by growth of the system on selective media comprising aminopterin (HAT media). The successfully fused cells are diluted and aliquots of the dilution placed in wells of a microtiter plate where growth of the culture is continued. Antibody-producing clones are identified by detection of antibody in the supernatant fluid of the wells by immunoassay procedures, such as ELISA, as originally described by Engvall, E., *Meth. Enzymol.* 70:419 (1980), and modified methods thereof. Selected positive clones can be expanded and their monoclonal antibody product harvested for use. Detailed procedures for monoclonal antibody production are described in Davis, L. *et al.*, *Basic Methods in Molecular Biology*, Elsevier, New York. Section 21-2 (1989).

### 3. Polyclonal Antibody Production by Immunization

Polyclonal antiserum containing antibodies to heterogenous epitopes of a single protein can be prepared by immunizing suitable animals with the expressed protein described above, which can be unmodified or modified to enhance immunogenicity. Effective polyclonal antibody production is affected by many factors related both to the antigen and the host species. For example, small molecules tend to be less immunogenic than others and may require the use of carriers and adjuvant. Also, host animals vary in response to site of inoculations and dose, with both inadequate or excessive doses of antigen resulting in low titer antisera. Small doses (ng level) of antigen administered at multiple intradermal sites appears to be most reliable. An effective immunization protocol for rabbits can be found in Vaitukaitis, J. *et al.*, *J. Clin. Endocrinol. Metab.* 33:988-991 (1971).

Booster injections can be given at regular intervals, and antiserum harvested when antibody titer thereof, as determined semi-quantitatively, for example, by double immunodiffusion in agar against known concentrations of the antigen, begins to fall. See, for example, Ouchterlony, O. *et al.*, Chap. 19 in: *Handbook of Experimental Immunology*, Wier, D., ed, Blackwell (1973). Plateau concentration of antibody is usually in the range of 0.1 to 0.2 mg/ml of serum (about 12M). Affinity of the antisera for the antigen is determined by preparing competitive binding curves, as described, for example, by Fisher, D., Chap. 42 in: *Manual of Clinical Immunology*, second edition, Rose and Friedman, eds., Amer. Soc. For Microbiology, Washington, D. C. (1980)

Antibody preparations prepared according to either protocol are useful in quantitative immunoassays which determine concentrations of antigen-bearing substances in biological samples; they are also used semi- quantitatively or qualitatively to identify the presence of antigen in a biological sample. In addition, antibodies are useful in various animal models of pneumococcal disease as a means of evaluating the protein used to make the antibody as a potential vaccine target or as a means of evaluating the antibody as a potential immunotherapeutic or immunoprophylactic reagent.



#### 4. Preparation of PCR Primers and Amplification of DNA

Various fragments of the *Streptococcus pneumoniae* genome, such as those of Tables 1-3 and SEQ ID NOS:1-391 can be used, in accordance with the present invention, to prepare PCR primers for a variety of uses. The PCR primers are preferably at least 15 bases, and more preferably at least 18 bases in length. When selecting a primer sequence, it is preferred that the primer pairs have approximately the same G/C ratio, so that melting temperatures are approximately the same. The PCR primers and amplified DNA of this Example find use in the Examples that follow.

#### 5. Gene expression from DNA Sequences Corresponding to ORFs

A fragment of the *Streptococcus pneumoniae* genome provided in Tables 1-3 is introduced into an expression vector using conventional technology. Techniques to transfer cloned sequences into expression vectors that direct protein translation in mammalian, yeast, insect or bacterial expression systems are well known in the art. Commercially available vectors and expression systems are available from a variety of suppliers including Stratagene (La Jolla, California), Promega (Madison, Wisconsin), and Invitrogen (San Diego, California). If desired, to enhance expression and facilitate proper protein folding, the codon context and codon pairing of the sequence may be optimized for the particular expression organism, as explained by Hatfield *et al.*, U. S. Patent No. 5,082,767, incorporated herein by this reference.

The following is provided as one exemplary method to generate polypeptide(s) from cloned ORFs of the *Streptococcus pneumoniae* genome fragment. Bacterial ORFs generally lack a poly A addition signal. The addition signal sequence can be added to the construct by, for example, splicing out the poly A addition sequence from pSG5 (Stratagene) using BglI and SalI restriction endonuclease enzymes and incorporating it into the mammalian expression vector pXT1 (Stratagene) for use in eukaryotic expression systems. pXT1 contains the LTRs and a portion of the gag gene of Moloney Murine Leukemia Virus. The positions of the LTRs in the construct allow efficient stable transfection. The vector includes the Herpes Simplex thymidine kinase promoter and the selectable neomycin gene. The *Streptococcus pneumoniae* DNA is obtained by PCR from the bacterial vector using oligonucleotide primers complementary to the *Streptococcus pneumoniae* DNA and containing restriction endonuclease sequences for PstI incorporated into the 5' primer and BglII at the 5' end of the corresponding *Streptococcus pneumoniae* DNA 3' primer, taking care to ensure that the *Streptococcus pneumoniae* DNA is positioned such that its followed with the poly A addition sequence. The purified fragment obtained from the resulting PCR reaction is digested with PstI, blunt ended with an exonuclease, digested with BglII, purified and ligated to pXT1, now containing a poly A addition sequence and digested BglII.

The ligated product is transfected into mouse NIH 3T3 cells using Lipofectin (Life Technologies, Inc., Grand Island, New York) under conditions outlined in the product specification. Positive transfectants are selected after growing the transfected cells in 600 ug/ml G418 (Sigma, St. Louis, Missouri). The protein is preferably released into the supernatant. However if the protein has membrane binding domains, the protein may additionally be retained within the cell or expression may be restricted to the cell surface. Since it may be necessary to purify and locate the transfected product, synthetic 15-mer peptides synthesized from the predicted *Streptococcus pneumoniae* DNA sequence are injected into mice to generate antibody to the polypeptide encoded by the *Streptococcus pneumoniae* DNA.

Alternatively and if antibody production is not possible, the *Streptococcus pneumoniae* DNA sequence is additionally incorporated into eukaryotic expression vectors and expressed as, for example, a globin fusion. Antibody to the globin moiety then is used to purify the chimeric protein. Corresponding protease cleavage sites are engineered between the globin moiety and the polypeptide encoded by the *Streptococcus pneumoniae* DNA so that the latter may be freed from the formed by simple protease digestion. One useful expression vector for generating globin chimerics is pSG5 (Stratagene). This vector encodes a rabbit globin. Intron II of the rabbit globin gene facilitates splicing of the expressed transcript, and the polyadenylation signal incorporated into the construct increases the level of expression. These techniques are well known to those skilled in the art of molecular biology. Standard methods are published in methods texts such as Davis *et al.*, cited elsewhere herein, and many of the methods are available from the technical assistance representatives from Stratagene, Life Technologies, Inc., or Promega. Polypeptides of the invention also may be produced using *in vitro* translation systems such as *in vitro* Express<sup>TM</sup> Translation Kit (Stratagene).

While the present invention has been described in some detail for purposes of clarity and understanding, one skilled in the art will appreciate that various changes in form and detail can be made without departing from the true scope of the invention.

All patents, patent applications and publications referred to above are hereby incorporated by reference.

TABLE 1

S. pneumoniae - Coding regions containing known sequences

Contig ID	ORF ID	Start (nt)	Stop (nt)	match accession	match gene name	percent ident	HSP nt length	ORF nt length
1	1	437	1003	gb U41735	Streptococcus pneumoniae peptide methionine sulfoxide reductase (msrA) and homoserine kinase homolog (thrB) genes, complete cds	92	200	567
2	5	6169	5720	gb U40407	Streptococcus pneumoniae SZ2 dextran glucosidase gene and insertion sequence IS1202 transposase gene, complete cds	96	450	450
2	6	6592	6167	emb 283335 SP28	S.pneumoniae dexB, capl(A,B,C,D,E,F,G,H,I,J,K) genes, dTDP-rhamnose biosynthesis genes and aliA gene	98	426	426
3	11	9770	9147	emb 283335 SP28	S.pneumoniae dexB, capl(A,B,C,D,E,F,G,H,I,J,K) genes, dTDP-rhamnose biosynthesis genes and aliA gene	94	624	624
3	12	10489	9671	emb 283335 SP28	S.pneumoniae dexB, capl(A,B,C,D,E,F,G,H,I,J,K) genes, dTDP-rhamnose biosynthesis genes and aliA gene	91	819	819
3	13	11546	12019	gb U43526	Streptococcus pneumoniae neuraminidase B (nanB) gene, complete cds, and neuraminidase (nanA) gene, partial cds	99	474	474
3	14	12017	13375	gb U43526	Streptococcus pneumoniae neuraminidase B (nanB) gene, complete cds, and neuraminidase (nanA) gene, partial cds	99	1359	1359
3	15	13421	14338	gb U43526	Streptococcus pneumoniae neuraminidase B (nanB) gene, complete cds, and neuraminidase (nanA) gene, partial cds	99	918	918
3	16	14329	15171	gb U43526	Streptococcus pneumoniae neuraminidase B (nanB) gene, complete cds, and neuraminidase (nanA) gene, partial cds	99	843	843
3	17	15132	17282	gb U43526	Streptococcus pneumoniae neuraminidase B (nanB) gene, complete cds, and neuraminidase (nanA) gene, partial cds	99	2151	2151
3	18	17267	18397	gb U43526	Streptococcus pneumoniae neuraminidase B (nanB) gene, complete cds, and neuraminidase (nanA) gene, partial cds	99	1069	1131
4	1	46	1188	emb V11463 SPDN	Streptococcus pneumoniae dnaC, rpoD, cpoA genes and ORF3 and ORF5	99	1143	1143
4	2	1198	2529	emb V11463 SPDN	Streptococcus pneumoniae dnaC, rpoD, cpoA genes and ORF3 and ORF5	99	876	1332
5	7	11297	11473	gb U41735	Streptococcus pneumoniae peptide methionine sulfoxide reductase (msrA) and homoserine kinase homolog (thrB) genes, complete cds	82	175	177
6	7	7125	7364	emb Z77726 SPIS	S.pneumoniae DNA for insertion sequence IS1318 (1372 bp)	93	238	240
6	8	7322	7570	emb Z77725 SPIS	S.pneumoniae DNA for insertion sequence IS1381 (966 bp)	95	160	249
6	9	7533	7985	emb Z77725 SPIS	S.pneumoniae DNA for insertion sequence IS1381 (966 bp)	99	453	453
6	23	20197	19733	emb 283335 SP28	S.pneumoniae dexB, capl(A,B,C,D,E,F,G,H,I,J,K) genes, dTDP-rhamnose biosynthesis genes and aliA gene	96	465	465
7	10	8305	7682	emb 283335 SP28	S.pneumoniae dexB, capl(A,B,C,D,E,F,G,H,I,J,K) genes, dTDP-rhamnose biosynthesis genes and aliA gene	95	624	624

S. pneumoniae - Coding regions containing known sequences

TABLE 1

Contig ID	ORF ID	Start (nt)	Stop (nt)	match accession	match gene name	percent ident	HSP nt length	ORF nt length
7	11	9024	8206	emb 283335 SP28	S.pneumoniae dexB, cap1(A,B,C,D,E,F,G,H,I,J,K) genes, dTDP-rhamnose biosynthesis genes and alia gene	95	819	819
10	13	9304	8078	gb L29323	Streptococcus pneumoniae methyl transferase (mtr) gene cluster, complete cds	93	513	1227
11	2	548	919	emb 279691 SOOR	S.pneumoniae yor1(A,B,C,D,E), ftsL, pbpX and regR genes	99	316	372
11	3	892	1980	emb 279691 SOOR	S.pneumoniae yor1(A,B,C,D,E), ftsL, pbpX and regR genes	99	1089	1089
11	5	3040	3477	emb 279691 SOOR	S.pneumoniae yor1(A,B,C,D,E), ftsL, pbpX and regR genes	99	259	438
11	6	3480	3247	emb 279691 SOOR	S.pneumoniae yor1(A,B,C,D,E), ftsL, pbpX and regR genes	99	234	234
11	7	3601	4557	emb 279691 SOOR	S.pneumoniae yor1(A,B,C,D,E), ftsL, pbpX and regR genes	98	957	957
11	8	4506	4886	emb 279691 SOOR	S.pneumoniae yor1(A,B,C,D,E), ftsL, pbpX and regR genes	99	381	381
11	9	4884	7142	emb X16367 SPPB	Streptococcus pneumoniae pbpX gene for penicillin binding protein 2X	99	2259	2259
11	10	7132	8124	emb X16367 SPPB	Streptococcus pneumoniae pbpX gene for penicillin binding protein 2X	98	70	993
13	1	53	1126	gb X31296	S.pneumoniae recP gene, complete cds	99	437	1074
14	3	1837	2148	emb 283335 SP28	S.pneumoniae dexB, cap1(A,B,C,D,E,F,G,H,I,J,K) genes, dTDP-rhamnose biosynthesis genes and alia gene	87	96	312
14	4	2518	2108	gb X36180	Streptococcus pneumoniae transposase, (comA and comB) and SAICAR synthetase (purC) genes, complete cds	98	411	411
15	9	8942	8511	gb U09239	Streptococcus pneumoniae type 19F capsular polysaccharide biosynthesis operon, (cpsA cpsB cpsC cpsD cpsE cpsF cpsG cpsH cpsI cpsJ cpsK cpsL cpsM cpsN cpsO cpsP cpsQ cpsR cpsS cpsT cpsU cpsV cpsW cpsX cpsY cpsZ cpsAA cpsAB cpsAC cpsAD cpsAE cpsAF cpsAG cpsAH cpsAI cpsAJ cpsAK cpsAL cpsAM cpsAN cpsAO cpsAP cpsAQ cpsAR cpsAS cpsAT cpsAU cpsAV cpsAW cpsAX cpsAY cpsAZ cpsBA cpsBB cpsBC cpsBD cpsBE cpsBF cpsBG cpsBH cpsBI cpsBJ cpsBK cpsBL cpsBM cpsBN cpsBO cpsBP cpsBQ cpsBR cpsBS cpsBT cpsBU cpsBV cpsBW cpsBX cpsBY cpsBZ cpsCA cpsCB cpsCC cpsCD cpsCE cpsCF cpsCG cpsCH cpsCI cpsCJ cpsCK cpsCL cpsCM cpsCN cpsCO cpsCP cpsCQ cpsCR cpsCS cpsCT cpsCU cpsCV cpsCW cpsCX cpsCY cpsCZ cpsDA cpsDB cpsDC cpsDD cpsDE cpsDF cpsDG cpsDH cpsDI cpsDJ cpsDK cpsDL cpsDM cpsDN cpsDO cpsDP cpsDQ cpsDR cpsDS cpsDT cpsDU cpsDV cpsDW cpsDX cpsDY cpsDZ cpsEA cpsEB cpsEC cpsED cpsEE cpsEF cpsEG cpsEH cpsEI cpsEJ cpsEK cpsEL cpsEM cpsEN cpsEO cpsEP cpsEQ cpsER cpsES cpsET cpsEU cpsEV cpsEW cpsEX cpsEY cpsEZ cpsFA cpsFB cpsFC cpsFD cpsFE cpsFF cpsFG cpsFH cpsFI cpsFJ cpsFK cpsFL cpsFM cpsFN cpsFO cpsFP cpsFQ cpsFR cpsFS cpsFT cpsFU cpsFV cpsFW cpsFX cpsFY cpsFZ cpsGA cpsGB cpsGC cpsGD cpsGE cpsGF cpsGG cpsGH cpsGI cpsGJ cpsGK cpsGL cpsGM cpsGN cpsGO cpsGP cpsGQ cpsGR cpsGS cpsGT cpsGU cpsGV cpsGW cpsGX cpsGY cpsGZ cpsHA cpsHB cpsHC cpsHD cpsHE cpsHF cpsHG cpsHH cpsHI cpsHJ cpsHK cpsHL cpsHM cpsHN cpsHO cpsHP cpsHQ cpsHR cpsHS cpsHT cpsHU cpsHV cpsHW cpsHX cpsHY cpsHZ cpsIA cpsIB cpsIC cpsID cpsIE cpsIF cpsIG cpsIH cpsII cpsIJ cpsIK cpsIL cpsIM cpsIN cpsIO cpsIP cpsIQ cpsIR cpsIS cpsIT cpsIU cpsIV cpsIW cpsIX cpsIY cpsIZ cpsJA cpsJB cpsJC cpsJD cpsJE cpsJF cpsJG cpsJH cpsJI cpsJJ cpsJK cpsJL cpsJM cpsJN cpsJO cpsJP cpsJQ cpsJR cpsJS cpsJT cpsJU cpsJV cpsJW cpsJX cpsJY cpsJZ cpsKA cpsKB cpsKC cpsKD cpsKE cpsKF cpsKG cpsKH cpsKI cpsKJ cpsKL cpsKM cpsKN cpsKO cpsKP cpsKQ cpsKR cpsKS cpsKT cpsKU cpsKV cpsKW cpsKX cpsKY cpsKZ cpsLA cpsLB cpsLC cpsLD cpsLE cpsLF cpsLG cpsLH cpsLI cpsLJ cpsLK cpsLL cpsLM cpsLN cpsLO cpsLP cpsLQ cpsLR cpsLS cpsLT cpsLU cpsLV cpsLW cpsLX cpsLY cpsLZ cpsMA cpsMB cpsMC cpsMD cpsME cpsMF cpsMG cpsMH cpsMI cpsMJ cpsMK cpsML cpsMN cpsMO cpsMP cpsMQ cpsMR cpsMS cpsMT cpsMU cpsMV cpsMW cpsMX cpsMY cpsMZ cpsNA cpsNB cpsNC cpsND cpsNE cpsNF cpsNG cpsNH cpsNI cpsNJ cpsNK cpsNL cpsNM cpsNO cpsNP cpsNQ cpsNR cpsNS cpsNT cpsNU cpsNV cpsNW cpsNX cpsNY cpsNZ cpsOA cpsOB cpsOC cpsOD cpsOE cpsOF cpsOG cpsOH cpsOI cpsOJ cpsOK cpsOL cpsOM cpsON cpsOO cpsOP cpsOQ cpsOR cpsOS cpsOT cpsOU cpsOV cpsOW cpsOX cpsOY cpsOZ cpsPA cpsPB cpsPC cpsPD cpsPE cpsPF cpsPG cpsPH cpsPI cpsPJ cpsPK cpsPL cpsPM cpsPN cpsPO cpsPP cpsPQ cpsPR cpsPS cpsPT cpsPU cpsPV cpsPW cpsPX cpsPY cpsPZ cpsQA cpsQB cpsQC cpsQD cpsQE cpsQF cpsQG cpsQH cpsQI cpsQJ cpsQK cpsQL cpsQM cpsQN cpsQO cpsQP cpsQQ cpsQR cpsQS cpsQT cpsQU cpsQV cpsQW cpsQX cpsQY cpsQZ cpsRA cpsRB cpsRC cpsRD cpsRE cpsRF cpsRG cpsRH cpsRI cpsRJ cpsRK cpsRL cpsRM cpsRN cpsRO cpsRP cpsRQ cpsRR cpsRS cpsRT cpsRU cpsRV cpsRW cpsRX cpsRY cpsRZ cpsSA cpsSB cpsSC cpsSD cpsSE cpsSF cpsSG cpsSH cpsSI cpsSJ cpsSK cpsSL cpsSM cpsSN cpsSO cpsSP cpsSQ cpsSR cpsSS cpsST cpsSU cpsSV cpsSW cpsSX cpsSY cpsSZ cpsTA cpsTB cpsTC cpsTD cpsTE cpsTF cpsTG cpsTH cpsTI cpsTJ cpsTK cpsTL cpsTM cpsTN cpsTO cpsTP cpsTQ cpsTR cpsTS cpsTT cpsTU cpsTV cpsTW cpsTX cpsTY cpsTZ cpsUA cpsUB cpsUC cpsUD cpsUE cpsUF cpsUG cpsUH cpsUI cpsUJ cpsUK cpsUL cpsUM cpsUN cpsUO cpsUP cpsUQ cpsUR cpsUS cpsUT cpsUU cpsUV cpsUW cpsUX cpsUY cpsUZ cpsVA cpsVB cpsVC cpsVD cpsVE cpsVF cpsVG cpsVH cpsVI cpsVJ cpsVK cpsVL cpsVM cpsVN cpsVO cpsVP cpsVQ cpsVR cpsVS cpsVT cpsVU cpsVV cpsVW cpsVX cpsVY cpsVZ cpsWA cpsWB cpsWC cpsWD cpsWE cpsWF cpsWG cpsWH cpsWI cpsWJ cpsWK cpsWL cpsWM cpsWN cpsWO cpsWP cpsWQ cpsWR cpsWS cpsWT cpsWU cpsWV cpsWW cpsWX cpsWY cpsWZ cpsXA cpsXB cpsXC cpsXD cpsXE cpsXF cpsXG cpsXH cpsXI cpsXJ cpsXK cpsXL cpsXM cpsXN cpsXO cpsXP cpsXQ cpsXR cpsXS cpsXT cpsXU cpsXV cpsXW cpsXX cpsXY cpsXZ cpsYA cpsYB cpsYC cpsYD cpsYE cpsYF cpsYG cpsYH cpsYI cpsYJ cpsYK cpsYL cpsYM cpsYN cpsYO cpsYP cpsYQ cpsYR cpsYS cpsYT cpsYU cpsYV cpsYW cpsYX cpsYY cpsYZ cpsZA cpsZB cpsZC cpsZD cpsZE cpsZF cpsZG cpsZH cpsZI cpsZJ cpsZK cpsZL cpsZM cpsZN cpsZO cpsZP cpsZQ cpsZR cpsZS cpsZT cpsZU cpsZV cpsZW cpsZX cpsZY cpsZZ	89	340	432
17	7	3910	3458	emb 277726 SPIS	S.pneumoniae DNA for insertion sequence IS1318 (1372 bp)	98	453	453
17	8	4304	3873	emb 277727 SPIS	S.pneumoniae DNA for insertion sequence IS1318 (823 bp)	96	382	432
19	1	41	529	emb X94909 SPIG	S.pneumoniae iga gene	75	368	489
19	2	534	757	gb L07752	Streptococcus pneumoniae attachment site (attB), DNA sequence	99	167	204
19	3	946	1827	gb L07752	Streptococcus pneumoniae attachment site (attB), DNA sequence	94	100	882
20	1	937	182	gb U33315	Streptococcus pneumoniae orfL gene, partial cds, competence stimulating peptide precursor (comC), histidine protein kinase (comD) and response regulator (comE) genes, complete cds, trna-Arg and trna-Gln genes	99	756	756
20	2	2271	931	gb U33315	Streptococcus pneumoniae orfL gene, partial cds, competence stimulating peptide precursor (comC), histidine protein kinase (comD) and response regulator (comE) genes, complete cds, trna-Arg and trna-Gln genes	98	1341	1341

**TABLE 1** *S. pneumoniae* - Coding regions containing known sequences

Contig ID	ORF ID	Start (nt)	Stop (nt)	match accession	match gene name	percent ident	HSP nt length	ORF nt length
20	3	3175	2684	gb U76218	<i>Streptococcus pneumoniae</i> competence stimulating peptide precursor ComC (comC), histidine kinase homolog ComD (comD), and response regulator homolog ComE (comE) genes, complete cds	99	492	492
20	4	3322	4527	gb AF000658	<i>Streptococcus pneumoniae</i> R801 tRNA-Arg gene, partial sequence, and putative serine protease (sphtra), SPSPoj (spspoj), initiator protein (spdnaa) and beta subunit of DNA polymerase III (spdnan) genes, complete cds	99	1206	1206
20	5	4573	5343	gb AF000658	<i>Streptococcus pneumoniae</i> R801 tRNA-Arg gene, partial sequence, and putative serine protease (sphtra), SPSPoj (spspoj), initiator protein (spdnaa) and beta subunit of DNA polymerase III (spdnan) genes, complete cds	99	771	771
20	6	5532	6917	gb AF000658	<i>Streptococcus pneumoniae</i> R801 tRNA-Arg gene, partial sequence, and putative serine protease (sphtra), SPSPoj (spspoj), initiator protein (spdnaa) and beta subunit of DNA polymerase III (spdnan) genes, complete cds	99	1386	1386
20	7	6995	8212	gb AF000658	<i>Streptococcus pneumoniae</i> R801 tRNA-Arg gene, partial sequence, and putative serine protease (sphtra), SPSPoj (spspoj), initiator protein (spdnaa) and beta subunit of DNA polymerase III (spdnan) genes, complete cds	99	1218	1218
20	8	8214	8471	gb AF000658	<i>Streptococcus pneumoniae</i> R801 tRNA-Arg gene, partial sequence, and putative serine protease (sphtra), SPSPoj (spspoj), initiator protein (spdnaa) and beta subunit of DNA polymerase III (spdnan) genes, complete cds	98	258	258
20	9	8534	9670	gb AF000658	<i>Streptococcus pneumoniae</i> R801 tRNA-Arg gene, partial sequence, and putative serine protease (sphtra), SPSPoj (spspoj), initiator protein (spdnaa) and beta subunit of DNA polymerase III (spdnan) genes, complete cds	99	134	1137
22	14	11887	12267	emb Z77726 SPIS	<i>S. pneumoniae</i> DNA for insertion sequence IS1318 (1372 bp)	99	226	381
22	15	12708	12256	emb Z77727 SPIS	<i>S. pneumoniae</i> DNA for insertion sequence IS1318 (823 bp)	97	353	453
22	16	13165	12662	emb Z77726 SPIS	<i>S. pneumoniae</i> DNA for insertion sequence IS1318 (1372 bp)	98	504	504
22	23	18398	18910	emb Z86112 SP28	<i>S. pneumoniae</i> genes encoding galacturonosyl transferase and transposase and insertion sequence IS1515	95	463	513
22	24	18829	19299	emb Z86112 SP28	<i>S. pneumoniae</i> genes encoding galacturonosyl transferase and transposase and insertion sequence IS1515	99	443	471
23	5	5624	4203	emb X52474 SPPL	<i>S. pneumoniae</i> ply gene for pneumolysin	99	1422	1422
23	6	6063	5629	gb M17717	<i>S. pneumoniae</i> pneumolysin gene, complete cds	98	197	435
26	1	5500	2	emb X94909 SPIG	<i>S. pneumoniae</i> iga gene	87	3487	5499
26	2	5823	5584	gb U47687	<i>Streptococcus pneumoniae</i> immunoglobulin A1 protease (iga) gene, complete cds	99	151	240
26	3	6878	5685	gb U47687	<i>Streptococcus pneumoniae</i> immunoglobulin A1 protease (iga) gene, complete cds	100	50	1194

TABLE 1  
S. pneumoniae - Coding regions containing known sequences

Contig ID	ORF ID	Start (nt)	Stop (nt)	match accession	match gene name	percent ident	HSP nt length	ORF nt length
26	8	14498	14854	emb 283335 SP28	S.pneumoniae dexB, caps(A,B,C,D,E,F,G,H,I,J,K) genes, dTDP-rhamnose biosynthesis genes and aIIA gene	99	338	357
26	9	14763	14924	emb 283335 SP28	S.pneumoniae dexB, caps(A,B,C,D,E,F,G,H,I,J,K) genes, dTDP-rhamnose biosynthesis genes and aIIA gene	100	94	162
26	10	14922	15173	gb U04047	Streptococcus pneumoniae SS2 dextran glucosidase gene and insertion sequence IS1202 transposase gene, complete cds	97	242	252
28	1	80	505	emb 283335 SP28	S.pneumoniae dexB, caps(A,B,C,D,E,F,G,H,I,J,K) genes, dTDP-rhamnose biosynthesis genes and aIIA gene	99	426	426
28	2	503	952	gb U04047	Streptococcus pneumoniae SS2 dextran glucosidase gene and insertion sequence IS1202 transposase gene, complete cds	97	450	450
28	3	780	1298	gb U04047	Streptococcus pneumoniae SS2 dextran glucosidase gene and insertion sequence IS1202 transposase gene, complete cds	96	181	519
34	1	207	1523	gb L08611	Streptococcus pneumoniae maltose/maltodextrin uptake (malX) and two maltodextrin permease (malC and malD) genes, complete cds	99	1317	1317
34	2	1477	2367	gb L08611	Streptococcus pneumoniae maltose/maltodextrin uptake (malX) and two maltodextrin permease (malC and malD) genes, complete cds	96	795	891
34	3	2593	3420	gb L21856	Streptococcus pneumoniae malA gene, complete cds; malR gene, complete cds	96	446	828
34	4	2790	2647	gb L21856	Streptococcus pneumoniae malA gene, complete cds; malR gene, complete cds	98	137	144
34	5	3418	4416	gb L21856	Streptococcus pneumoniae malA gene, complete cds; malR gene, complete cds	96	999	999
34	9	7764	7507	gb U41735	Streptococcus pneumoniae peptide methionine sulfoxide reductase (msrA) and homoserine kinase homolog (thrB) genes, complete cds	93	201	258
34	16	10562	10257	emb X63602 SP80	S.pneumoniae mmsA-Box			
35	4	1176	1439	emb 283335 SP28	S.pneumoniae dexB, caps(A,B,C,D,E,F,G,H,I,J,K) genes, dTDP-rhamnose biosynthesis genes and aIIA gene	92	238	306
35	5	1458	1961	gb U09239	Streptococcus pneumoniae type 19F capsular polysaccharide biosynthesis operon, (cps19FABCEFGHIJLKLMNO) genes, complete cds, and aIIA gene, partial cds	87	248	264
35	17	16172	15477	emb X85787 SPCP	S.pneumoniae dexB, caps(A,B,C,D,E,F,G,H,I,J,K) genes, dTDP-rhamnose biosynthesis genes and aIIA gene	98	264	504
35	18	16961	16170	emb 283335 SP28	S.pneumoniae dexB, caps(A,B,C,D,E,F,G,H,I,J,K) genes, dTDP-rhamnose biosynthesis genes and aIIA gene	97	696	696
35	19	17620	16871	gb U09239	Streptococcus pneumoniae type 19F capsular polysaccharide biosynthesis operon, (cps19FABCEFGHIJLKLMNO) genes, complete cds, and aIIA gene, partial cds	86	792	792
						83	750	750

TABLE 1  
S. pneumoniae - Coding regions containing known sequences

Contig ID	ORF ID	Start (nt)	Stop (nt)	match accession	match gene name	Percent ident	HSP nt length	ORF nt length
35	20	19061	17604	[emb]X85787 SPCP	S.pneumoniae dexB, cps14A, cps14B, cps14C, cps14D, cps14E, cps14F, cps14G, cps14H, cps14I, cps14J, cps14K, cps14L, taaA genes	94	1458	1458
36	19	18960	18352	[gb]U40786	Streptococcus pneumoniae surface antigen A variant precursor (psaA) and 18 kDa protein genes, complete cds, and ORF1 gene, partial cds	99	609	609
36	20	19934	18966	[gb]U53509	Streptococcus pneumoniae surface adhesin A precursor (psaA) gene, complete cds	99	969	969
37	1	2743	179	[emb]Z67739 SPPA	S.pneumoniae parC, parE and transposase genes and unknown orf	99	2565	2565
37	2	2985	2824	[emb]Z67739 SPPA	S.pneumoniae parC, parE and transposase genes and unknown orf	100	162	162
37	3	5034	3070	[emb]Z67739 SPPA	S.pneumoniae parC, parE and transposase genes and unknown orf	99	1965	1965
37	4	5134	5790	[emb]Z67739 SPPA	S.pneumoniae parC, parE and transposase genes and unknown orf	99	657	657
37	5	6171	5833	[emb]Z67739 SPPA	S.pneumoniae parC, parE and transposase genes and unknown orf	96	339	339
38	19	12969	13268	[gb]M28679	S.pneumoniae promoter region DNA	100	64	300
39	2	1256	2137	[gb]U41735	Streptococcus pneumoniae peptide methionine sulfoxide reductase (msrA) and homoserine kinase homolog (thrB) genes, complete cds	99	882	882
39	3	2405	3370	[gb]U41735	Streptococcus pneumoniae peptide methionine sulfoxide reductase (msrA) and homoserine kinase homolog (thrB) genes, complete cds	99	966	966
40	9	5253	7208	[gb]M29686	S.pneumoniae mismatch repair (hmxB) gene, complete cds	99	1956	1956
41	1	3	1037	[emb]Z17307 SPRE	S.pneumoniae recA gene encoding RecA	99	1027	1035
41	2	1328	2713	[emb]Z34303 SPCI	Streptococcus pneumoniae cin operon encoding the cinA, recA, dinP, lytA genes, and downstream sequences	99	1386	1386
41	3	3083	4045	[gb]M13812	S.pneumoniae autolysin (lytA) gene, complete cds	99	963	963
41	4	3272	3096	[gb]M13812	S.pneumoniae autolysin (lytA) gene, complete cds	100	177	177
41	5	3603	3860	[gb]M13812	S.pneumoniae autolysin (lytA) gene, complete cds	100	258	258
41	6	4755	5162	[gb]U36660	Streptococcus pneumoniae ORF, complete cds	98	408	408
41	7	5270	5716	[gb]U36660	Streptococcus pneumoniae ORF, complete cds	98	447	447
41	8	6112	6918	[gb]U36660	Streptococcus pneumoniae ORF, complete cds	98	431	807
41	9	6916	7119	[gb]U36660	Streptococcus pneumoniae ORF, complete cds	100	204	204
41	10	7082	7660	[gb]U36660	Streptococcus pneumoniae ORF, complete cds	97	552	579
41	11	7680	7979	[gb]U36660	Streptococcus pneumoniae ORF, complete cds	98	81	300
41	12	9169	8717	[emb]Z77727 SPIS	S.pneumoniae DNA for insertion sequence IS1318 (823 bp)	97	353	453



TABLE I

S. pneumoniae - Coding regions containing known sequences

Contig ID	ORF ID	Start (nt)	Stop (nt)	match accession	match gene name	percent ident	HSP nt length	ORF nt length
41	13	9533	9132	emb 277725 SPIS	S.pneumoniae DNA for insertion sequence IS1381 (966 bp)	95	160	402
41	14	9669	9475	emb 282001 SP28	S.pneumoniae pcpsA gene and open reading frames	100	189	195
44	5	7190	7555	emb 282001 SP28	S.pneumoniae pcpsA gene and open reading frames	99	366	366
44	6	8059	7607	emb 277726 SPIS	S.pneumoniae DNA for insertion sequence IS1318 (1372 bp)	97	453	453
44	7	8423	8022	emb 277725 SPIS	S.pneumoniae DNA for insertion sequence IS1381 (966 bp)	95	160	402
44	8	8539	8365	emb 282001 SP28	S.pneumoniae pcpsA gene and open reading frames	100	189	195
48	9	6480	4687	gb LJ9074	Streptococcus pneumoniae pyruvate oxidase (spxB) gene, complete cds	99	1794	1794
49	2	231	2603	gb LJ0561	Streptococcus pneumoniae Exp7 gene, partial cds	100	216	2373
53	6	2407	2156	gb U04047	Streptococcus pneumoniae SSZ dextran glucosidase gene and insertion sequence IS1202 transposase gene, complete cds	97	242	252
53	7	2566	2405	emb 283335 SP28	S.pneumoniae dexB, capl(A,B,C,D,E,F,G,H,I,J,K) genes, dTDP-rhamnose biosynthesis genes and alia gene	100	94	162
53	8	2831	2475	emb 283335 SP28	S.pneumoniae dexB, capl(A,B,C,D,E,F,G,H,I,J,K) genes, dTDP-rhamnose biosynthesis genes and alia gene	99	338	357
54	13	12409	11105	emb 283335 SP28	S.pneumoniae dexB, capl(A,B,C,D,E,F,G,H,I,J,K) genes, dTDP-rhamnose biosynthesis genes and alia gene	67	591	1305
55	22	20488	19949	emb 284379 HS28	S.pneumoniae dfr gene (isolate 92)	99	540	540
61	11	11864	9900	emb 216082 PNAL	Streptococcus pneumoniae alib gene	98	1965	1965
63	1	3	239	gb H18729	S.pneumoniae mismatch repair protein (hexA) gene, complete cds	100	237	237
63	2	233	2611	gb H18729	S.pneumoniae mismatch repair protein (hexA) gene, complete cds	99	2330	2379
63	3	2557	2823	gb H18729	S.pneumoniae mismatch repair protein (hexA) gene, complete cds	99	266	267
63	4	2958	4664	gb H18729	S.pneumoniae mismatch repair protein (hexA) gene, complete cds	95	69	1707
67	6	3770	3399	gb L20670	Streptococcus pneumoniae hyaluronidase gene, complete cds	96	372	372
67	7	7161	4171	gb L20670	Streptococcus pneumoniae hyaluronidase gene, complete cds	99	2938	2991
70	1	1	702	gb H14340	S.pneumoniae DpnI gene region encoding dpcN and dpcD, complete cds	100	693	702
70	2	678	1160	gb H14340	S.pneumoniae DpnI gene region encoding dpcN and dpcD, complete cds	100	483	483
70	3	2490	1210	gb H14339	S.pneumoniae DpnII gene region encoding dpcM, dpcN, complete cds	98	462	1281
70	7	4230	4424	gb J04234	S.pneumoniae exodeoxyribonuclease (exoA) gene, complete cds	99	147	195
70	8	5197	4316	gb J04234	S.pneumoniae exodeoxyribonuclease (exoA) gene, complete cds	99	881	882

TABLE 1

S. pneumoniae - Coding regions containing known sequences

Contig ID	ORF ID	Start (nt)	Stop (nt)	match accession	match gene name	Percent ident	HSP nt length	ORF nt length
70	13	8108	9874	gb L20562	Streptococcus pneumoniae Exp8 gene, partial cds	93	234	1767
71	22	27964	28341	emb X63602 SPBO	S. pneumoniae mmsA-Box			
72	5	4607	3552	emb Z26850 SPAT	S. pneumoniae (M222) genes for ATPase a subunit, ATPase b subunit and ATPase c subunit	93	233	378
73	1	471	133	emb X63602 SPBO	S. pneumoniae mmsA-Box	97	102	1056
73	3	3658	977	gb J04479	S. pneumoniae DNA polymerase I (polA) gene, complete cds	91	193	339
73	8	4864	5379	gb H36180	Streptococcus pneumoniae transposase, (comA and comB) and SAICAR synthetase (purC) genes, complete cds	99	2682	2682
77	3	2622	1999	emb Z83335 SPZ8	S. pneumoniae dexB, capl(A,B,C,D,E,F,G,H,I,J,K) genes, dTDP-rhamnose biosynthesis genes and allA gene	98	318	516
77	4	3341	2523	emb Z83335 SPZ8	S. pneumoniae dexB, capl(A,B,C,D,E,F,G,H,I,J,K) genes, dTDP-rhamnose biosynthesis genes and allA gene	95	624	624
78	1	341	3	emb X77249 SPR6	S. pneumoniae (R6) ciar/ciaH genes	91	819	819
78	2	1095	325	emb X77249 SPR6	S. pneumoniae (R6) ciar/ciaH genes	99	339	339
82	10	11436	10816	gb U90721	Streptococcus pneumoniae signal peptidase I (spi) gene, complete cds	99	771	771
82	11	12402	11434	gb U93576	Streptococcus pneumoniae Hfl (rnhB) gene, complete cds	97	621	621
82	12	12381	12704	gb U93576	Streptococcus pneumoniae Hfl (rnhB) gene, complete cds	98	953	969
83	8	3212	3550	emb Z77727 SPIS	S. pneumoniae DNA for insertion sequence IS1318 (823 bp)	100	51	324
83	10	4662	6851	gb H36180	Streptococcus pneumoniae transposase, (comA and comB) and SAICAR synthetase (purC) genes, complete cds	97	290	339
83	11	6849	8213	gb H36180	Streptococcus pneumoniae transposase, (comA and comB) and SAICAR synthetase (purC) genes, complete cds	99	2190	2190
83	12	8236	9090	gb H36180	Streptococcus pneumoniae transposase, (comA and comB) and SAICAR synthetase (purC) genes, complete cds	99	1365	1365
83	13	9283	13017	gb L15190	Streptococcus pneumoniae SAICAR synthetase (purC) gene, complete cds	99	855	855
83	23	22147	23313	gb L36923	Streptococcus pneumoniae beta-N-acetylhexosaminidase (strH) gene, complete cds	100	107	3735
83	24	23268	23450	gb L36923	Streptococcus pneumoniae beta-N-acetylhexosaminidase (strH) gene, complete cds	98	218	1167
83	25	27527	23505	gb L36923	Streptococcus pneumoniae beta-N-acetylhexosaminidase (strH) gene, complete cds	98	172	183
83	25	27527	23505	gb L36923	Streptococcus pneumoniae beta-N-acetylhexosaminidase (strH) gene, complete cds	99	3826	4023

TABLE 1  
S. pneumoniae - Coding regions containing known sequences

Contig ID	ORF ID	Start (nt)	Stop (nt)	match accession	match gene name	percent ident	HSP nt length	ORF nt length
83	26	28472	27771	gb L36923	Streptococcus pneumoniae beta-N-acetylhexosaminidase (strH) gene, complete cds	99	416	702
84	4	4554	6173	emb Z83335 SP28	S. pneumoniae dexB, capI(A,B,C,D,E,F,G,H,I,J,K) genes, dTDP-rhamnose biosynthesis genes and aIIA gene	98	697	1620
87	6	5951	5316	emb Z7725 SP15	S. pneumoniae DNA for insertion sequence IS1381 (966 bp)	96	439	636
88	5	2957	3511	gb M36180	Streptococcus pneumoniae transposase, (comA and comB) and SAICAR synthetase (purC) genes, complete cds	94	555	555
88	6	3466	4269	gb M36180	Streptococcus pneumoniae transposase, (comA and comB) and SAICAR synthetase (purC) genes, complete cds	94	804	804
89	13	9878	10093	gb M36180	Streptococcus pneumoniae transposase, (comA and comB) and SAICAR synthetase (purC) genes, complete cds	97	211	216
89	14	10062	10412	emb Z83335 SP28	S. pneumoniae dexB, capI(A,B,C,D,E,F,G,H,I,J,K) genes, dTDP-rhamnose biosynthesis genes and aIIA gene	97	335	351
93	10	5303	4941	emb X63602 SP80	S. pneumoniae mmaA-Box	89	237	363
97	4	1708	1520	gb U41735	Streptococcus pneumoniae peptide methionine sulfoxide reductase (msrA) and homoserine kinase homolog (thrB) genes, complete cds	91	140	189
99	1	89	700	emb Z83335 SP28	S. pneumoniae dexB, capI(A,B,C,D,E,F,G,H,I,J,K) genes, dTDP-rhamnose biosynthesis genes and aIIA gene	93	592	612
99	2	1773	775	emb X17337 SPAM	Streptococcus pneumoniae aml locus conferring aminopterin resistance	99	998	999
99	3	2794	1712	emb X17337 SPAM	Streptococcus pneumoniae aml locus conferring aminopterin resistance	99	1083	1083
99	4	3712	2788	emb X17337 SPAM	Streptococcus pneumoniae aml locus conferring aminopterin resistance	100	945	945
99	5	5249	3714	emb X17337 SPAM	Streptococcus pneumoniae aml locus conferring aminopterin resistance	100	1536	1536
99	6	7262	5277	emb X17337 SPAM	Streptococcus pneumoniae aml locus conferring aminopterin resistance	99	1986	1986
101	1	216	1538	emb X54225 SPEN	S. pneumoniae epuA and endA genes for 7 kDa protein and membrane endonuclease	99	146	1323
101	2	1492	1719	emb X54225 SPEN	S. pneumoniae epuA and endA genes for 7 kDa protein and membrane endonuclease	99	228	228
101	3	1694	1855	emb X54225 SPEN	S. pneumoniae epuA and endA genes for 7 kDa protein and membrane endonuclease	100	162	162
101	4	1701	2582	emb X54225 SPEN	S. pneumoniae epuA and endA genes for 7 kDa protein and membrane endonuclease	100	882	882
103	7	5556	5041	emb Z95914 SP29	Streptococcus pneumoniae sodA gene	100	396	516
104	2	1347	1556	emb Z7727 SP15	S. pneumoniae DNA for insertion sequence IS1318 (823 bp)	83	206	210

TABLE 1

S. pneumoniae - Coding regions containing known sequences

Contig ID	ORF ID	Start (nt)	Stop (nt)	match accession	match gene name	percent ident	HSP nt length	ORF nt length
105	5	5381	5028	emb Z67739 SPPA	S. pneumoniae parC, parE and transposase genes and unknown orf	98	353	354
105	6	6089	5379	emb Z67739 SPPA	S. pneumoniae parC, parE and transposase genes and unknown orf	98	84	711
107	4	2785	1880	emb X16022 SPPE	S. pneumoniae penA gene	98	72	906
107	5	2913	4988	emb X16022 SPPE	S. pneumoniae penA gene	99	1692	2076
107	6	4981	5595	emb X13136 SPPE	Streptococcus pneumoniae penA gene for penicillin binding protein 2B lacking N-term. (penicillin resistant strain)	91	107	615
108	9	9068	8718	emb Z67739 SPPA	S. pneumoniae parC, parE and transposase genes and unknown orf	95	342	351
108	12	11308	10922	emb Z67739 SPPA	S. pneumoniae parC, parE and transposase genes and unknown orf	99	199	387
109	3	2768	2241	emb Z77725 SPIS	S. pneumoniae DNA for insertion sequence IS1381 (966 bp)	96	61	528
109	4	2688	2855	emb Z77726 SPIS	S. pneumoniae DNA for insertion sequence IS1318 (1372 bp)	96	148	168
109	5	2862	3269	emb Z77727 SPIS	S. pneumoniae DNA for insertion sequence IS1318 (823 bp)	97	353	408
109	6	5320	3584	gb M18729	S. pneumoniae mismatch repair protein (hexA) gene, complete cds	100	371	1737
113	1	431	3	gb M36180	Streptococcus pneumoniae transposase, (comA and comB) and SAICAR synthetase (purC) genes, complete cds	95	429	429
113	10	9788	8532	emb X99400 SPDA	S. pneumoniae dacA gene and ORF	99	1257	1257
113	11	9870	10985	emb X99400 SPDA	S. pneumoniae dacA gene and ORF	99	1116	1116
114	3	2530	2030	gb M36180	Streptococcus pneumoniae transposase, (comA and comB) and SAICAR synthetase (purC) genes, complete cds	95	481	501
115	11	11303	10932	gb U04047	Streptococcus pneumoniae SS2 dextran glucosidase gene and insertion sequence IS1202 transposase gene, complete cds	97	372	372
117	1	897	3302	emb X72967 SPNA	S. pneumoniae nanA gene	99	2402	2406
117	2	3277	3831	emb X72967 SPNA	S. pneumoniae nanA gene	99	237	555
117	3	4327	3899	gb M36180	Streptococcus pneumoniae transposase, (comA and comB) and SAICAR synthetase (purC) genes, complete cds	98	429	429
121	2	1369	1941	gb U72720	Streptococcus pneumoniae heat shock protein 70 (dnaK) gene, complete cds and DnaJ (dnaJ) gene, partial cds	99	202	573
121	3	2412	4253	gb U72720	Streptococcus pneumoniae heat shock protein 70 (dnaK) gene, complete cds and DnaJ (dnaJ) gene, partial cds	99	1842	1842
122	8	5066	5587	gb U04047	Streptococcus pneumoniae SS2 dextran glucosidase gene and insertion sequence IS1202 transposase gene, complete cds	64	451	522

TABLE 1

S. pneumoniae - Coding regions containing known sequences

Contig ID	ORF ID	Start (nt)	Stop (nt)	match accession	match gene name	percent ident	HSP nt length	ORF nt length
125	1	1811	189	gb H36180	Streptococcus pneumoniae transposase, (comA and comB) and SAICAR synthetase (purC) genes, complete cds	92	99	1623
128	15	12496	11204	emb Z83335 SP28	S.pneumoniae dexB, cap1(A,B,C,D,E,F,G,H,I,J,K) genes, dTDP-rhamnose biosynthesis genes and allA gene	91	705	1293
134	1	1	492	emb Y10818 SPY1	S.pneumoniae spsA gene	99	203	492
134	2	556	2652	gb AF019904	Streptococcus pneumoniae choline binding protein A (cbpA) gene, partial cds	86	685	2097
134	3	1160	837	emb Y10818 SPY1	S.pneumoniae spsA gene	86	324	324
134	4	3952	2882	gb AF019904	Streptococcus pneumoniae choline binding protein A (cbpA) gene, partial cds	98	215	1071
134	8	7992	9848	gb U12567	Streptococcus pneumoniae P13 glycerol-3-phosphate dehydrogenase (glpD) gene, partial cds, and glycerol uptake facilitator (glpF) and ORF3 genes, complete cds	99	285	1857
134	9	9846	10622	gb U12567	Streptococcus pneumoniae P13 glycerol-3-phosphate dehydrogenase (glpD) gene, partial cds, and glycerol uptake facilitator (glpF) and ORF3 genes, complete cds	99	570	777
134	10	10805	11122	gb U12567	Streptococcus pneumoniae P13 glycerol-3-phosphate dehydrogenase (glpD) gene, partial cds, and glycerol uptake facilitator (glpF) and ORF3 genes, complete cds	100	318	318
137	13	7970	8443	gb U09239	Streptococcus pneumoniae type 19F capsular polysaccharide biosynthesis operon, (cps)9(ABCDEFGHIJKLMNO) genes, complete cds, and allA gene, partial cds	90	420	474
137	14	8590	8775	emb Z83335 SP28	S.pneumoniae dexB, cap1(A,B,C,D,E,F,G,H,I,J,K) genes, dTDP-rhamnose biosynthesis genes and allA gene	94	174	186
137	15	8773	8967	emb Z83335 SP28	S.pneumoniae dexB, cap1(A,B,C,D,E,F,G,H,I,J,K) genes, dTDP-rhamnose biosynthesis genes and allA gene	98	195	195
137	16	9223	9687	emb Z77726 SP15	S.pneumoniae DNA for insertion sequence IS1318 (1372 bp)	96	446	465
137	17	9641	10051	emb Z77727 SP15	S.pneumoniae DNA for insertion sequence IS1318 (823 bp)	96	293	411
139	10	12998	12702	emb X63602 SPB0	S.pneumoniae mmsA-Box	90	234	297
141	8	7805	8938	emb Z49988 SPNM	Streptococcus pneumoniae mmsA gene	99	338	1134
141	9	8936	10972	emb Z49988 SPNM	Streptococcus pneumoniae mmsA gene	99	2037	2037
141	10	11472	12467	emb Z49988 SPNM	Streptococcus pneumoniae mmsA gene	100	76	996
142	2	257	814	gb H60215	Streptococcus pneumoniae uvs402 protein gene, complete cds	98	174	558
142	3	787	957	gb H60215	Streptococcus pneumoniae uvs402 protein gene, complete cds	100	142	171
142	4	980	3022	gb H60215	Streptococcus pneumoniae uvs402 protein gene, complete cds	95	1997	2043

S. pneumoniae - Coding regions containing known sequences

TABLE 1

Contig ID	ORF ID	Start (nt)	Stop (nt)	match accession	match gene name	percent ident	HSP nt length	ORF nt length
142	5	3020	3595	gb W80215	Streptococcus pneumoniae uvs402 protein gene, complete cds	100	153	576
145	1	1	219	emb Z35135 SPAL	S.pneumoniae alla gene for emA-like gene A			
145	2	171	1994	gb L20556	Streptococcus pneumoniae p1pa gene, partial cds	97	185	219
145	3	2287	7599	emb Z47210 SPDE	S.pneumoniae dexB, cap3A, cap3B and cap3C genes and orfA	99	1811	1824
145	4	9934	7766	gb M90527	Streptococcus pneumoniae penicillin-binding protein (ponA) gene, complete cds	99	1052	5313
145	5	10488	9922	gb M90527	Streptococcus pneumoniae penicillin-binding protein (ponA) gene, complete cds	99	2169	2169
146	1	159	4	emb Z82002 SP28	S.pneumoniae pcgB and pcgC genes	98	156	156
146	2	344	90	emb Z82002 SP28	S.pneumoniae pcgB and pcgC genes	98	255	255
146	16	11795	10794	emb Z82002 SP28	S.pneumoniae pcgB and pcgC genes	85	276	1002
147	11	10678	10202	emb Z21702 SPUN	S.pneumoniae ung gene and mutX genes encoding uracil-DNA glycosylase and 8-oxodGTP nucleoside triphosphatase	98	477	477
147	12	11338	10676	emb Z21702 SPUN	S.pneumoniae ung gene and mutX genes encoding uracil-DNA glycosylase and 8-oxodGTP nucleoside triphosphatase	99	663	663
148	12	9009	8815	gb U41735	Streptococcus pneumoniae peptide methionine sulfoxide reductase (msrA) and homoserine kinase homolog (thcB) genes, complete cds	90	180	195
156	4	1154	1402	emb X63602 SPBO	S.pneumoniae emsA-Box	94	185	249
159	13	9048	8521	gb M36180	Streptococcus pneumoniae transposase, (comA and comB) and SAICAR synthetase (purC) genes, complete cds	98	526	528
160	1	1	147	emb Z26851 SPAT	S.pneumoniae (R6) genes for ATPase a subunit, ATPase b subunit and ATPase c subunit	100	142	147
160	2	179	898	emb Z26851 SPAT	S.pneumoniae (R6) genes for ATPase a subunit, ATPase b subunit and ATPase c subunit	99	720	720
160	3	906	1406	emb Z26850 SPAT	S.pneumoniae (M222) genes for ATPase a subunit, ATPase b subunit and ATPase c subunit	95	501	501
160	4	1373	1942	emb Z26850 SPAT	S.pneumoniae (M222) genes for ATPase a subunit, ATPase b subunit and ATPase c subunit	87	306	570
161	1	1	984	emb X77249 SPR6	S.pneumoniae (R6) clbA/clbH genes	99	984	984
161	7	6910	7497	emb X83917 SPGY	S.pneumoniae orf1gyrB and gyrB gene encoding DNA gyrase B subunit	99	437	588
161	8	7443	9386	emb X83917 SPGY	S.pneumoniae orf1gyrB and gyrB gene encoding DNA gyrase B subunit	98	1912	1944
163	1	2	2155	gb L20559	Streptococcus pneumoniae Exp5 gene, partial cds	98	327	2154

TABLE 1

S. pneumoniae - Coding regions containing known sequences

Contig ID	ORF ID	Start (nt)	Stop (nt)	match accession	match gene name	percent ident	HSP nt length	ORF nt length
165	1	32	1618	gb J01796	S.pneumoniae malX and malM genes encoding membrane protein and amyomaltase, complete cds, and malP gene encoding phosphorylase	99	1587	1587
165	2	1608	3902	gb J01796	S.pneumoniae malX and malM genes encoding membrane protein and amyomaltase, complete cds, and malP gene encoding phosphorylase	100	280	2295
166	1	378	4	emb Y11463 SPDN	Streptococcus pneumoniae dnaG, rpoD, cpoA genes and ORF3 and ORF5	100	375	375
166	2	1507	320	emb Y11463 SPDN	Streptococcus pneumoniae dnaG, rpoD, cpoA genes and ORF3 and ORF5	99	1188	1188
166	3	3240	1432	emb Y11463 SPDN	Streptococcus pneumoniae dnaG, rpoD, cpoA genes and ORF3 and ORF5	99	563	1809
167	1	1077	328	emb Z71552 SPAD	Streptococcus pneumoniae dnaG, rpoD, cpoA genes and ORF3 and ORF5	94	155	750
167	2	1844	999	emb Z71552 SPAD	Streptococcus pneumoniae dnaG, rpoD, cpoA genes and ORF3 and ORF5	98	405	846
167	3	2714	1842	emb Z71552 SPAD	Streptococcus pneumoniae dnaG, rpoD, cpoA genes and ORF3 and ORF5	97	604	873
167	4	3399	2641	emb Z71552 SPAD	Streptococcus pneumoniae dnaG, rpoD, cpoA genes and ORF3 and ORF5	99	703	759
168	1	1	2259	gb J20558	Streptococcus pneumoniae Exp4 gene, partial cds	99	282	2259
170	10	7338	7685	emb Z77726 SPIS	S.pneumoniae DNA for insertion sequence IS1318 (1372 bp)	95	315	348
172	6	2462	4981	gb U47625	Streptococcus pneumoniae formate acetyltransferase (exp72) gene, partial cds	97	365	2520
175	1	373	20	gb M36180	Streptococcus pneumoniae transposase, (comA and comB) and SAICAR synthetase (purC) genes, complete cds	89	353	354
175	4	1843	3621	emb Z47210 SPDE	S.pneumoniae dexB, capJA, capJB and capJC genes and orfs	95	89	1779
176	5	3984	2980	emb Z67739 SPPA	S.pneumoniae parC, parE and transposase genes and unknown orf	100	573	1005
178	1	3	425	emb Z67739 SPPA	S.pneumoniae parC, parE and transposase genes and unknown orf	95	423	423
179	1	426	70	emb Z83335 SP28	S.pneumoniae dexB, capI(A,B,C,D,E,F,G,H,I,J,K) genes, dTDP-rhamnose biosynthesis genes and aIIA gene	99	338	357
180	3	3084	1855	emb X95718 SPGY	S.pneumoniae gyrA gene	99	381	1230
186	1	714	4	emb Z79691 SOOR	S.pneumoniae yorI(A,B,C,D,E), ftsL, pbpX and regR genes	98	59	711
186	2	2254	608	emb Z79691 SOOR	S.pneumoniae yorI(A,B,C,D,E), ftsL, pbpX and regR genes	98	315	1647
186	3	707	880	emb Z79691 SOOR	S.pneumoniae yorI(A,B,C,D,E), ftsL, pbpX and regR genes	98	174	174
189	1	2	259	gb U72720	Streptococcus pneumoniae heat shock protein 70 (dnaK) gene, complete cds and DnaJ (dnaJ) gene, partial cds	99	258	258
189	2	600	385	gb U72720	Streptococcus pneumoniae heat shock protein 70 (dnaK) gene, complete cds and DnaJ (dnaJ) gene, partial cds	98	204	216

TABLE 1

S. pneumoniae - Coding regions containing known sequences

Contig ID	ORF ID	Start (nt)	Stop (nt)	match accession	match gene name	percent ident	HSP nt length	ORF nt length
189	3	1018	851	gb U72720	Streptococcus pneumoniae heat shock protein 70 (dnaK) gene, complete cds and DnaJ (dnaJ) gene, partial cds	99	168	168
189	4	1012	2154	gb U72720	Streptococcus pneumoniae heat shock protein 70 (dnaK) gene, complete cds and DnaJ (dnaJ) gene, partial cds	99	1062	1143
191	9	7829	7524	emb X63602 SP80	S.pneumoniae msaA-Box	95	234	306
194	1	1	729	gb M36180	Streptococcus pneumoniae transposase, (comA and comB) and SAICAR synthetase (purC) genes, complete cds	91	728	729
199	2	1117	881	emb Z83335 SP28	S.pneumoniae dexB, capl(A,B,C,D,E,F,G,H,I,J,K) genes, RTDP-rhamnose biosynthesis genes and alia gene	96	211	237
199	4	1499	1762	emb Z83335 SP28	S.pneumoniae dexB, capl(A,B,C,D,E,F,G,H,I,J,K) genes, dTDP-rhamnose biosynthesis genes and alia gene	89	248	264
199	5	1781	2284	emb Z83335 SP28	S.pneumoniae dexB, capl(A,B,C,D,E,F,G,H,I,J,K) genes, dTDP-rhamnose biosynthesis genes and alia gene	98	504	504
203	1	1977	337	gb J20563	Streptococcus pneumoniae Exp9 gene, partial cds	99	342	1641
204	1	1145	3	gb J36131	Streptococcus pneumoniae exp10 gene, complete cds, recA gene, 5' end	99	1143	1143
208	1	59	2296	gb U89711	Streptococcus pneumoniae pneumococcal surface protein A PspA (pspa) gene, complete cds	90	471	2238
213	3	2455	2123	emb Z83335 SP28	S.pneumoniae dexB, capl(A,B,C,D,E,F,G,H,I,J,K) genes, dTDP-rhamnose biosynthesis genes and alia gene	96	332	333
216	1	368	12	emb Z83335 SP28	S.pneumoniae dexB, capl(A,B,C,D,E,F,G,H,I,J,K) genes, dTDP-rhamnose biosynthesis genes and alia gene	99	338	357
216	3	2650	2227	gb M28678	S.pneumoniae promoter sequence DNA	98	86	324
222	1	417	4	emb Z83335 SP28	S.pneumoniae dexB, capl(A,B,C,D,E,F,G,H,I,J,K) genes, dTDP-rhamnose biosynthesis genes and alia gene	94	414	414
227	3	5266	4238	emb AJ000336 SP	Streptococcus pneumoniae ldh gene	99	1029	1029
239	1	1	804	gb M31296	S.pneumoniae recP gene, complete cds	95	484	804
247	3	1625	1807	gb M36180	Streptococcus pneumoniae transposase, (comA and comB) and SAICAR synthetase (purC) genes, complete cds	94	178	183
249	3	921	1364	emb Z83335 SP28	S.pneumoniae dexB, capl(A,B,C,D,E,F,G,H,I,J,K) genes, dTDP-rhamnose biosynthesis genes and alia gene	94	443	444
253	1	362	3	gb M36180	Streptococcus pneumoniae transposase, (comA and comB) and SAICAR synthetase (purC) genes, complete cds	99	360	360
253	5	1238	2050	emb Z83335 SP28	S.pneumoniae dexB, capl(A,B,C,D,E,F,G,H,I,J,K) genes, dTDP-rhamnose biosynthesis genes and alia gene	95	420	813



TABLE 1  
S. pneumoniae - Coding regions containing known sequences

Contig ID	ORF ID	Start (nt)	Stop (nt)	match accession	match gene name	percent ident	HSP nt length	ORF nt length
253	6	2069	2572	emb Z83335 SP28	S.pneumoniae dexB, capl(A,B,C,D,E,F,G,H,I,J,K) genes, dTDP-rhamnose biosynthesis genes and aliA gene	97	504	504
255	1	3	800	emb Z82002 SP28	S.pneumoniae pcgB and pcgC genes			
255	2	798	1841	emb Z82002 SP28	S.pneumoniae pcgB and pcgC genes	97	531	798
255	3	2493	1969	emb Z67739 SPPA	S.pneumoniae parC, parE and transposase genes and unknown orf	97	672	1044
257	2	985	770	emb X17337 SPAM	Streptococcus pneumoniae aml locus conferring aminopterin resistance	92	435	525
257	3	1245	907	gb M36180	Streptococcus pneumoniae transposase, (comA and comB) and SAICAR synthetase (purC) genes, complete cds	96	117	216
267	2	495	1208	gb U16156	Streptococcus pneumoniae dihydropteroate synthase (sulA), dihydrofolate synthetase (sulB), guanosine triphosphate cyclohydrolase (sulC), aldolase-pyrophosphokinase (sulD) genes, complete cds	97	339	339
267	3	1291	2277	gb U16156	Streptococcus pneumoniae dihydropteroate synthase (sulA), dihydrofolate synthetase (sulB), guanosine triphosphate cyclohydrolase (sulC), aldolase-pyrophosphokinase (sulD) genes, complete cds	97	755	987
267	4	2261	3601	gb U16156	Streptococcus pneumoniae dihydropteroate synthase (sulA), dihydrofolate synthetase (sulB), guanosine triphosphate cyclohydrolase (sulC), aldolase-pyrophosphokinase (sulD) genes, complete cds	98	1341	1341
267	5	3561	4136	gb U16156	Streptococcus pneumoniae dihydropteroate synthase (sulA), dihydrofolate synthetase (sulB), guanosine triphosphate cyclohydrolase (sulC), aldolase-pyrophosphokinase (sulD) genes, complete cds	99	576	576
267	6	4164	4949	gb U16156	Streptococcus pneumoniae dihydropteroate synthase (sulA), dihydrofolate synthetase (sulB), guanosine triphosphate cyclohydrolase (sulC), aldolase-pyrophosphokinase (sulD) genes, complete cds	99	748	786
267	7	5544	5140	gb U16156	Streptococcus pneumoniae dihydropteroate synthase (sulA), dihydrofolate synthetase (sulB), guanosine triphosphate cyclohydrolase (sulC), aldolase-pyrophosphokinase (sulD) genes, complete cds	100	186	405
268	4	1793	1990	emb X63602 SP90	S.pneumoniae msaA-Box			
271	1	562	104	gb M29686	S.pneumoniae mismatch repair (hexB) gene, complete cds	89	194	198
291	1	75	524	gb U04047	Streptococcus pneumoniae SSZ dextran glucosidase gene and insertion sequence IS1202 transposase gene, complete cds	93	160	459
291	2	1001	525	emb Z83335 SP28	S.pneumoniae dexB, capl(A,B,C,D,E,F,G,H,I,J,K) genes, dTDP-rhamnose biosynthesis genes and aliA gene	96	450	450
291	3	807	559	emb Z83335 SP28	S.pneumoniae dexB, capl(A,B,C,D,E,F,G,H,I,J,K) genes, dTDP-rhamnose biosynthesis genes and aliA gene	87	205	477
291	4	1374	1099	gb M36180	Streptococcus pneumoniae transposase, (comA and comB) and SAICAR synthetase (purC) genes, complete cds	90	170	249
						85	264	276

**TABLE I**  
**S. pneumoniae - Coding regions containing known sequences**

Contig ID	ORF ID	Start (nt)	Stop (nt)	match accession	match gene name	percent ident	HSP nt length	ORF nt length
293	1	3	1673	emb 267740 SPCY	S.pneumoniae gyrB gene and unknown orf	98	553	1671
296	1	1434	151	emb 247210 SPDE	S.pneumoniae dexB, cap3A, cap3B and cap3C genes and orfs	99	430	1284
317	1	157	510	emb 267739 SPPA	S.pneumoniae parC, parE and transposase genes and unknown orf	89	353	354
325	2	1237	485	emb 283335 SPZ8	S.pneumoniae dexB, cap1(A,B,C,D,E,F,G,H,I,J,K) genes, dTDP-rhamnose biosynthesis genes and alia gene	91	299	753
326	1	1	462	emb 282001 SPZ8	S.pneumoniae pcpA gene and open reading frames	100	233	462
327	1	603	64	emb 283335 SPZ8	S.pneumoniae dexB, cap1(A,B,C,D,E,F,G,H,I,J,K) genes, dTDP-rhamnose biosynthesis genes and alia gene	94	89	540
334	1	153	545	gb U41735	Streptococcus pneumoniae peptide methionine sulfoxide reductase (msrA) and homoserine kinase homolog (thrB) genes, complete cds	87	91	393
336	1	308	93	emb 236850 SPAT	S.pneumoniae (M222) genes for ATPase a subunit, ATPase b subunit and ATPase c subunit	97	102	216
360	1	1	519	emb 267739 SPPA	S.pneumoniae parC, parE and transposase genes and unknown orf	95	435	519
360	4	1598	1960	emb 283335 SPZ8	S.pneumoniae dexB, cap1(A,B,C,D,E,F,G,H,I,J,K) genes, dTDP-rhamnose biosynthesis genes and alia gene	94	353	363
362	1	673	2	emb 283335 SPZ8	S.pneumoniae dexB, cap1(A,B,C,D,E,F,G,H,I,J,K) genes, dTDP-rhamnose biosynthesis genes and alia gene	95	63	672
362	2	1168	728	gb U04047	Streptococcus pneumoniae SS2 dextran glucosidase gene and insertion sequence IS1202 transposase gene, complete cds	96	441	441
384	1	347	111	emb X85787 SPCP	S.pneumoniae dexB, cps14A, cps14B, cps14C, cps14D, cps14E, cps14F, cps14G, cps14H, cps14I, cps14J, cps14K, cps14L, tsaA genes	94	54	237

TABLE 2

S. pneumoniae - Putative coding regions of novel proteins similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)	match accession	match gene name	% sim	% ident	length (nt)
228	2	1760	1942	pir F60663 F606	translation elongation factor Tu - Streptococcus oralis	100	100	183
319	1	2	205	gi 984927	neomycin phosphotransferase [Cloning vector pBSL99]	100	100	204
260	1	2	1138	pir F60663 F606	translation elongation factor Tu - Streptococcus oralis	99	98	1137
25	2	486	1394	gi 1574495	hypothetical [Haemophilus influenzae]	98	96	909
94	2	685	1002	gi 110627	phosphoenolpyruvate:sugar phosphotransferase system HPr [Streptococcus mutans]	98	93	318
312	1	190	2	gi 347999	ATP-dependent protease proteolytic subunit [Streptococcus salivarius]	98	95	189
329	1	1	807	gi 924848	inosine monophosphate dehydrogenase [Streptococcus pyogenes]	98	94	807
336	2	290	589	gi 987050	lacZ gene product [unidentified cloning vector]	98	98	300
181	9	5948	7366	gi 153755	phospho-beta-D-galactosidase (EC 3.2.1.85) [Lactococcus lactis cremoris]	97	94	1419
312	2	1044	361	gi 347998	uracil phosphoribosyltransferase [Streptococcus salivarius]	97	88	684
32	8	6575	7486	sp P37214 ERA_S	GTP-BINDING PROTEIN ERA HOMOLOG	96	91	912
94	3	951	2741	gi 153615	phosphoenolpyruvate:sugar phosphotransferase system enzyme I [Streptococcus salivarius]	96	92	1791
127	1	1	168	gi 581299	initiation factor IF-1 [Lactococcus lactis]	96	89	168
128	14	10438	11154	gi 1276873	DeoD [Streptococcus thermophilus]	96	93	717
181	4	1362	1598	gi 46606	lacD polypeptide (AA 1-326) [Staphylococcus aureus]	96	80	237
218	1	1	834	gi 1743856	intragenic coaggregation-relevant adhesin [Streptococcus gordonii]	96	93	834
319	2	115	441	gi 208225	heat-shock protein 92/neomycin phosphotransferase fusion protein (hap82-neo) [unidentified cloning vector]	96	96	327
54	12	8622	10967	gnl PID d100972	pyruvate formate-lyase [Streptococcus mutans]	95	89	2346
181	2	606	1289	gi 149396	lacD [Lactococcus lactis]	95	89	684
46	3	3410	3045	gi 1850606	YlxM [Streptococcus mutans]	94	86	366
89	10	7972	7337	gi 703442	thymidine kinase [Streptococcus gordonii]	94	86	636
148	9	6431	7354	gi 995767	UDP-glucose pyrophosphorylase [Streptococcus pyogenes]	94	85	924
160	7	4430	5848	gi 153573	H+ ATPase [Enterococcus faecalis]	94	87	1419
2	3	4598	3513	gi 153763	plasma receptor [Streptococcus pyogenes]	93	86	1086
12	8	7877	6204	gi 1103865	formyl-tetrahydrofolate synthetase [Streptococcus mutans]	93	84	1674

TABLE 2

S. pneumoniae - Putative coding regions of novel proteins similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)	match accession	match gene name	% sim	% ident	length (nt)
65	11	4734	5120	gi 40150	Jul4 protein (AA 1-122) [Bacillus subtilis]	93	87	387
68	1	53	1297	gi 47341	antitumor protein [Streptococcus pyogenes]	93	87	1245
80	1	3	299	gm pid d101166	ribosomal protein S7 [Bacillus subtilis]	93	84	297
127	3	695	1093	gi 142462	ribosomal protein S11 [Bacillus subtilis]	93	86	399
160	5	1924	3462	gi 1773264	ATPase, alpha subunit [Streptococcus mutans]	93	85	1539
211	5	3757	3047	gi 535273	aminopeptidase C [Streptococcus thermophilus]	93	82	711
262	1	16	564	gi 149394	lacB [Lactococcus lactis]	93	90	549
366	1	197	3	gi 295259	tryptophan synthase beta subunit [Synechocystis sp.]	93	91	195
25	3	1392	1976	gi 1574496	hypothetical [Haemophilus influenzae]	92	80	585
36	21	20781	19927	gi 310632	hydrophobic membrane protein [Streptococcus gordonii]	92	86	855
181	3	1265	1534	gi 149396	lacD [Lactococcus lactis]	92	83	270
181	7	3682	4060	gi 149410	enzyme III [Lactococcus lactis]	92	83	399
32	4	5631	3937	gm pid e294090	fibronectin-binding protein-like protein A [Streptococcus gordonii]	91	85	1695
46	2	3054	1462	gi 1850607	signal recognition particle Ffh [Streptococcus mutans]	91	84	1593
65	10	4442	4726	pir S17865 S178	ribosomal protein S17 - Bacillus stearothermophilus	91	80	285
77	2	260	1900	gi 287871	groEL gene product [Lactococcus lactis]	91	82	1641
84	1	2	2056	gi 871784	Clp-like ATP-dependent protease binding subunit [Bos taurus]	91	79	2055
99	8	10750	9272	gi 153740	sucrose phosphorylase [Streptococcus mutans]	91	84	1479
99	9	11947	11072	gi 153739	membrane protein [Streptococcus mutans]	91	78	876
127	5	2065	2469	pir S07223 RSBS	ribosomal protein L17 - Bacillus stearothermophilus	91	78	405
132	6	9539	9390	gi 143065	hubst [Bacillus stearothermophilus]	91	89	150
137	8	4765	6153	gm pid d100347	Na <sup>+</sup> -ATPase beta subunit [Enterococcus hirae]	91	79	1389
151	7	11119	9734	gi 1815634	glutamine synthetase type 1 [Streptococcus agalactiae]	91	82	1386
201	2	1798	278	gi 2208998	dextran glucosidase DaxS [Streptococcus suis]	91	79	1521
222	2	673	1839	gi 153741	ATP-binding protein [Streptococcus mutans]	91	85	1167
293	5	4113	4400	gi 1196921	unknown protein [insertion sequence IS861]	91	71	288
32	7	6166	6570	pir A36933 A369	diacylglycerol kinase homolog - Streptococcus mutans	90	77	405

TABLE 2

S. pneumoniae - Putative coding regions of novel proteins similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)	match accession	match gene name	% sim	% ident	length (nt)
33	2	841	527	gi11196921	unknown protein [Insertion sequence IS861]	90	70	315
48	27	20908	19757	gnl pid e274705	lactate oxidase (Streptococcus iniae)	90	80	1152
55	21	19777	18515	gnl pid e221213	ClpX protein [Bacillus subtilis]	90	75	1263
56	2	717	977	gi11710133	flagellar filament cap [Borrelia burgdorferi]	90	50	261
65	1	1	606	gi11165303	L3 [Bacillus subtilis]	90	75	606
114	1	2	988	gi1153562	aspartate beta-semialdehyde dehydrogenase (EC 1.2.1.11) [Streptococcus mutans]	90	80	987
120	1	1345	827	gi1407880	ORP1 [Streptococcus equisimilis]	90	75	519
159	12	7690	8298	gi1143012	GMP synthetase [Bacillus subtilis]	90	84	609
166	4	4076	3282	gi11661179	high affinity branched chain amino acid transport protein [Streptococcus mutans]	90	78	795
183	1	28	1395	gi1308858	ATP:pyruvate 2-O-phosphotransferase [Lactococcus lactis]	90	76	1368
191	3	2891	1662	gi1149521	cryptophan synthase beta subunit [Lactococcus lactis]	90	78	1230
198	2	1551	436	gi12323342	[AF014460] CcpA [Streptococcus mutans]	90	76	1116
305	1	37	783	gi11573351	asparagine synthetase A (asnA) [Haemophilus influenzae]	90	80	747
8	3	2285	3343	gi1149434	putative [Lactococcus lactis]	89	78	1059
46	8	7577	7362	pir A45436 A454	ribosomal protein L19 - Bacillus stearothermophilus	89	76	216
49	9	8363	10342	gi1153792	recP peptide [Streptococcus pneumoniae]	89	83	1980
51	14	18410	19447	gi1308857	ATP-D-fructose 6-phosphate 1-phosphotransferase [Lactococcus lactis]	89	81	1038
57	11	9686	10669	gnl pid d100932	H2O-forming NADH Oxidase [Streptococcus mutans]	89	77	984
65	5	2418	2786	gi11165307	S19 [Bacillus subtilis]	89	81	369
65	8	3806	4225	sp P14577 RL16	50S RIBOSOMAL PROTEIN L16	89	82	420
65	18	8219	8719	gi1143417	ribosomal protein S5 [Bacillus stearothermophilus]	89	76	501
73	9	6337	5315	gi11532204	prf [Listeria monocytogenes]	89	70	1023
76	3	3360	1465	gnl pid e200671	lepA gene product [Bacillus subtilis]	89	76	1896
99	10	12818	11919	gi1153738	membrane protein [Streptococcus mutans]	89	73	900
120	2	3552	1300	gi1407881	stringent response-like protein [Streptococcus equisimilis]	89	79	2253
122	5	4512	2791	gnl pid e280490	unknown [Streptococcus pneumoniae]	89	81	1722

TABLE 2

S. pneumoniae - Putative coding regions of novel proteins similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)	match accession	match gene name	% sim	% ident	length (nt)
176	1	669	4	gi 47394	5-oxoprolyl-peptidase [Streptococcus pyogenes]	89	78	666
177	6	3050	3934	gi 912423	putative [Lactococcus lactis]	89	71	885
181	8	4033	5751	gi 149411	enzyme III [Lactococcus lactis]	89	80	1719
211	4	3149	2793	gi 535273	aminopeptidase C [Streptococcus thermophilus]	89	83	357
361	1	431	838	gi 1196922	unknown protein [insertion sequence IS861]	89	70	408
34	17	11839	10535	sp P30053 SYN_S	HISTIDYL-TRNA SYNTHETASE (EC 6.1.1.21) (HISTIDINE-TRNA LIGASE) (HISRS)	88	78	1305
38	3	1646	2623	gi 2058544	putative ABC transporter subunit ComYA [Streptococcus gordonii]	88	78	978
54	1	3	227	gnl PID d101320	YggU [Bacillus subtilis]	88	66	225
57	2	611	1468	gnl PID e134943	putative reductase 1 [Saccharomyces cerevisiae]	88	75	858
65	13	5497	6069	pir A29102 R5BS	ribosomal protein L5 - Bacillus stearothermophilus	88	75	573
65	20	9030	9500	gi 2078381	ribosomal protein L15 [Staphylococcus aureus]	88	83	471
78	3	3636	1108	gnl PID d100781	lysoyl-aminopeptidase [Lactococcus lactis]	88	80	2529
106	12	12965	12054	gi 2407215	(AF017421) putative heat shock protein HtpX [Streptococcus gordonii]	88	72	912
107	2	219	962	gnl PID e139862	putative acylneuraminidase lyase [Clostridium tertium]	88	75	744
111	8	14073	10420	gi 402363	rRNA polymerase beta-subunit [Bacillus subtilis]	88	74	3654
126	9	13096	12062	gnl PID e111468	unknown [Bacillus subtilis]	88	74	1035
140	17	19143	18874	gi 1573659	H. influenzae predicted coding region HI0659 [Haemophilus influenzae]	88	61	270
144	1	394	555	gnl PID e274705	lactate oxidase [Streptococcus infiae]	88	75	162
148	4	2723	3493	gi 1591672	phosphate transport system ATP-binding protein [Methanococcus jannaschii]	88	68	771
160	8	5853	6278	gi 1773267	ATPase, epsilon subunit [Streptococcus mutans]	88	65	426
177	4	1770	2885	gi 149426	putative [Lactococcus lactis]	88	72	1116
211	6	4140	3613	gi 1535273	aminopeptidase C [Streptococcus thermophilus]	88	74	528
231	4	580	957	gi 40186	homologous to E.coli ribosomal protein L27 [Bacillus subtilis]	88	78	378
260	5	2387	2998	gi 1196922	unknown protein [insertion sequence IS861]	88	69	612
291	6	2017	3375	gnl PID d100571	adenylosuccinate synthetase [Bacillus subtilis]	88	75	1359
319	4	658	317	gi 603578	serine/threonine kinase [Phytophthora capsici]	88	88	342
40	5	4353	4514	gi 153672	lactose repressor [Streptococcus mutans]	87	56	162

TABLE 2

S. pneumoniae - Putative coding regions of novel proteins similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)	match accession	match gene name	% sim	% ident	length (nt)
49	10	10660	10929	gi 1196921	unknown protein [Insertion sequence IS861]	87	72	270
65	7	3140	3808	gi 1165309	S3 [Bacillus subtilis]	87	73	669
65	15	6623	7039	gi 1044978	ribosomal protein S8 [Bacillus subtilis]	87	73	417
75	8	5411	6625	gi 1877422	galactokinase [Streptococcus mutans]	87	78	1215
80	2	703	2805	gnl PID d101166	elongation factor G [Bacillus subtilis]	87	76	2103
82	1	541	248	gi 1196921	unknown protein [Insertion sequence IS861]	87	69	294
140	23	25033	23897	gnl PID e254999	phenylalanyl-tRNA synthetase beta subunit [Bacillus subtilis]	87	74	1137
214	14	10441	8516	gi 2281305	glucose inhibited division protein homolog GIDA [Lactococcus lactis cremoris]	87	75	1926
220	2	2742	874	gnl PID e324358	product highly similar to elongation factor EF-G [Bacillus subtilis]	87	73	1869
260	4	2056	2389	gi 1196921	unknown protein [Insertion sequence IS861]	87	72	294
323	1	27	650	gi 897795	30S ribosomal protein [Pedococcus acidilactici]	87	73	624
357	1	154	570	gi 1044978	ribosomal protein S8 [Bacillus subtilis]	87	73	417
49	11	10927	11445	gi 1196922	unknown protein [Insertion sequence IS861]	86	63	519
59	12	7461	9224	gi 951051	relaxase [Streptococcus pneumoniae]	86	68	1764
65	4	1553	2401	pir A02759 R5BS	ribosomal protein L2 - Bacillus stearothermophilus	86	77	849
65	23	10957	11610	gi 44074	adenylate kinase [Lactococcus lactis]	86	76	654
82	4	4374	4856	gi 153745	mannitol-specific enzyme III [Streptococcus mutans]	86	72	483
102	4	4270	4986	gnl PID e264705	OMP decarboxylase [Lactococcus lactis]	86	76	717
106	6	7824	6880	gnl PID e137598	aspartate transcarbamylase [Lactobacillus leichmannii]	86	68	945
107	1	1	273	gnl PID e339862	putative acylneuraminase lyase [Clostridium tertium]	86	71	273
111	7	10432	6710	gnl PID e228283	DNA-dependent RNA polymerase [Streptococcus pyogenes]	86	60	3723
131	9	5704	4892	gi 1661193	polipoprotein diacylglycerol transferase [Streptococcus mutans]	86	71	813
134	7	6430	7980	gi 2388637	glycerol kinase [Enterococcus faecalis]	86	73	1551
146	11	7473	6583	gi 1591731	malonate kinase [Methanococcus jannaschii]	86	72	891
153	2	595	2010	gi 2160707	dipeptidase [Lactococcus lactis]	86	78	1416
154	1	2	1435	gi 1857246	6-phosphogluconate dehydrogenase [Lactococcus lactis]	86	74	1434

TABLE 2

S. pneumoniae - Putative coding regions of novel proteins similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)	match accession	match gene name	% sim	% ident	length (nt)
161	5	5025	6284	gi 47529	Unknown [Streptococcus salivarius]	86	66	1260
184	1	2	1483	gi 642667	NADP-dependent glyceraldehyde-3-phosphate dehydrogenase [Streptococcus mutans]	86	73	1482
210	8	3659	6571	gi 153661	translational initiation factor IF2 [Enterococcus faecium]	86	76	2913
250	1	2	187	gi 1573551	asparagine synthetase A (asnA) [Haemophilus influenzae]	86	68	186
36	4	2644	3909	gi 2149909	cell division protein [Enterococcus faecalis]	85	73	1266
38	4	2475	3587	gi 2058545	putative ABC transporter subunit ComYB [Streptococcus gordonii]	85	72	1113
38	5	3577	3915	gi 2058546	ComYC [Streptococcus gordonii]	85	80	339
57	5	2797	3789	gnl PID d101316	Yqj3 [Bacillus subtilis]	85	72	993
82	5	4915	6054	gi 153746	mannotol-phosphate dehydrogenase [Streptococcus mutans]	85	68	1140
83	15	14690	15793	gi 143371	phosphoribosyl aminoimidazole synthetase (PUR-M) [Bacillus subtilis]	85	69	1104
87	2	1417	2388	gi 1184967	SerR [Streptococcus mutans]	85	69	972
108	3	2666	3154	gi 153566	ORF (19k protein) [Enterococcus faecalis]	85	67	489
127	2	312	692	gi 1044989	ribosomal protein S13 [Bacillus subtilis]	85	72	381
128	3	1534	2409	gi 1685110	tetrahydrofolate dehydrogenase/cyclohydrolase [Streptococcus thermophilus]	85	71	876
137	7	2962	4767	gnl PID d100347	Na <sup>+</sup> -ATPase alpha subunit [Enterococcus hirae]	85	74	1806
170	2	2622	709	gnl PID d102006	[AB001488] FUNCTION UNKNOWN, SIMILAR PRODUCT IN E. COLI, H. INFLUENZAE AND NEISSERIA MENINGITIDIS. [Bacillus subtilis]	85	70	1914
187	5	3760	4386	gi 727436	putative 20-kDa protein [Lactococcus lactis]	85	65	627
233	2	728	1873	gi 1163116	ORF-5 [Streptococcus pneumoniae]	85	67	1146
234	3	962	1255	gi 2293155	[AF008220] YtiA [Bacillus subtilis]	85	61	294
240	1	309	1931	gi 143597	CTP synthetase [Bacillus subtilis]	85	70	1623
6	1	199	1521	gi 508979	GTP-binding protein [Bacillus subtilis]	84	72	1323
10	4	4375	3443	gnl PID e339862	putative acylneuraminate lyase [Clostridium tertium]	84	70	933
14	1	63	2093	gi 520753	DNA topoisomerase I [Bacillus subtilis]	84	69	2031
19	4	1793	2593	gi 2352484	[AF005098] RNaseH II [Lactococcus lactis]	84	68	801
20	17	17720	19687	gnl PID d100584	cell division protein [Bacillus subtilis]	84	71	1968
22	28	21723	20884	gi 299163	alanine dehydrogenase [Bacillus subtilis]	84	68	840



TABLE 2

S. pneumoniae - Putative coding regions of novel proteins similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)	match accession	match gene name	% sim	% ident	length (nt)
30	10	7730	6792	gnl PID d100296	[fructokinase [Streptococcus mutans]]	84	75	939
33	9	5650	5300	gi 147194	[phnA protein [Escherichia coli]]	84	71	351
36	22	21551	20772	gi 310631	[ATP binding protein [Streptococcus gordonii]]	84	72	780
48	4	2837	2505	gi 882609	[6-phospho-beta-glucosidase [Escherichia coli]]	84	69	333
58	1	41	1316	gi 450849	[amylase [Streptococcus bovis]]	84	73	1476
59	10	6715	7116	gi 951053	[ORF10, putative [Streptococcus pneumoniae]]	84	74	402
62	3	21	644	gi 806487	[ORF211; putative [Lactococcus lactis]]	84	66	624
65	17	7779	8207	gi 1044980	[ribosomal protein L18 [Bacillus subtilis]]	84	73	429
65	21	9507	10397	gi 44073	[SecY protein [Lactococcus lactis]]	84	68	891
106	4	5474	2262	gnl PID e19387	[carbamoyl-phosphate synthase [Lactobacillus plantarum]]	84	73	3213
159	1	147	4	gi 806487	[ORF211; putative [Lactococcus lactis]]	84	63	144
163	4	4690	5910	gi 2293164	[AF008220] SAM synthase [Bacillus subtilis]]	84	69	1221
192	1	46	1308	gi 495046	[tripeptidase [Lactococcus lactis]]	84	73	1263
348	1	671	6	gi 1787753	[AE000245] f346; 79 pct identical to 336 amino acids of ADH1_ZYMO SW: P20368 but has 10 additional N-ter residues [Escherichia coli]]	84	71	666
3	4	1572	3575	gi 143766	[ChrSv] (EC 6.1.1.3) [Bacillus subtilis]]	83	65	2004
9	6	3893	3417	gnl PID d100576	[single strand DNA binding protein [Bacillus subtilis]]	83	68	477
17	15	7426	8457	gi 540738	[comA protein [Streptococcus pneumoniae]]	83	66	1032
20	12	13860	14144	gnl PID d100583	[unknown [Bacillus subtilis]]	83	61	285
23	4	3358	2606	gi 1788294	[AE000290] o238; This 238 aa orf is 40 pct identical (5 gaps) to 231 residues of an approx. 248 aa protein YEB_COLI SW: P24237 [Escherichia coli]]	83	74	753
28	6	3304	3005	gi 1573659	[H. influenzae predicted coding region H10659 [Haemophilus influenzae]]	83	57	300
35	7	5108	3867	gi 311707	[hypothetical nucleotide binding protein [Acholeplasma laidlawii]]	83	63	1242
55	19	17932	17528	gi 537085	[ORF_f141 [Escherichia coli]]	83	59	405
55	20	18339	17919	gi 496558	[orfX [Bacillus subtilis]]	83	69	621
65	6	2795	3142	gi 1165308	[l22 [Bacillus subtilis]]	83	64	348
68	6	6877	6683	gi 1213494	[immunoglobulin A1 protease [Streptococcus pneumoniae]]	83	54	195

TABLE 2

S. pneumoniae - Putative coding regions of novel proteins similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)	match accession	match gene name	% sim	% ident	length (nt)
87	15	15112	14771	gnl PID e323522	putative rpoZ protein [Bacillus subtilis]			
96	12	8963	9631	gi 47394	5-oxopropyl-peptidase [Streptococcus pyogenes]	83	54	342
98	1	3	263	gi 1183885	glutamine-binding subunit [Bacillus subtilis]	83	73	669
120	4	7170	5233	gi 310630	zinc metalloprotease [Streptococcus gordonii]	83	55	261
127	7	2998	4347	gi 1500567	M. Jannaschii predicted coding region M1665 [Methanococcus jannaschii]	83	72	1938
137	1	3	440	gi 472918	v-type Na-ATPase [Enterococcus hirae]	83	72	1350
160	6	3466	4356	gi 1773265	ATPase, gamma subunit [Streptococcus mutans]	83	60	438
214	4	2278	2964	gi 663279	transposase [Streptococcus pneumoniae]	83	67	891
226	3	2367	2020	gi 142154	thioredoxin [Synechococcus PCC6301]	83	72	687
303	1	3	1049	gi 40046	phosphoglucose isomerase A (AA 1-449) [Bacillus stearothermophilus]	83	58	348
303	2	1155	1931	gi 289282	glutanyl-tRNA synthetase [Bacillus subtilis]	83	67	1047
6	17	15370	14318	gi 1633147	ribose-phosphate pyrophosphokinase [Bacillus caldolyticus]	83	67	777
7	1	299	96	gi 143648	ribosomal protein L28 [Bacillus subtilis]	82	64	1053
9	3	1479	1090	gi 385178	unknown [Bacillus subtilis]	82	69	204
9	7	4213	3899	gnl PID d100576	ribosomal protein S6 [Bacillus subtilis]	82	46	390
12	6	4688	3942	gnl PID d100571	unknown [Bacillus subtilis]	82	60	315
22	17	13422	14837	gi 520754	putative [Bacillus subtilis]	82	68	747
22	18	14897	15658	gnl PID d101929	uridine monophosphate kinase [Synechocystis sp.]	82	69	1416
33	16	11471	10641	gnl PID d101190	ORF4 [Streptococcus mutans]	82	62	762
35	9	7400	6255	gi 1881543	UDP-N-acetylglucosamine-2-epimerase [Streptococcus pneumoniae]	82	68	831
40	10	8003	7533	gi 1173519	riboflavin synthase beta subunit [Actinobacillus pleuropneumoniae]	82	68	1146
48	32	23159	23437	gi 1930092	outer membrane protein [Campylobacter jejuni]	82	68	471
52	14	13833	14765	gi 142521	deoxyribodipyrimidine photolyase [Bacillus subtilis]	82	61	279
60	4	4737	1849	gnl PID d102221	[AB001610] uvrA [Deinococcus radiodurans]	82	61	933
62	4	2131	1457	gi 2246749	[AF009622] thioredoxin reductase [Listeria monocytogenes]	82	66	2889
71	11	16586	17518	gnl PID e322063	ss-1,4-galactosyltransferase [Streptococcus pneumoniae]	82	63	675
73	13	9222	7637	gnl PID d100586	unknown [Bacillus subtilis]	82	60	933
						82	65	1386

TABLE 2

S. pneumoniae - Putative coding regions of novel proteins similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)	match accession	match gene name	% sim	% ident	length (nt)
74	1	1	3771	gnl PID d101199	alkaline amylopullulanase (Bacillus sp.)	82	68	3771
83	9	3696	3983	gnl PID e305362	unnamed protein product (Streptococcus thermophilus)	82	52	288
86	11	10776	9394	gi 563583	[5-enolpyruvylshikimate-3-phosphate synthase (Lactococcus lactis)	82	67	1383
89	12	8295	9752	gi 40025	homologous to E. coli 50K (Bacillus subtilis)	82	66	1458
115	9	10347	8812	gnl PID d102090	(AB001927) phospho-beta-galactosidase 1 (Lactobacillus gasei)	82	74	1536
118	1	1	1332	gnl PID d100579	seryl-tRNA synthetase (Bacillus subtilis)	82	71	1332
151	3	4657	6246	pir S06097 S060	type I site-specific deoxyribonuclease (EC 3.1.21.3) CfrA chain S - Citrobacter freundii	82	66	1590
173	6	4183	3503	gi 2313836	(AE000584) conserved hypothetical protein (Helicobacter pylori)	82	68	681
177	12	5481	7442	gnl PID d101999	(AB001341) MCRB (Escherichia coli)	82	58	1962
193	2	178	576	pir S08564 R3BS	ribosomal protein S9 - Bacillus stearothermophilus	82	70	399
245	2	258	845	gi 146402	[ScA type I restriction-modification enzyme S subunit (Escherichia coli)	82	68	588
9	5	3400	3146	gnl PID d100576	ribosomal protein S18 (Bacillus subtilis)	81	66	255
16	7	7484	8413	gi 1100074	cryptophanyl-tRNA synthetase (Clostridium longisporum)	81	70	930
20	11	10308	13820	gnl PID d100583	transcription-repair coupling factor (Bacillus subtilis)	81	63	3513
38	2	1232	1606	gi 2058543	putative DNA binding protein (Streptococcus gordonii)	81	63	375
45	2	3061	1751	gi 460259	enolase (Bacillus subtilis)	81	67	1311
46	1	2	1267	gi 431231	luciferase (Bacillus caldolyticus)	81	61	1266
48	3	2453	1440	gnl PID d100453	Mannosephosphate isomerase (Streptococcus mutans)	81	70	1014
54	2	1106	336	gi 154752	transport protein (Agrobacterium tumefaciens)	81	64	771
65	22	10306	10821	gi 44073	SecY protein (Lactococcus lactis)	81	66	516
89	4	3874	2603	gi 556886	serine hydroxymethyltransferase (Bacillus subtilis)	81	69	1272
99	16	19126	18929	gi 2313526	(AE000557) H. pylori predicted coding region HP0411 (Helicobacter pylori)	81	75	198
106	7	8373	7822	gnl PID e199384	pyrR (Lactobacillus plantarum)	81	61	552
108	6	5054	6877	gi 1469939	group B oligopeptidase PcpB (Streptococcus agalactiae)	81	66	1824
113	15	15899	18283	pir S09411 S094	[spoIIIE protein - Bacillus subtilis	81	65	2385
128	5	3359	3634	gi 1685111	orf1091 (Streptococcus thermophilus)	81	69	276

TABLE 2

S. pneumoniae - Putative coding regions of novel proteins similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)	match accession	match gene name	% sim	% ident	length (nt)
151	1	830	3211	gi 304896	EcoE type I restriction-modification enzyme R subunit (Escherichia coli)	81	59	2382
159	11	6722	7837	gi 2239288	GMP synthetase (Bacillus subtilis)	81	69	1116
170	1	739	458	gnl PID d102006	(AB001488) FUNCTION UNKNOWN. (Bacillus subtilis)	81	55	282
191	2	1759	893	gi 149522	tryptophan synthase alpha subunit (Lactococcus lactis)	81	65	867
214	3	2290	1994	gi 157587	reverse transcriptase endonuclease (Drosophila virilis)	81	43	297
217	4	4415	4008	gi 466473	cellobiose phosphotransferase enzyme II' (Bacillus stearothermophilus)	81	59	408
262	2	569	868	gi 153675	tagatase 6-P kinase (Streptococcus mutans)	81	68	300
299	1	663	4	gnl PID e301154	StySKI methylase (Salmonella enterica)	81	60	660
366	2	376	83	gi 149521	tryptophan synthase beta subunit (Lactococcus lactis)	81	65	294
12	10	8766	9242	gi 1216490	DNA/pentothenate metabolism flavoprotein (Streptococcus mutans)	80	64	477
17	11	6030	5748	gnl PID e305362	unnamed protein product (Streptococcus thermophilus)	80	67	303
17	16	8455	9066	gi 703126	leucocin A translocator (Leuconostoc gelidum)	80	59	612
18	3	2440	1613	gi 1591672	phosphate transport system ATP-binding protein (Methanococcus jannaschii)	80	58	828
27	3	4248	1579	gi 452309	valyl-tRNA synthetase (Bacillus subtilis)	80	69	2670
28	7	3671	3288	gi 1573660	H. influenzae predicted coding region HI0660 (Haemophilus influenzae)	80	63	384
32	2	902	1933	gnl PID e264499	ldihydroxotrate dehydrogenase B (Lactococcus lactis)	80	66	1032
39	1	1	1266	gnl PID e234078	hom (Lactococcus lactis)	80	63	1266
52	5	4363	3593	gi 1183884	ATP-binding subunit (Bacillus subtilis)	80	57	771
54	5	4550	4744	gi 2198820	(AF004225) Cux/CDP(1B1); Cux/CDP homeoprotein (Mus musculus)	80	60	195
59	11	7109	7486	gi 951052	ORF9, putative (Streptococcus pneumoniae)	80	68	378
65	3	1230	1550	pir A02815 R585	ribosomal protein L23 - Bacillus stearothermophilus	80	69	321
65	12	5174	5503	pir A02819 R585	ribosomal protein L24 - Bacillus stearothermophilus	80	70	310
66	9	9884	10687	gi 2313836	(AE000584) conserved hypothetical protein (Helicobacter pylori)	80	66	804
82	2	648	2438	gi 622991	mannitol transport protein (Bacillus stearothermophilus)	80	65	1791
85	1	950	630	gi 528995	polyketide synthase (Bacillus subtilis)	80	46	321
89	8	6870	5779	gi 853776	peptide chain release factor 1 (Bacillus subtilis)	80	63	1092
93	12	8718	7438	gnl PID d101959	hypothetical protein (Synecocystis sp.)	80	60	1281

TABLE 2

S. pneumoniae - Putative coding regions of novel proteins similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)	match accession	match gene name	% sim	% ident	length (nt)
106	5	6854	5751	gnl PID e19386	glutaminase of carbamoyl-phosphate synthase [Lactobacillus plantarum]	80	65	1104
109	2	2160	1450	gi 40056	phoP gene product [Bacillus subtilis]	80	59	711
124	9	4246	3953	gnl PID d102254	30S ribosomal protein S16 [Bacillus subtilis]	80	65	294
128	8	5148	6428	gi 2281308	phosphoenolpyruvate carboxylase [Lactococcus lactis cremoris]	80	66	1281
137	19	12665	11376	gi 159109	NADP-dependent glutamate dehydrogenase [Giardia intestinalis]	80	68	1290
140	19	19699	19457	gi 517210	putative transposase [Streptococcus pyogenes]	80	70	243
158	2	2474	984	gi 1877423	galactose-1-P-uridylyl transferase [Streptococcus mutans]	80	65	1491
171	10	7474	7728	gi 397800	cyclophilin C-associated protein [Mus musculus]	80	60	255
181	1	2	619	gi 149395	lacC [Lactococcus lactis]	80	66	618
313	1	27	539	gi 143467	ribosomal protein S4 [Bacillus subtilis]	80	70	513
329	2	1652	858	gi 533080	RecP protein [Streptococcus pyogenes]	80	63	795
371	1	2	958	gi 442360	ClpC adenosine triphosphatase [Bacillus subtilis]	80	58	957
8	7	4312	5580	gi 149435	putative [Lactococcus lactis]	79	64	1269
23	1	1175	135	gi 1542975	AbcB [Thermomonas thermophilus]	79	61	1041
33	14	9244	8201	gnl PID e253891	UDP-glucose 4-epimerase [Bacillus subtilis]	79	62	1044
36	3	1242	2633	gnl PID e34218	ftsA [Enterococcus hirae]	79	58	1392
38	13	7155	8378	gi 405134	acetate kinase [Bacillus subtilis]	79	58	1224
55	7	9011	8229	gi 1146234	dihydrodipicolinate reductase [Bacillus subtilis]	79	56	783
65	19	8661	8915	gi 2078380	ribosomal protein L30 [Staphylococcus aureus]	79	68	255
69	4	3678	2128	gnl PID e311452	unknown [Bacillus subtilis]	79	64	1551
69	9	7881	7279	gi 677850	hypothetical protein [Staphylococcus aureus]	79	59	603
72	10	8491	9783	gnl PID d101091	hypothetical protein [Synecocystis sp.]	79	62	1293
80	3	2906	7300	gi 143342	polymerase III [Bacillus subtilis]	79	65	4395
82	14	13326	15689	gnl PID e255093	hypothetical protein [Bacillus subtilis]	79	65	2364
86	13	12233	11118	gi 683582	prephenate dehydrogenase [Lactococcus lactis]	79	58	1116
92	3	940	1734	gi 537286	triosephosphate isomerase [Lactococcus lactis]	79	65	795
98	6	4023	4742	gnl PID d100262	tlvG protein [Salmonella typhimurium]	79	63	720

TABLE 2

S. pneumoniae - Putative coding regions of novel proteins similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)	match accession	match gene name	% sim	% ident	length (nt)
99	12	16315	16150	gi153736	a-galactosidase (Streptococcus mutans)	79	64	2166
107	7	5684	6406	gi1460080	D-alanine:D-alanine ligase-related protein (Enterococcus faecalis)	79	58	723
113	9	6858	8303	gi1466082	ppsl: BL496_C2_189 (Mycobacterium leprae)	79	64	1446
151	10	13424	12213	gi1450686	3-phosphoglycerate kinase (Thermotoga maritima)	79	60	1212
162	2	1158	3017	gi1506700	CapD (Staphylococcus aureus)	79	67	1860
177	5	2876	3052	gi1912423	putative (Lactococcus lactis)	79	61	177
177	8	4198	4363	gi1149429	putative (Lactococcus lactis)	79	61	177
187	3	2728	2907	gnl PID d102002	(AB001488) FUNCTION UNKNOWN. (Bacillus subtilis)	79	61	366
189	7	3589	4350	gnl PID e183449	putative ATP-binding protein of ABC-type (Bacillus subtilis)	79	53	180
191	5	4249	3449	gi1149519	indoleglycerol phosphate synthase (Lactococcus lactis)	79	66	801
211	3	1805	2737	gi1147404	mannose permease subunit II-M-Man (Escherichia coli)	79	57	933
212	3	3863	3621	gnl PID e209004	glutaredoxin-like protein (Lactococcus lactis)	79	58	243
215	1	987	715	gi12293242	(AF008220) arginine succinate synthase (Bacillus subtilis)	79	64	273
323	2	530	781	gi1897795	30S ribosomal protein (Pediococcus acidilactici)	79	67	252
380	1	694	2	gi11184680	polynucleotide phosphorylase (Bacillus subtilis)	79	64	693
384	2	655	239	gi1143328	phoP protein (put.); putative (Bacillus subtilis)	79	59	417
6	3	2820	4091	gi1853767	UDP-N-acetylglucosamine 1-carboxyvinyltransferase (Bacillus subtilis)	78	62	1272
8	1	50	1786	gi1149432	putative (Lactococcus lactis)	78	63	1737
9	1	351	124	gi1897793	y98 gene product (Pediococcus acidilactici)	78	59	228
15	8	7364	8314	gnl PID d100585	cysteine synthetase A (Bacillus subtilis)	78	63	951
20	10	9738	10310	gnl PID d100583	stage V sporulation (Bacillus subtilis)	78	58	573
20	16	17165	17713	gi149105	hypoxanthine phosphoribosyltransferase (Lactococcus lactis)	78	59	549
22	22	17388	18416	gnl PID d101315	yqfE (Bacillus subtilis)	78	60	1029
22	27	20971	20612	gi1299163	alanine dehydrogenase (Bacillus subtilis)	78	59	360
34	8	7407	7105	gi141015	aspartate-tRNA ligase (Escherichia coli)	78	55	303
35	8	6257	5196	gi11657644	Cap8E (Staphylococcus aureus)	78	60	1062

TABLE 2

S. pneumoniae - Putative coding regions of novel proteins similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)	match accession	match gene name	% sim	% ident	length (nt)
40	11	9287	8001	gi 1173518	GTP cyclohydrolase II/ 3,4-dihydroxy-2-butanone-4-phosphate synthase (Actinobacillus pleuropneumoniae)	78	58	1287
46	31	22422	23183	gi 2314330	(AE000623) glutamine ABC transporter, ATP-binding protein (glnQ) (Helicobacter pylori)	78	58	762
52	2	2101	1430	gi 1183887	integral membrane protein (Bacillus subtilis)	78	54	672
55	14	13605	12712	gnl PID d102026	(AB002150) YbbP (Bacillus subtilis)	78	58	894
55	17	16637	15612	gnl PID e313027	hypothetical protein (Bacillus subtilis)	78	51	1026
71	14	19756	19598	gi 179764	calcium channel: alpha-1D subunit (Homo sapiens)	78	57	159
74	11	15031	14018	gi 1573279	Holliday junction DNA helicase (ruvB) (Haemophilus influenzae)	78	57	1014
75	9	6623	7972	gi 1877423	galactose-1-P-uridylyl transferase (Streptococcus mutans)	78	62	1350
81	12	12125	13906	gi 1573607	L-fucose isomerase (fucI) (Haemophilus influenzae)	78	66	1782
82	3	2423	4417	gi 153744	ORF X; putative (Streptococcus mutans)	78	64	1995
83	18	16926	18500	gi 143373	phosphoribosyl aminimidazole carboxy formyl formyltransferase/inosine monophosphate cyclohydrolase (PUR-H(J)) (Bacillus subtilis)	78	63	1575
83	20	20212	20775	gi 143364	phosphoribosyl aminimidazole carboxylase I (PUR-E) (Bacillus subtilis)	78	64	564
92	2	165	878	gnl PID d101190	ORF2 (Streptococcus mutans)	78	62	714
98	8	5863	6909	gi 2331287	(AF013188) release factor 2 (Bacillus subtilis)	78	63	1047
113	3	1071	2741	gi 580914	dnazX (Bacillus subtilis)	78	64	1671
127	4	1133	2071	gi 142463	RNA polymerase alpha-core-subunit (Bacillus subtilis)	78	59	939
132	1	2782	497	gi 1561763	pullulanase (Bacteroides thetaiotaomicron)	78	58	2286
135	4	2698	3537	gi 1788036	(AE000269) NH3-dependent NAD synthetase (Escherichia coli)	78	66	840
140	24	26853	25423	gi 1100077	phospho-beta-glucosidase (Clostridium longisporum)	78	64	1431
150	5	4690	4514	gi 149464	amino peptidase (Lactococcus lactis)	78	42	177
152	1	1	795	gi 639915	NADH dehydrogenase subunit (Thunbergia alata)	78	43	795
162	4	4997	4110	gnl PID e23528	putative YhaP protein (Bacillus subtilis)	78	64	888
181	10	8651	7947	gi 149402	lactose repressor (lacI; alt.) (Lactococcus lactis)	78	48	705
200	4	3627	4958	gnl PID d100172	invertase (Zymomonas mobilis)	78	61	1332
203	3	3230	3015	gi 1174237	CycK (Pseudomonas fluorescens)	78	57	216

TABLE 2

S. pneumoniae - Putative coding regions of novel proteins similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)	match accession	match gene name	% sim	% ident	length (nt)
210	9	6789	7172	gi 580902	ORF6 gene product [Bacillus subtilis]	78	42	384
214	6	3810	2797	gnl pid d102049	P. haemolytica O-sialoglycoprotein endopeptidase; P36175 (660) transmembrane [Bacillus subtilis]	78	60	1014
214	13	6322	8163	gi 1377831	unknown [Bacillus subtilis]	78	62	1842
217	1	9	2717	gi 488430	alcohol dehydrogenase 2 [Entamoeba histolytica]	78	64	2709
222	3	2316	3098	gi 1573047	spore germination and vegetative growth protein (gerC2) [Haemophilus influenzae]	78	65	783
268	1	742	8	gi 517210	putative transposase [Streptococcus pyogenes]	78	65	735
276	1	223	753	gnl pid d100306	ribosomal protein L1 [Bacillus subtilis]	78	65	531
312	3	1567	1079	gi 289261	comE ORF2 [Bacillus subtilis]	78	54	489
339	1	117	794	gi 1916729	Cadd [Staphylococcus aureus]	78	53	678
342	2	762	265	gi 1842439	phosphatidylglycerophosphate synthase [Bacillus subtilis]	78	59	498
383	1	737	3	gi 1184680	polynucleotide phosphorylase [Bacillus subtilis]	78	64	735
7	15	11923	11018	gi 1399855	carboxyltransferase beta subunit [Synecococcus PCC7942]	77	63	906
8	2	1698	2255	gi 149433	putative [Lactococcus lactis]	77	59	558
17	14	6948	7550	gi 520738	comA protein [Streptococcus pneumoniae]	77	60	603
30	12	9761	8967	gi 1000451	Trep [Bacillus subtilis]	77	43	795
36	14	11421	12131	gi 1573766	phosphoglyceromutase (gpmA) [Haemophilus influenzae]	77	64	711
55	3	3836	4096	gi 1708640	YeaB [Bacillus subtilis]	77	55	261
61	8	8377	8054	gi 1890649	multidrug resistance protein LmrA [Lactococcus lactis]	77	51	324
65	2	607	1254	gi 40103	ribosomal protein L4 [Bacillus stearothermophilus]	77	63	648
68	8	7509	7240	gi 47551	MRP [Streptococcus suis]	77	68	270
69	1	1083	118	gnl pid e311493	unknown [Bacillus subtilis]	77	57	966
77	5	4583	4026	gnl pid e281578	hypothetical 12.2 kd protein [Bacillus subtilis]	77	60	558
83	14	13104	14552	gi 1590947	amidophosphoribosyltransferase [Methanococcus jannaschii]	77	56	1449
94	4	3006	5444	gnl pid e329895	(AJ000496) cyclic nucleotide-gated channel beta subunit [Rattus norvegicus]	77	66	2439
96	11	8518	8880	gi 551879	ORF 1 [Lactococcus lactis]	77	62	363
99	11	14082	12799	gi 153737	sugar-binding protein [Streptococcus mutans]	77	61	1284



TABLE 2  
S. pneumoniae - Putative coding regions of novel proteins similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)	match accession	match gene name	% sim	% ident	length (nt)
106	2	361	1176	gi 148921	LicD protein (Haemophilus influenzae)	77	51	816
108	4	3152	4030	gi 1574730	telurite resistance protein (tehB) (Haemophilus influenzae)	77	58	879
118	4	3520	3131	gi 1573900	D-alanine permease (dagA) (Haemophilus influenzae)	77	57	390
124	4	1796	1071	gi 1573162	tRNA (guanine-N1)-methyltransferase (trmD) (Haemophilus influenzae)	77	58	726
126	4	5909	4614	gnl PID d101163	Srb (Bacillus subtilis)	77	62	1296
128	2	630	1373	gnl PID d101328	YqjZ (Bacillus subtilis)	77	58	744
130	1	1	1287	gnl PID e325013	hypothetical protein (Bacillus subtilis)	77	61	1287
139	5	4388	3639	gi 2293302	(AF008220) YtqA (Bacillus subtilis)	77	59	750
140	11	10931	9582	gi 289284	cysteineyl-tRNA synthetase (Bacillus subtilis)	77	64	1350
140	18	19451	19263	gi 517210	putative transposase (Streptococcus pyogenes)	77	66	189
141	2	976	1693	gnl PID e157887	URF5 (aa 1-573) (Drosophila yakuba)	77	50	708
141	4	2735	5293	gi 556258	secA (Listeria monocytogenes)	77	59	2559
144	2	671	2173	gnl PID d100585	lysyl-tRNA synthetase (Bacillus subtilis)	77	61	1503
163	5	6412	7398	gi 511015	dihydroorotate dehydrogenase A (Lactococcus lactis)	77	62	987
164	10	7841	7074	gnl PID d100964	homologue of iron dicitrate transport ATP-binding protein PecE of E. coli (Bacillus subtilis)	77	52	768
191	8	7257	5791	gi 149516	anthranilate synthase alpha subunit (Lactococcus lactis)	77	57	1467
198	8	5377	5177	gi 1573856	hypothetical (Haemophilus influenzae)	77	66	201
213	1	202	462	gi 1743860	Brca2 (Mus musculus)	77	50	261
250	2	231	509	gnl PID e334776	YlbW protein (Bacillus subtilis)	77	60	279
289	3	1737	1276	gnl PID d100947	Ribosome Protein L10 (Bacillus subtilis)	77	62	462
292	2	1399	668	gi 143004	transfer RNA-Gln synthetase (Bacillus stearothermophilus)	77	58	732
7	3	2734	1166	gnl PID d101824	peptide-chain-release factor 3 (Synchocystis sp.)	76	53	1569
7	23	18474	18235	gi 455157	acyl carrier protein (Cryptomonas phi)	76	57	240
9	8	5706	4342	gi 1146247	asparaginyl-tRNA synthetase (Bacillus subtilis)	76	61	1365
10	5	4531	4385	gnl PID e314495	hypothetical protein (Clostridium perfringens)	76	53	147
18	2	1615	842	gi 1591672	phosphate transport system ATP-binding protein (Methanococcus jannaschii)	76	56	774

**TABLE 2**  
S. pneumoniae - Putative coding regions of novel proteins similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)	match accession	match gene name	% sim	% ident	length (nt)
22	37	27796	28173	gnl PID e13389	translation initiation factor IF3 (AA 1-172) [Bacillus stearothermophilus]	76	64	378
35	6	3869	2682	gi 1773346	CapSG [Staphylococcus aureus]	76	61	1188
48	28	21113	21787	gi 2314328	(AE000622) glutamine ABC transporter, permease protein (glnP) [Helicobacter pylori]	76	52	675
52	12	12881	13786	gi 142521	deoxyribodipyrimidine photolyase [Bacillus subtilis]	76	58	906
55	10	11521	10571	gnl PID e283110	femD [Staphylococcus aureus]	76	61	951
57	8	7824	6359	gi 290561	tol188 [Escherichia coli]	76	47	1266
62	5	2406	2095	gnl PID e313024	hypothetical protein [Bacillus subtilis]	76	59	312
65	9	4223	4441	gi 40148	l29 protein (AA 1-66) [Bacillus subtilis]	76	58	219
68	2	1328	2371	gnl PID e284233	anabolic ornithine carbamoyltransferase [Lactobacillus plantarum]	76	61	1044
69	8	7297	6005	gnl PID d101420	Pyrimidine nucleoside phosphorylase [Bacillus stearothermophilus]	76	61	1293
73	12	7839	7267	gnl PID e243629	unknown [Mycobacterium tuberculosis]	76	53	573
74	5	8433	7039	gnl PID d102048	C. thermocellum beta-glucosidase; P26208 (985) [Bacillus subtilis]	76	60	1395
80	5	7643	7936	gi 2314030	(AE000599) conserved hypothetical protein [Helicobacter pylori]	76	61	296
82	15	16019	16996	gi 1573900	D-alanine permease (dagA) [Haemophilus influenzae]	76	56	978
83	19	18616	19884	gi 143374	phosphoribosyl glycinamide synthetase (PUR-D; gtg start codon) [Bacillus subtilis]	76	60	1269
86	14	13409	12231	gi 143806	AroF [Bacillus subtilis]	76	58	1179
87	1	3	1442	gi 153804	sucrose-6-phosphate hydrolase [Streptococcus mutans]	76	59	1440
87	16	15754	15110	gnl PID e323500	putative Gmk protein [Bacillus subtilis]	76	56	645
93	4	1769	1539	gi 1574820	1,4-alpha-glucan branching enzyme (glgB) [Haemophilus influenzae]	76	46	231
94	1	51	365	gi 144313	6.0 kd ORF [Plasmid ColEI]	76	73	315
116	2	2151	1678	gi 153841	pneumococcal surface protein A [Streptococcus pneumoniae]	76	59	474
123	6	3442	5895	gi 1314297	ClpC ATPase [Listeria monocytogenes]	76	59	2454
126	2	2156	2932	gnl PID d101328	Yqiz [Bacillus subtilis]	76	61	777
128	10	6973	7797	gi 944944	purine nucleoside phosphorylase [Bacillus subtilis]	76	60	825
131	11	6186	5812	gi 1674310	(AE000058) Mycoplasma pneumoniae, MG085 homolog, from H. genitalium [Mycoplasma pneumoniae]	76	47	375

**TABLE 2**  
S. pneumoniae - Putative coding regions of novel proteins similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)	match accession	match gene name	% sim	% ident	length (nt)
139	4	3641	3192	gi 2293102	[AF008220] YtqA [Bacillus subtilis]	76	53	450
140	14	14872	12536	gi 1184680	[polynucleotide phosphorylase [Bacillus subtilis]	76	62	2337
143	2	2583	3905	gi 143795	[transfer RNA-Tyr synthetase [Bacillus subtilis]	76	61	1323
170	6	5095	6114	gnl pid d100959	[ycpQ [Bacillus subtilis]	76	44	1020
180	2	1927	557	gi 40019	[ORF 821 (aa 1-821) [Bacillus subtilis]	76	53	1371
191	7	5815	5228	gi 551880	[anthranilate synthase beta subunit [Lactococcus lactis]	76	61	588
195	3	3829	2444	gi 2149905	[D-glutamic acid adding enzyme [Enterococcus faecalis]	76	60	1386
200	3	1914	3629	gi 431272	[lysis protein [Bacillus subtilis]	76	58	1716
201	1	431	207	gi 2208998	[dextran glucosidase DexS [Streptococcus suis]	76	57	225
214	2	1283	2380	gi 663278	[transposase [Streptococcus pneumoniae]	76	55	1098
225	3	2338	3411	gi 1552775	[ATP-binding protein [Escherichia coli]	76	56	1074
233	1	2	724	gi 1163115	[neuraminidase B [Streptococcus pneumoniae]	76	60	723
347	1	523	38	gi 537033	[ORF_356 [Escherichia coli]	76	60	486
356	2	842	165	gi 2149905	[D-glutamic acid adding enzyme [Enterococcus faecalis]	76	61	678
366	3	734	348	gi 149520	[phosphoribosyl anthranilate isomerase [Lactococcus lactis]	76	69	387
5	8	12599	11484	gi 1574293	[fimbrial transcription regulation repressor (pilB) [Haemophilus influenzae]	75	61	1116
6	13	12553	11894	gnl pid d102050	[ydh [Bacillus subtilis]	75	51	660
9	10	7282	6062	gi 142538	[aspartate aminotransferase [Bacillus sp.]	75	55	1221
10	12	8080	7940	gi 149493	[SCRPI methylase [Lactococcus lactis]	75	56	141
18	5	4266	3301	gnl pid d101319	[YggH [Bacillus subtilis]	75	52	966
22	4	1838	2728	gi 1373157	[orf-X; hypothetical protein; Method: conceptual translation supplied by author [Bacillus subtilis]	75	62	891
30	11	9015	7828	gi 153801	[enzyme scr-II [Streptococcus mutans]	75	64	1188
31	5	2362	2030	gi 2293211	[AF008220] putative thioredoxin [Bacillus subtilis]	75	53	333
32	9	7484	8359	gnl pid d100560	[formamidopyrimidine-DNA glycosylase [Streptococcus mutans]	75	61	876
33	4	1735	1448	gi 413976	[ipa-52r gene product [Bacillus subtilis]	75	53	288
33	10	6470	5769	gi 533105	[unknown [Bacillus subtilis]	75	56	702

TABLE 2

S. pneumoniae - Putative coding regions of novel proteins similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)	match accession	match gene name	% sim	% ident	length (nt)
33	12	6878	7183	pir A00205 FECL	ferredoxin (4Fe-4S) - Clostridium thermaceticum	75	56	306
36	1	181	2	gi 2088739	(AF003141) strong similarity to the FAPB/P2/CRBP family of transporters [Caenorhabditis elegans]	75	43	180
38	22	114510	115379	gi 1574058	hypothetical [Haemophilus influenzae]	75	56	870
48	33	23398	24066	gi 1930092	outer membrane protein [Campylobacter jejuni]	75	56	669
51	1	2	319	gi 43985	infs-like gene [Lactobacillus delbrueckii]	75	55	318
51	10	8318	11683	gi 537192	CG Site No. 620; alternate gene names hsp, hsp, har, rmy apparent frameshift in GenBank Accession Number X06545 [Escherichia coli]	75	50	3366
54	18	19366	20759	gi 666069	orf2 gene product [Lactobacillus leichmannii]	75	58	1194
57	9	8448	7822	gi 290561	ol88 [Escherichia coli]	75	50	627
65	14	6072	6356	gi 606241	30S ribosomal subunit protein S14 [Escherichia coli]	75	64	285
70	4	3071	2472	gi 1256617	adenine phosphoribosyltransferase [Bacillus subtilis]	75	57	600
71	24	30399	29404	gi 1574390	C4-dicarboxylate transport protein [Haemophilus influenzae]	75	57	996
73	2	910	455	gnl PID e249656	YneF [Bacillus subtilis]	75	57	456
79	1	1810	491	gi 1146219	28.2% of identity to the Escherichia coli GTP-binding protein Era; putative [Bacillus subtilis]	75	59	1320
82	6	6360	6536	gi 1655715	BatD [Rhodobacter capsulatus]	75	55	177
83	6	1938	2975	gnl PID e323529	putative Plax protein [Bacillus subtilis]	75	56	1038
93	11	7368	5317	gi 39989	methylonyl-tRNA synthetase [Bacillus stearothermophilus]	75	58	2032
93	13	9409	8699	gi 1591493	glutamine transport ATP-binding protein Q [Methanococcus jannaschii]	75	54	711
95	1	1795	47	gnl PID e323510	YioV protein [Bacillus subtilis]	75	57	1749
103	2	362	1186	gnl PID e266928	unknown [Mycobacterium tuberculosis]	75	64	825
104	1	691	915	gi 460026	repressor protein [Streptococcus pneumoniae]	75	54	225
113	5	2951	3883	gnl PID d101119	ABC transporter subunit [Synechocystis sp.]	75	55	933
121	1	320	1390	gi 2145131	repressor of class I heat shock gene expression HrcA [Streptococcus mutans]	75	58	1071
127	6	2614	3000	gi 1500451	M. jannaschii predicted coding region MJ1558 [Methanococcus jannaschii]	75	44	387
137	18	10082	10687	gi 393116	P-glycoprotein 5 [Entamoeba histolytica]	75	52	606
149	11	8499	9338	gnl PID d100582	unknown [Bacillus subtilis]	75	55	840

TABLE 2  
S. pneumoniae - Putative coding regions of novel proteins similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)	match accession	match gene name	% sim	% ident	length (nt)
151	6	9100	7673	gi140467	HsdS polypeptide, part of CfrA family [Citrobacter freundii]	75	57	1428
158	1	986	3	gnl PID e253891	UDP-glucose 4-epimerase [Bacillus subtilis]	75	63	984
172	8	5653	6774	gi142978	glycerol dehydrogenase [Bacillus stearothermophilus]	75	56	1122
172	9	7139	9730	gnl PID e268456	unknown [Mycobacterium tuberculosis]	75	58	2592
173	1	261	79	gnl PID e236469	C10C5.6 [Caenorhabditis elegans]	75	50	183
185	3	3086	2014	gi1574806	spermidine/putrescine transport ATP-binding protein (potA) [Haemophilus influenzae]	75	56	1053
191	6	5235	4213	gi149518	phosphoribosyl anthranilate transferase [Lactococcus lactis]	75	61	1023
226	2	1774	1181	gi12314588	(AE000642) conserved hypothetical protein [Helicobacter pylori]	75	65	594
231	1	1	153	gi140173	homolog of E. coli ribosomal protein L21 [Bacillus subtilis]	75	57	153
234	1	2	418	gi12293259	(AF008220) Ytqi [Bacillus subtilis]	75	59	417
279	1	552	151	gi1119198	unknown protein [Bacillus subtilis]	75	50	402
291	7	3558	3827	gi140011	(ORF17 [AA 1-161] [Bacillus subtilis])	75	48	270
375	2	137	628	gi1410137	(ORF13 [Bacillus subtilis])	75	58	492
6	120	16721	17560	gi12293323	(AF008220) YtdI [Bacillus subtilis]	74	53	840
7	6	4682	6052	gi13354211	PEP112-like protein [Bacillus subtilis]	74	60	1371
18	4	3341	2427	gnl PID d101319	YqgI [Bacillus subtilis]	74	54	915
21	6	5885	4800	gi1072381	glutaryl-aminopeptidase [Lactococcus lactis]	74	59	1086
24	2	739	546	gi12314762	(AE000655) ABC transporter, permease protein (yaeB) [Helicobacter pylori]	74	46	192
25	1	2	367	gnl PID d100932	H2O-forming NADH Oxidase [Streptococcus mutans]	74	63	366
38	18	11432	12964	gi1537034	(ORF_0488 [Escherichia coli])	74	57	1533
48	10	8924	6669	gi1513069	P-type adenosine triphosphatase [Listeria monocytogenes]	74	53	2256
55	11	11964	11401	gnl PID e283110	femD [Staphylococcus aureus]	74	64	564
61	2	1782	427	gi12293216	(AF008220) putative UDP-N-acetylmuramate-alanine ligase [Bacillus subtilis]	74	55	1356
76	10	9414	8065	gnl PID d101325	YqjB [Bacillus subtilis]	74	54	1350
83	2	666	926	pir C33496 C334	hisc homolog - Bacillus subtilis	74	55	261
86	9	8985	8080	gi1683585	prephenate dehydratase [Lactococcus lactis]	74	55	906

TABLE 2

S. pneumoniae - Putative coding regions of novel proteins similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)	match accession	match gene name	% sim	% ident	length (nt)
102	5	5005	5652	gi 141394	OMP-PRP transferase (Bacillus subtilis)	74	57	648
103	5	4364	3267	gnl PID e323524	YloN protein (Bacillus subtilis)	74	62	1098
108	7	6864	7592	gnl PID e257631	methyltransferase (Lactococcus lactis)	74	56	729
131	2	478	146	gnl PID d101320	YggZ (Bacillus subtilis)	74	45	333
133	2	1380	919	gnl PID e313025	hypothetical protein (Bacillus subtilis)	74	60	462
137	9	6167	6787	gnl PID d100479	Na <sup>+</sup> -ATPase subunit D (Enterococcus hirae)	74	53	621
149	4	3008	3883	gnl PID d100581	high level kasamycin resistance (Bacillus subtilis)	74	55	876
157	2	243	824	gi 1573373	methylated-DNA--protein-cysteine methyltransferase (dat1) (Haemophilus influenzae)	74	48	582
164	6	3515	4249	gi 1410131	OREX7 (Bacillus subtilis)	74	48	735
167	7	3446	5201	gi 1413927	lipa-3r gene product (Bacillus subtilis)	74	55	246
171	1	1	1818	gnl PID d102231	beta-galactosidase (Bacillus circulans)	74	62	1818
172	4	1064	2392	gi 1466474	cellobiose phosphotransferase enzyme II'' (Bacillus stearothermophilus)	74	50	1329
185	1	326	3	gi 1573646	Mg(2+) transport ATPase protein C (mgTC) (SP:P22037) (Haemophilus influenzae)	74	68	324
188	2	1089	2018	gi 1573008	ATP dependent translocator homolog (asbA) (Haemophilus influenzae)	74	44	930
189	11	6491	7174	gi 1661199	sakacin A production response regulator (Streptococcus mutans)	74	60	684
210	2	520	1287	gi 2293207	(AF008220) YmoQ (Bacillus subtilis)	74	60	768
261	1	836	192	gi 666983	putative ATP binding subunit (Bacillus subtilis)	74	55	645
263	3	1619	3655	gi 663232	similarity with S. cerevisiae hypothetical 137.7 kD protein in subtelomeric Y' repeat region (Saccharomyces cerevisiae)	74	42	2037
265	2	844	1227	gi 49272	Asparaginase (Bacillus licheniformis)	74	64	384
368	1	1	942	gi 603998	unknown (Saccharomyces cerevisiae)	74	39	942
7	16	13357	11921	gnl PID d101324	YqhX (Bacillus subtilis)	73	57	1437
17	10	5706	5449	gnl PID e305362	unnamed protein product (Streptococcus thermophilus)	73	47	258
31	2	522	244	gnl PID d100576	single strand DNA binding protein (Bacillus subtilis)	73	55	279
32	6	5667	6194	gnl PID d101315	YqfG (Bacillus subtilis)	73	58	528
34	15	10281	9790	gnl PID d102151	(AB001684) ORF42c (Clostridia vulgaris)	73	46	492

TABLE 2  
S. pneumoniae - Putative coding regions of novel proteins similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)	match accession	match gene name	% sim	% ident	length (nt)
40	12	9876	9226	gi 1173517	riboflavin synthase alpha subunit [Actinobacillus pleuropneumoniae]	73	55	651
55	2	3592	839	gnl pid d101887	[cation-transporting ATPase PacL [Synecocystis sp.]	73	60	2754
55	18	17494	16586	gnl pid e265580	unknown [Mycobacterium tuberculosis]	73	52	909
65	16	7213	7767	gi 143419	ribosomal protein L6 [Bacillus stearothermophilus]	73	60	555
66	3	3300	3659	gnl pid e269883	LacP [Lactobacillus casei]	73	52	360
70	10	5557	5733	gi 857631	envelope protein [Human immunodeficiency virus type 1]	73	60	177
71	4	6133	8262	gnl pid e322063	ss-1,4-galactosyltransferase [Streptococcus pneumoniae]	73	45	2130
72	1	3	851	gi 2293177	[AF008220] transporter [Bacillus subtilis]	73	50	849
76	7	7019	6195	gnl pid d101325	YqjF [Bacillus subtilis]	73	66	825
76	12	10009	9533	gi 1573086	uridine kinase [uridine monophosphokinase] (udk) [Haemophilus influenzae]	73	54	477
80	7	8113	9372	gi 1377823	aminopeptidase [Bacillus subtilis]	73	60	1260
97	5	3389	1668	gnl pid d101954	dihydroxyacid dehydratase [Synecocystis sp.]	73	54	1722
98	9	6912	7619	gnl pid e314991	FtsE [Mycobacterium tuberculosis]	73	54	708
108	11	10928	10440	gi 388109	regulatory protein [Enterococcus faecalis]	73	54	489
128	6	3632	4222	gi 1685111	orf1091 [Streptococcus thermophilus]	73	63	591
138	2	1575	394	gi 147326	transport protein [Escherichia coli]	73	60	1182
140	13	12538	11903	pir e53402 E534	serine O-acetyltransferase (EC 2.3.1.30) - Bacillus stearothermophilus	73	55	636
162	5	5701	4991	gnl pid e323511	putative yhaQ protein [Bacillus subtilis]	73	50	711
164	4	2323	2790	gi 1592076	hypothetical protein (SP:P25768) [Methanococcus jannaschii]	73	52	468
164	8	4815	5546	gi 410137	ORFX13 [Bacillus subtilis]	73	56	732
170	5	4394	5302	gnl pid d100959	homologue of unidentified protein of E. coli [Bacillus subtilis]	73	46	909
178	7	3893	4855	gi 46242	modulation protein B, 5'end [Rhizobium loti]	73	56	963
204	6	5096	4278	gnl pid e214719	PICR protein [Bacillus thuringiensis]	73	41	819
213	2	832	2037	gi 1565296	ribosomal protein S1 homologue; sequence specific DNA-binding protein [Leuconostoc lactis]	73	55	1206
231	2	84	287	gi 40173	homolog of E. coli ribosomal protein L21 [Bacillus subtilis]	73	61	204
237	1	2	505	gi 1773151	adenine phosphoribosyltransferase [Escherichia coli]	73	51	504

TABLE 2

S. pneumoniae - Putative coding regions of novel proteins similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)	match accession	match gene name	% sim	% ident	length (nt)
269	1	2	691	gnl pid d101328	YgiX [Bacillus subtilis]	73	36	690
289	2	1272	832	pir A02771 R7WC	ribosomal protein L7/L12 - Micrococcus luteus	73	66	441
343	1	14	484	gi 1788125	(AE000276) hypothetical 30.4 kD protein in manZ-cspC intergenic region [Escherichia coli]	73	47	471
356	1	222	4	gi 2149905	D-glutamic acid adding enzyme [Enterococcus faecalis]	73	50	219
7	5	3165	4691	gnl pid d101833	amidase [Synecocystis sp.]	72	52	1527
7	9	7195	7647	gi 146976	musB [Escherichia coli]	72	54	453
7	17	13743	13300	gnl pid e289141	similar to hydroxymyristoyl-(acyl carrier protein) dehydratase [Bacillus subtilis]	72	59	444
22	19	15637	16224	gnl pid d101929	ribosome releasing factor [Synecocystis sp.]	72	51	588
33	17	12111	11425	gnl pid d101190	ORF3 [Streptococcus mutans]	72	55	687
34	7	7147	5627	gi 396501	aspartyl-tRNA synthetase [Thermus thermophilus]	72	52	1521
38	23	15372	16085	pir H64108 H641	L-ribulose-phosphate 4-epimerase (araD) homolog - Haemophilus influenzae (strain Rd RW20)	72	54	714
39	5	5094	6905	gnl pid e254877	unknown [Mycobacterium tuberculosis]	72	56	1812
40	6	4469	4636	gi 153672	lactose repressor [Streptococcus mutans]	72	58	168
48	2	1459	1253	gi 310380	inhibin beta-A-subunit [Ovis aries]	72	33	207
48	29	21729	22424	gi 2314329	(AE000623) glutamine ABC transporter, permease protein (glnP) [Helicobacter pylori]	72	49	696
50	5	4529	3288	gi 1750108	YnbA [Bacillus subtilis]	72	54	1242
51	3	1044	2282	gi 2293230	(AF008220) YcbJ [Bacillus subtilis]	72	54	1239
52	13	13681	13938	gi 142521	deoxyribodipyrimidine photolyase [Bacillus subtilis]	72	45	258
55	1	841	35	gi 882518	ORF_0304; GTG start [Escherichia coli]	72	59	807
75	5	2832	3191	gnl pid e209866	mercuric resistance operon regulatory protein [Bacillus subtilis]	72	44	360
76	6	6229	5771	gi 142450	ahrC protein [Bacillus subtilis]	72	53	459
79	5	5065	4592	gi 2293279	(AF008220) YtcG [Bacillus subtilis]	72	46	474
87	14	14726	12309	gnl pid e323502	putative P1A protein [Bacillus subtilis]	72	52	2418
91	1	444	662	gi 500691	MYO1 gene product [Saccharomyces cerevisiae]	72	50	219
91	7	4516	4764	gi 829615	skeletal muscle sodium channel alpha-subunit [Equus caballus]	72	38	249



TABLE 2  
S. pneumoniae - Putative coding regions of novel proteins similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)	match accession	match gene name	% sim	% ident	length (nt)
95	2	2004	1717	gnl PID e323527	putative Asp23 protein [Bacillus subtilis]	72	40	288
109	1	1452	118	gi 143331	alkaline phosphatase regulatory protein [Bacillus subtilis]	72	52	1335
126	1	3	2192	gnl PID d101831	glutamine-binding periplasmic protein [Synechocystis sp.]	72	46	2190
130	3	1735	2478	gi 2415396	[AF015775] carboxypeptidase [Bacillus subtilis]	72	53	744
137	6	2585	2929	gi 472922	v-type Na-ATPase [Enterococcus hirae]	72	46	345
140	10	9601	9203	gi 49224	[URP 4] [Synechococcus sp.]	72	48	399
146	5	1906	1247	gnl PID e324945	hypothetical protein [Bacillus subtilis]	72	45	660
147	2	2084	1083	gnl PID e325016	hypothetical protein [Bacillus subtilis]	72	56	1002
147	5	6156	5146	gi 472327	TPP-dependent acetoin dehydrogenase beta-subunit [Clostridium magnum]	72	56	1011
148	8	5381	6433	gi 974332	NAD(P)H-dependent dihydroxyacetone-phosphate reductase [Bacillus subtilis]	72	54	1053
148	14	10256	9675	gnl PID d101319	YqgN [Bacillus subtilis]	72	50	582
159	8	4005	4949	gi 1788770	[AE000310] o463; 24 pct identical (44 gaps) to 338 residues from penicillin-binding protein 4", PBPE_BACSU SW: P32959 (451 aa) [Escherichia coli]	72	43	945
172	10	9907	10620	gi 763387	unknown [Saccharomyces cerevisiae]	72	55	714
220	3	2862	1602	gi 1574175	hypothetical [Haemophilus influenzae]	72	50	741
267	1	3	449	gi 290513	[470] [Escherichia coli]	72	48	447
281	2	899	540	gnl PID d100964	homologue of aspartokinase 2 alpha and beta subunits LysC of B. subtilis [Bacillus subtilis]	72	45	360
290	1	1018	14	gi 474195	This ORF is homologous to a 40.0 kd hypothetical protein in the htrB 3' region from E. coli, Accession Number X61000 (Mycoplasma-like organism)	72	54	1005
300	1	63	587	gi 746399	transcription elongation factor [Escherichia coli]	72	50	525
316	1	1326	4	gi 158127	protein kinase C [Drosophila melanogaster]	72	40	1323
342	1	227	3	gnl PID d101164	unknown [Bacillus subtilis]	72	54	225
354	1	1	1005	gnl PID d102048	C. thermocellum beta-glucosidase; P26208 (985) [Bacillus subtilis]	72	52	1005
6	10	8134	10467	gnl PID e264229	unknown [Mycobacterium tuberculosis]	71	57	2334
7	20	16231	15464	gi 18046	[3-oxoacyl-(acyl-carrier protein) reductase [Cuphea lanceolata]	71	52	768
15	1	1297	2	gnl PID d100571	replicative DNA helicase [Bacillus subtilis]	71	51	1296
15	4	4435	3869	gi 499384	[orf189] [Bacillus subtilis]	71	47	567

S. pneumoniae - Putative coding regions of novel proteins similar to known proteins

TABLE 2

Contig ID	ORF ID	Start (nt)	Stop (nt)	match accession	match gene name	% sim	% ident	length (nt)
18	6	5120	4218	gnl PID d101318	YqgG [Bacillus subtilis]	71	51	903
29	1	1	540	gi 1773142	similar to the 20.2kd protein in TETB-EXOA region of B. subtilis [Escherichia coli]	71	56	540
38	20	13327	113830	gi 537036	ORF_0158 [Escherichia coli]	71	48	504
51	12	15015	12676	gi 149528	dipeptidyl peptidase IV [Lactococcus lactis]	71	55	2340
55	23	21040	20585	gi 2343285	[AF015453] surface located protein [Lactobacillus rhamnosus]	71	58	456
60	2	705	265	gnl PID d101320	YqgZ [Bacillus subtilis]	71	44	441
71	18	24679	26226	gi 580920	rodD (gtA) polypeptide (AA 1-673) [Bacillus subtilis]	71	44	1548
71	25	30587	30360	gi 606028	ORF_0414; Geneplot suggests frameshift near start but none found [Escherichia coli]	71	50	228
72	6	5239	6729	gi 580835	lysine decarboxylase [Bacillus subtilis]	71	48	1491
72	14	11991	12878	gi 624085	similar to rat beta-alanine synthetase encoded by GenBank Accession Number S27881; contains ATP/GTP binding motif [Paramacium buraria Chlorella virus 1]	71	54	888
73	11	7269	7033	gi 1906594	PN1 [Rattus norvegicus]	71	42	237
74	6	10385	8517	gi 1573733	prolyl-tRNA synthetase (proS) [Haemophilus influenzae]	71	52	1869
81	9	5772	6578	gi 147404	mannose permease subunit II-N-Man [Escherichia coli]	71	45	807
86	5	4602	3604	gnl PID e322063	ss-1,4-galactosyltransferase [Streptococcus pneumoniae]	71	53	999
105	4	3619	4707	gi 2323341	[AF014460] PepQ [Streptococcus mutans]	71	58	1089
106	13	13557	12955	gi 1519287	Lema [Listeria monocytogenes]	71	48	603
114	2	1029	1979	gi 310303	mosA [Rhizobium meliloti]	71	55	951
122	2	564	1205	gi 1649037	glutamine transport ATP-binding protein GLNQ [Salmonella typhimurium]	71	50	642
132	5	9018	7063	gnl PID d102049	H. influenzae hypothetical ABC transporter; P44808 (774) [Bacillus subtilis]	71	51	1956
140	1	1141	227	gi 1673788	(AB000015) Mycoplasma pneumoniae, fructose-bisphosphate aldolase; similar to Swiss-Prot Accession Number P13243, from B. subtilis [Mycoplasma pneumoniae]	71	49	915
140	5	5635	4973	gnl PID d100964	homologue of hypothetical protein in a rapamycin synthesis gene cluster of Streptomyces hygroscopicus [Bacillus subtilis]	71	48	663
141	7	7369	7845	gnl PID d102005	(AB001488) FUNCTION UNKNOWN, SIMILAR PRODUCT IN S. COLI AND MYCOPLASMA PNEUMONIAE. [Bacillus subtilis]	71	51	477

TABLE 2

S. pneumoniae - Putative coding regions of novel proteins similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)	match accession	match gene name	% sim	% ident	length (nt)
193	1	1	165	gi 46912	ribosomal protein L13 [Staphylococcus carnosus]	71	59	165
194	3	2205	1594	gi 535351	CodY [Bacillus subtilis]	71	52	612
199	3	1510	1319	gi 2182574	[AE000090] Y4pE [Rhizobium sp. NGR234]	71	45	192
208	2	2616	3752	gi 1787378	[AE000213] hypothetical protein in purB 5' region [Escherichia coli]	71	57	1137
209	2	2022	1141	gi 41432	sepC gene product [Escherichia coli]	71	46	882
210	5	1911	3071	gi 49316	ORF2 gene product [Bacillus subtilis]	71	45	1161
210	6	3069	3386	gi 580900	ORF3 gene product [Bacillus subtilis]	71	48	318
212	2	3561	1381	gi 557567	ribonucleotide reductase R1 subunit [Mycobacterium tuberculosis]	71	53	2181
233	3	2003	2920	gm PID d101320	YqgR [Bacillus subtilis]	71	50	918
244	1	13	1053	gm PID d100964	homologue of aspartokinase 2 alpha and beta subunits LysC of B. subtilis [Bacillus subtilis]	71	55	1041
251	2	1008	1874	gi 755601	unknown [Bacillus subtilis]	71	46	867
282	2	906	712	gi 1353874	unknown [Rhodospirillum rubrum]	71	46	195
312	4	2137	1565	gm PID d102245	[AB005554] yxBF [Bacillus subtilis]	71	34	573
338	1	3	683	gi 1591045	hypothetical protein (SP:P31466) [Methanococcus jannaschii]	71	48	681
346	1	3	164	gi 1591234	hypothetical protein (SP:P42297) [Methanococcus jannaschii]	71	36	162
374	1	619	2	gi 397526	clumping factor [Staphylococcus aureus]	71	23	618
377	1	688	2	gi 397526	clumping factor [Staphylococcus aureus]	71	23	687
3	8	7419	6958	gm PID e269486	unknown [Bacillus subtilis]	70	42	462
3	10	8395	9075	gm PID e255543	putative iron dependant repressor [Staphylococcus epidermidis]	70	46	681
7	14	11024	10254	gm PID d100290	undefined open reading frame [Bacillus stearothermophilus]	70	55	771
7	18	14213	13719	gm PID d101090	biotin carboxyl carrier protein of acetyl-CoA carboxylase [Synchocystis sp.]	70	56	495
9	2	1057	287	gm PID d100581	unknown [Bacillus subtilis]	70	52	771
12	4	2610	1789	gm PID d101195	yycJ [Bacillus subtilis]	70	52	822
21	2	2586	1846	gi 2293447	[AF008930] ATPase [Bacillus subtilis]	70	54	741
22	13	10955	11512	gi 1165295	Ydr50cp [Saccharomyces cerevisiae]	70	50	558
30	6	4315	3980	gi 39478	ATP binding protein of transport ATPases [Bacillus firmus]	70	51	336

TABLE 2  
S. pneumoniae - Putative coding regions of novel proteins similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)	match accession	match gene name	% sim	% ident	length (nt)
31	1	370	113	gi 662792	single-stranded DNA binding protein (unidentified eubacterium)	70	36	258
33	15	10639	9521	gi 1161219	homologous to D-amino acid dehydrogenase enzyme (Pseudomonas aeruginosa)	70	50	1119
38	6	3812	4312	gi 2058547	ComYD (Streptococcus gordonii)	70	48	501
38	25	17986	18477	gi 537033	ORF_4356 (Escherichia coli)	70	58	492
40	13	11054	9846	gi 1173516	riboflavin-specific deaminase (Actinobacillus pleuropneumoniae)	70	52	1209
42	2	722	1954	gi 1146183	putative (Bacillus subtilis)	70	51	1233
43	3	2373	1612	gi 1591493	glutamine transport ATP-binding protein Q (Methanococcus jannaschii)	70	48	762
45	8	9197	8049	gnl PID d102036	subunit of ADP-glucose pyrophosphorylase (Bacillus stearothermophilus)	70	54	1149
59	2	567	956	gnl PID d100302	neopullulanase (Bacillus sp.)	70	42	390
60	3	1874	795	gnl PID e276466	aminopeptidase P (Lactococcus lactis)	70	48	1080
61	4	5553	2437	gnl PID e275074	SNF (Bacillus cereus)	70	51	3117
61	7	7914	6802	gi 1573037	cystathionine gamma-synthase (metB) (Haemophilus influenzae)	70	52	1113
63	7	5372	7222	gnl PID d100974	unknown (Bacillus subtilis)	70	54	1851
68	7	7126	6962	gi 1263014	emm18.1 gene product (Streptococcus pyogenes)	70	37	165
72	12	10081	10911	gi 2313093	(AE000524) carboxymoraximidine decarboxylase (nspC) (Helicobacter pylori)	70	56	831
75	10	7888	8124	gi 1877423	galactose-1-P-uridylyl transferase (Streptococcus mutans)	70	59	237
79	3	3424	2525	gi 39881	ORF 311 (AA 1-311) (Bacillus subtilis)	70	47	900
87	10	9369	7124	gnl PID e323506	putative Pkn2 protein (Bacillus subtilis)	70	52	2046
96	14	10640	11788	gi 1573209	tRNA-guanine transglycosylase (tgt) (Haemophilus influenzae)	70	52	1149
113	2	574	1086	gi 433630	A180 (Saccharomyces cerevisiae)	70	59	513
123	5	2901	3461	gnl PID d100585	unknown (Bacillus subtilis)	70	45	561
125	5	4593	4282	gnl PID e276474	capacitative calcium entry channel 1 (Bos taurus)	70	35	312
129	5	4500	3454	gnl PID d101314	Yqer (Bacillus subtilis)	70	47	1047
133	3	2608	1394	gi 2293312	(AF008220) Ytfp (Bacillus subtilis)	70	50	1215
135	1	420	662	gnl PID e265530	Yorfe (Streptococcus pneumoniae)	70	47	243
137	3	438	932	gi 472919	v-type Na-ATPase (Enterococcus hirae)	70	57	495
138	1	440	3	gi 147336	transmembrane protein (Escherichia coli)	70	42	438

TABLE 2

S. pneumoniae - Putative coding regions of novel proteins similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)	match accession	match gene name	% sim	% ident	length (nt)
140	16	18796	16364	gi 976441	N5-methyltetrahydrofolate homocysteine methyltransferase (Saccharomyces cerevisiae)	70	53	2433
167	10	8263	6695	gi 149535	D-alanine activating enzyme [Lactobacillus casei]	70	52	1569
204	4	3226	2747	gnl pid d102049	E. coli hypothetical protein; P31805 (267) (Bacillus subtilis)	70	51	480
207	3	2627	2869	gnl pid e309213	racGAP [Dictyostelium discoideum]	70	45	243
282	3	1136	882	gi 1353874	unknown [Rhodobacter capsulatus]	70	50	255
6	21	17554	18453	gnl pid e233879	hypothetical protein [Bacillus subtilis]	69	44	900
6	22	18482	19471	gi 580883	ipa-88d gene product [Bacillus subtilis]	69	53	990
22	6	4682	5824	gi 2209379	[AF006720] ProJ [Bacillus subtilis]	69	48	1143
22	9	7992	8651	gnl pid d100580	unknown [Bacillus subtilis]	69	51	660
22	12	9871	10767	gnl pid d100581	unknown [Bacillus subtilis]	69	51	897
27	7	5857	5348	gnl pid d102012	[AB001488] FUNCTION UNKNOWN. [Bacillus subtilis]	69	28	510
36	10	7294	10116	gi 437916	iso-leucyl-tRNA synthetase [Staphylococcus aureus]	69	53	2823
38	1	2	1090	gi 141900	alcohol dehydrogenase (EC 1.1.1.1) [Alcaligenes eutrophus]	69	48	1089
40	14	11333	11944	gi 1573280	Holliday junction DNA helicase (ruva) [Haemophilus influenzae]	69	44	612
40	15	11942	12517	gi 1573653	DNA-3-methyladenine glycosidase 1 (tagI) [Haemophilus influenzae]	69	50	576
45	6	6947	5490	gi 580887	starch (bacterial glycogen) synthase [Bacillus subtilis]	69	47	1458
48	34	24932	24153	gnl pid e233870	hypothetical protein [Bacillus subtilis]	69	36	780
49	6	6183	6521	gi 396297	similar to phosphotransferase system enzyme II [Escherichia coli]	69	50	339
49	8	7586	8338	gi 396420	similar to Alcaligenes eutrophus ptkG D-ribulose-5-phosphate 3 epimerase [Escherichia coli]	69	49	753
55	6	8262	7033	gi 1146238	poly(A) polymerase [Bacillus subtilis]	69	50	1230
59	3	954	2333	gnl pid e313038	hypothetical protein [Bacillus subtilis]	69	54	1380
62	3	1170	1418	gnl pid d101915	hypothetical protein [Synecocystis sp.]	69	49	249
63	8	7298	7762	gi 293017	ORF3 (put.); putative [Lactococcus lactis]	69	42	465
66	4	3657	5081	gi 153755	phospho-beta-D-galactosidase (EC 3.2.1.85) [Lactococcus lactis cremoris]	69	49	1425
66	5	5126	6829	gi 433809	enzyme II [Streptococcus mutans]	69	46	1704
71	6	10017	10664	gnl pid e322063	as-1.4-galactosyltransferase [Streptococcus pneumoniae]	69	39	648

TABLE 2  
S. pneumoniae - Putative coding regions of novel proteins similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)	match accession	match gene name	% sim	% ident	length (nt)
71	21	27730	27966	gnl PID d100649	OE-cadherin (Drosophila melanogaster)	69	30	237
77	1	1	237	gi 287870	groES gene product [Lactococcus lactis]	69	44	237
81	5	3622	4101	gi 1573605	fucose operon protein (fucU) [Haemophilus influenzae]	69	52	480
83	1	40	714	psl C33496 C334	hisc homolog - Bacillus subtilis	69	46	675
83	16	15742	16335	gi 143372	phosphoribosyl glycineamide formyltransferase (PUR-N) [Bacillus subtilis]	69	46	594
85	2	1212	916	gi 194097	IFN-response element binding factor 1 [Mus musculus]	69	48	297
91	5	3678	4274	gi 1574712	anaerobic ribonucleoside-triphosphate reductase activating protein (nrdo)	69	44	597
98	5	3247	4032	gnl PID d100262	LivP protein (Salmonella typhimurium)	69	51	786
108	5	4085	5056	gnl PID e257629	transcription factor [Lactococcus lactis]	69	49	972
126	3	3078	4568	gnl PID d101329	YqjJ [Bacillus subtilis]	69	49	1491
131	6	4121	2889	gnl PID d101314	Yqer [Bacillus subtilis]	69	47	1233
136	2	1505	2299	gnl PID d100581	unknown [Bacillus subtilis]	69	47	795
149	5	3852	4763	gnl PID e323525	YioQ protein [Bacillus subtilis]	69	50	912
149	12	9336	10655	gi 151571	Homology with E. coli and P. aeruginosa lysA gene; product of unknown function; putative (Pseudomonas syringae)	69	52	1320
153	4	3191	3829	gi 1710373	BrnQ [Bacillus subtilis]	69	44	639
169	3	849	2324	gnl PID d100582	temperature sensitive cell division [Bacillus subtilis]	69	49	1476
180	1	566	3	gi 488139	alpha-amylase [unidentified cloning vector]	69	50	564
212	1	1196	231	gi 1395209	ribonucleotide reductase R2-2 small subunit [Mycobacterium tuberculosis]	69	53	966
226	1	2	661	pir JQ2285 JQ22	modulin-26 - soybean	69	41	660
233	5	3249	4766	gi 472918	v-type Na-ATPase [Enterococcus hirae]	69	56	1518
235	3	660	1766	gi 146945	methylase [Haemophilus influenzae]	69	43	1107
243	2	865	2361	gnl PID d100225	ORF5 [Barley yellow dwarf virus]	69	69	1497
251	3	2899	1967	gi 2289231	macrolide-efflux protein [Streptococcus agalactiae]	69	51	933
310	1	1	282	gnl PID e322442	peptide deformylase [Clostridium beijerinckii]	69	55	282
369	1	868	2	gi 397526	clumping factor [Staphylococcus aureus]	69	22	867
370	1	749	3	gi 397526	clumping factor [Staphylococcus aureus]	69	21	747

TABLE 2  
S. pneumoniae - Putative coding regions of novel proteins similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)	match accession	match gene name	% sim	% ident	length (nt)
379	1	44	280	gnl PID d100649	DG-cadherin ( <i>Drosophila melanogaster</i> )	69	30	237
388	1	260	72	gi 1767524	(AE000223) hypothetical 32.7 kD protein in trpL-btuR intergenic region [ <i>Escherichia coli</i> ]	69	44	189
1	2	2006	3040	gnl PID d101809	ABC transporter [ <i>Synechocystis</i> sp.]	68	43	1035
12	5	3958	2600	gi 2182992	histidine kinase ( <i>Lactococcus lactis cremoris</i> )	68	45	1359
15	2	1790	1311	pir S16974 RSBS	ribosomal protein L9 - <i>Bacillus stearothermophilus</i>	68	56	480
16	6	7333	5701	gi 1787041	(AE000184) o530; This 530 aa orf is 33 pct identical (14 gaps) to 525 residues of an approx. 640 aa protein YHE5_HAEIN SW: P44808 [ <i>Escherichia coli</i> ]	68	45	1653
17	12	6479	6805	gi 553165	acetylcholinesterase ( <i>Homo sapiens</i> )	68	68	327
20	13	14128	14505	gi 142700	P competence protein (ttg start codon) (put.); putative [ <i>Bacillus subtilis</i> ]	68	40	378
22	32	24612	25397	gi 289262	comE ORF3 [ <i>Bacillus subtilis</i> ]	68	36	786
30	7	4548	4288	gi 311388	ORF1 ( <i>Azorhizobium caulinodans</i> )	68	46	261
36	5	3911	4585	gi 1573041	hypothetical ( <i>Haemophilus influenzae</i> )	68	54	675
46	6	5219	6040	gi 1790131	(AE000446) hypothetical 29.7 kD protein in lbpA-gyrB intergenic region [ <i>Escherichia coli</i> ]	68	47	822
54	10	6235	7086	gi 882579	CG Site No. 29739 [ <i>Escherichia coli</i> ]	68	55	852
55	5	7069	5165	gnl PID d101914	ABC transporter [ <i>Synechocystis</i> sp.]	68	45	1905
71	3	6134	5613	gi 1573353	outer membrane integrity protein (tolA) ( <i>Haemophilus influenzae</i> )	68	50	522
71	10	15342	16613	gi 580866	ipa-12d gene product [ <i>Bacillus subtilis</i> ]	68	31	1272
71	12	17560	18792	gi 44073	SecY protein [ <i>Lactococcus lactis</i> ]	68	35	1233
71	17	22295	24703	gi 1762349	involved in protein export [ <i>Bacillus subtilis</i> ]	68	50	2409
73	16	10208	9729	gi 1353537	dUTPase ( <i>Bacteriophage rit</i> )	68	51	480
86	18	17198	16011	gi 413943	ipa-19d gene product [ <i>Bacillus subtilis</i> ]	68	53	1188
87	17	17491	15866	gi 150209	ORF 1 [ <i>Mycoplama mycoides</i> ]	68	43	1626
89	6	5139	4354	gi 1498824	M. jamaehii predicted coding region MJ0062 ( <i>Methanococcus jamaehii</i> )	68	40	786
89	11	8021	8242	gi 150974	4-oxalocrotonate tautomerase ( <i>Pseudomonas putida</i> )	68	43	222
97	8	6755	5394	gi 2367358	(AE000491) hypothetical 52.9 kD protein in sldB-rpsF intergenic region [ <i>Escherichia coli</i> ]	68	41	1362

TABLE 2

S. pneumoniae - Putative coding regions of novel proteins similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)	match accession	match gene name	% sim	% ident	length (nt)
98	3	1418	2308	gnl pid d100261	Liva protein [Salmonella typhimurium]	68	40	891
99	13	16414	17280	gi 455363	regulatory protein [Streptococcus mutans]	68	50	867
115	3	5054	3693	gi 466474	cellobiose phosphotransferase enzyme II' [Bacillus stearothermophilus]	68	44	1362
124	7	3394	3221	gnl pid d100702	cutl4 protein [Schizosaccharomyces pombe]	68	56	174
125	2	2923	1922	gi 450566	transmembrane protein [Bacillus subtilis]	68	50	1002
132	2	4858	2888	gnl pid d101732	DNA ligase [Synechocystis sp.]	68	52	1971
140	7	7765	7580	gi 1209711	unknown [Saccharomyces cerevisiae]	68	47	186
150	1	539	3	gi 402490	ADP-ribosylarginine hydrolase [Mus musculus]	68	59	537
164	1	58	867	gnl pid e255114	glutamate racemase [Bacillus subtilis]	68	49	810
164	2	819	1835	gnl pid e255117	hypothetical protein [Bacillus subtilis]	68	50	1017
169	7	3946	4104	pir 854545 8545	hypothetical protein - Lactococcus lactis subsp. lactis plasmid pSL2	68	40	159
170	4	4247	4396	gi 304146	spore coat protein [Bacillus subtilis]	68	52	150
171	8	6002	7034	gi 38722	precursor (aa -20 to 381) [Acinetobacter calcoaceticus]	68	54	1053
198	3	2473	1871	gnl pid e313075	hypothetical protein [Bacillus subtilis]	68	46	603
211	2	969	1802	gi 1439528	EFIC-man [Lactobacillus curvatus]	68	45	834
214	8	4926	4231	gnl pid d102049	H. influenzae hypothetical protein; P43990 (182) [Bacillus subtilis]	68	50	696
217	6	4955	5170	gnl pid e326966	similar to B. vulgaris CMS-associated mitochondrial ... (reverse transcriptase) [Arabidopsis thaliana]	68	36	216
218	7	3930	4745	gi 2293198	(AF008220) Ytgp [Bacillus subtilis]	68	38	816
220	6	4628	4338	gnl pid e325791	(AJ000005) orf1 [Bacillus megaterium]	68	51	291
236	1	746	108	gi 410137	ORFX13 [Bacillus subtilis]	68	46	639
237	2	675	1451	gi 396348	homoserine transuccinylase [Escherichia coli]	68	49	777
250	4	771	1229	gi 310859	ORF2 [Synechococcus sp.]	68	50	459
254	1	517	155	gi 1787105	(AE000189) 0648 was 0669; This 669 aa orf is 40 pct identical (1 gaps) to 217 residues of an approx. 232 aa protein YBBA_HAEIN SW: P45247 [Escherichia coli]	68	44	363
337	1	1	774	gnl pid e261990	putative orf [Bacillus subtilis]	68	47	774
345	1	3	653	gi 149513	chymidylate synthase (EC 2.1.1.45) [Lactococcus lactis]	68	61	651



TABLE 2  
S. pneumoniae - Putative coding regions of novel proteins similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)	match accession	match gene name	% sim	% ident	length (nt)
386	2	417	4	gi1573353	outer membrane integrity protein (tolA) (Haemophilus influenzae)	68	51	414
2	4	5722	4897	gi1592141	M. jannaschii predicted coding region MJ1507 (Methanococcus jannaschii)	67	26	1026
3	6	5397	4591	gi12293175	(AF008220) signal transduction regulator (Bacillus subtilis)	67	44	807
5	2	2301	574	gi12313385	(AE000547) para-aminobenzoate synthetase (pabB) (Helicobacter pylori)	67	48	1728
6	19	16063	16758	gi1413931	lipa-7d gene product (Bacillus subtilis)	67	41	696
22	8	7094	7897	gi11928962	pyrroline-5-carboxylate reductase (Actinidia deliciosa)	67	51	804
29	10	8335	9072	gi1468745	gtcR gene product (Bacillus brevis)	67	41	738
31	3	1379	585	gi12425123	(AF019986) PkAB (Dictyostelium discoideum)	67	49	795
32	11	8849	10150	gi142029	ORF1 gene product (Escherichia coli)	67	47	1302
36	16	14830	15546	gi1592142	ABC transporter, probable ATP-binding subunit (Methanococcus jannaschii)	67	43	717
38	9	4958	5392	gn1PID e214803	T22B3.3 (Caenorhabditis elegans)	67	47	435
38	21	13775	14512	gi1537037	ORF_0216 (Escherichia coli)	67	52	738
45	9	10428	9181	gi1551710	branching enzyme (glgB) (EC 2.4.1.18) (Bacillus stearothermophilus)	67	51	1248
48	23	18344	17514	gi1413949	lipa-25d gene product (Bacillus subtilis)	67	50	831
50	2	1773	952	gn1PID d101330	YqjQ (Bacillus subtilis)	67	55	822
53	1	431	3	gi1574291	fimbrial transcription regulation repressor (pilB) (Haemophilus influenzae)	67	40	429
55	13	12740	11946	gn1PID e252990	ORF YDL037c (Saccharomyces cerevisiae)	67	51	795
61	9	9210	8329	gn1PID e264711	ATP-binding cassette transporter A (Staphylococcus aureus)	67	50	882
71	2	5614	6117	gi1197667	vitellogenin (Anolis pulchellus)	67	36	504
81	7	4489	4983	gi1142714	phosphoenolpyruvate:mannose phosphotransferase element IIB (Lactobacillus curvatus)	67	42	495
83	7	2957	3214	gi1276746	Acyl carrier protein (Porphyra purpurea)	67	37	258
86	8	8140	6809	gi1147744	PSR (Enterococcus hirae)	67	45	1332
97	3	986	1366	gn1PID d102235	(AB000631) unnamed protein product (Streptococcus mutans)	67	43	381
102	1	601	1413	gi1682765	mccB gene product (Escherichia coli)	67	36	813
106	3	1109	1987	gi1148921	LicD protein (Haemophilus influenzae)	67	43	879
115	4	5982	5656	gi1895750	putative cellobiose phosphotransferase enzyme III (Bacillus subtilis)	67	44	327

TABLE 2

S. pneumoniae - Putative coding regions of novel proteins similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)	match accession	match gene name	% sim	% ident	length (nt)
115	7	8421	8077	gi 466473	cellobiose phosphotransferase enzyme II' [Bacillus stearothermophilus]	67	51	345
127	13	8127	7021	gi 147326	transport protein [Escherichia coli]	67	45	1107
136	3	2215	2859	gnl PID d100581	unknown [Bacillus subtilis]	67	49	645
140	21	23317	20906	gnl PID d101912	phenylalanine tRNA synthetase [Synachocystis sp.]	67	43	2412
146	6	2894	1893	gi 2182994	histidine kinase [Lactococcus lactis cremoris]	67	44	1002
151	8	11476	11117	gnl PID d100085	ORF129 [Bacillus cereus]	67	48	360
160	10	7453	8646	gi 2281317	OrfB; similar to a Streptococcus pneumoniae putative membrane protein encoded by GenBank Accession Number X99400; inactivation of the OrfB gene leads to UV-sensitivity and to decrease of homologous recombination (plasmidic test) [Lactococcus 1]	67	46	1194
163	3	3099	4505	gnl PID d101317	YqfR [Bacillus subtilis]	67	47	1407
167	8	6704	5454	gi 1161933	DitB [Lactobacillus casei]	67	45	1251
169	4	2322	2879	gnl PID d101331	YqkG [Bacillus subtilis]	67	41	558
171	11	7656	8384	gi 153841	pneumococcal surface protein A [Streptococcus pneumoniae]	67	50	729
188	3	1930	3723	gi 1542975	ABC [Thermotoga bacterium thermophilus]	67	46	1794
189	6	3599	3141	gnl PID e325178	Hypothetical protein [Bacillus subtilis]	67	52	459
205	3	1663	2211	gi 606073	ORF_0169 [Escherichia coli]	67	47	549
207	4	2856	3456	gi 2276374	DtxR/iron regulated lipoprotein precursor [Corynebacterium diphtheriae]	67	49	561
217	3	4086	3703	gi 895750	putative cellobiose phosphotransferase enzyme III [Bacillus subtilis]	67	42	384
246	2	291	662	gi 1842438	unknown [Bacillus subtilis]	67	43	372
252	1	2	745	gi 2351768	PspA [Streptococcus pneumoniae]	67	41	744
265	3	1134	1811	gi 2313847	[AE000585] L-asparaginase II (ansB) [Helicobacter pylori]	67	42	678
295	1	1	375	gi 2276374	DtxR/iron regulated lipoprotein precursor [Corynebacterium diphtheriae]	67	43	375
3	1	4898	5146	gnl PID e255179	unknown [Mycobacterium tuberculosis]	66	56	249
3	1	389	3	gnl PID e269548	unknown [Bacillus subtilis]	66	48	387
3	20	19267	20805	gi 39956	IRGc [Bacillus subtilis]	66	50	1539
4	3	2545	2718	gi 1787564	[AE000228] phage shock protein C [Escherichia coli]	66	36	174
5	9	13197	12592	gi 1574291	fibrial transcription regulation repressor (pilB) [Haemophilus influenzae]	66	46	606

**TABLE 2**  
*S. pneumoniae* - Putative coding regions of novel proteins similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)	match accession	match gene name	% sim	% ident	length (nt)
9	4	2872	1451	gnl pid e266928	unknown [Mycobacterium tuberculosis]	66	43	1422
12	2	1469	1200	gi 520407	orf2; GTP start codon [Bacillus thuringiensis]	66	42	270
15	12	10979	9897	gi 2314738	[AE000653] translation elongation factor EF-Ts (tsf) [Helicobacter pylori]	66	49	1083
16	2	1312	734	gnl pid d102245	[AB005554] ybp [Bacillus subtilis]	66	35	579
22	3	1372	1851	gi 1480916	signal peptidase type II [Lactococcus lactis]	66	38	480
22	7	5828	7096	gnl pid e206261	gamma-glutamyl phosphate reductase [Streptococcus thermophilus]	66	51	1269
22	20	16194	17138	gnl pid e281914	YitL [Bacillus subtilis]	66	50	945
30	2	530	976	gi 2314379	[AE000627] ABC transporter, ATP-binding protein (YncG) [Helicobacter pylori]	66	40	447
32	1	199	984	gi 312444	[ORF2] [Bacillus caldolyticus]	66	49	786
33	13	8352	7234	gi 1387979	448 identity over 302 residues with hypothetical protein from <i>Synechocystis</i> sp. accession D64006_CD; expression induced by environmental stress; some similarity to glycosyl transferases; two potential membrane-spanning helices [Bacillus subtilis]	66	44	1119
34	6	5658	4708	gnl pid e250724	orf2 [Bacobacillus sake]	66	39	951
34	14	9792	9574	gi 1590997	M. jannaschii predicted coding region M0272 [Methanococcus jannaschii]	66	48	219
35	16	15163	14501	gi 1773352	Cap5M [Staphylococcus aureus]	66	46	663
36	9	6173	6976	gi 1518680	minicell-associated protein DivIVA [Bacillus subtilis]	66	35	804
36	11	10396	10824	bbs 155344	insulin activator factor, INSAP [human, Pancreatic insulinoma, Peptide Partial, 744 aa] [Homo sapiens]	66	43	429
48	1	28	1419	gnl pid e325204	hypothetical protein [Bacillus subtilis]	66	50	1392
48	7	3810	4112	gi 2182574	[AE000090] Y4pE [Rhizobium sp. NGR234]	66	40	303
52	4	3595	2789	gi 388565	major cell-binding factor [Campylobacter jejuni]	66	52	807
54	3	2662	1076	gnl pid d101831	glutamine-binding periplasmic protein [Synechocystis sp.]	66	43	1587
61	10	9740	9183	gnl pid e154144	mdr gene product [Staphylococcus aureus]	66	44	558
72	13	10893	11993	gi 2313129	[AE000526] H. pylori predicted coding region HP0049 [Helicobacter pylori]	66	44	1101
74	9	13267	12476	gi 1573941	hypothetical [Haemophilus influenzae]	66	43	792
75	1	2	868	gi 1574631	nicotinamide mononucleotide transporter (pmc) [Haemophilus influenzae]	66	48	867
75	7	5303	4275	gi 41312	put. EBG repressor protein [Escherichia coli]	66	40	1029

TABLE 2

S. pneumoniae - Putative coding regions of novel proteins similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)	match accession	match gene name	% sim	% ident	length (nt)
82	7	6813	8123	gnl pid e251128	trigger factor [Bacillus subtilis]	66	53	1311
83	3	905	1219	pir C33496 C334	hisc homolog - Bacillus subtilis	66	44	315
86	10	9407	8925	gi 683584	shikimate kinase [Lactococcus lactis]	66	41	483
88	10	7001	6060	gi 2098719	putative fibrillar-associated protein [Actinomyces naeslundii]	66	52	942
89	1	951	4	gi 410118	ORFX19 [Bacillus subtilis]	66	41	948
93	7	3661	2711	gi 1787936	(AE000260) f298; This 298 aa orf is 51 pct identical (5 gaps) to 297 residues of an approx. 304 aa protein YCSN_BACSU SM: R42972 [Escherichia coli]	66	49	951
104	3	1805	3049	gi 1465784	putative cell division protein ftsW [Enterococcus hirae]	66	48	1245
106	14	13576	14253	gi 40027	homologous to E.coli gidB [Bacillus subtilis]	66	52	678
107	3	965	1864	gi 144858	ORP A [Clostridium perfringens]	66	49	900
112	7	5718	6593	gi 609332	DprA [Haemophilus influenzae]	66	43	876
115	1	3	302	gi 727367	Myr1p [Saccharomyces cerevisiae]	66	56	300
122	1	3	566	gnl pid d101328	Vqiv [Bacillus subtilis]	66	36	564
126	8	11759	11046	gnl pid d101163	ORP3 [Bacillus subtilis]	66	48	714
128	11	8201	8431	gi 726288	growth associated protein GAP-43 [Xenopus laevis]	66	41	231
131	8	4894	4508	gi 486661	Tmm related protein [Saccharomyces cerevisiae]	66	39	387
140	3	3236	2574	gi 40056	phoP gene product [Bacillus subtilis]	66	36	663
140	15	16318	15434	gi 1658189	5,10-methylenetetrahydrofolate reductase [Erwinia carotovora]	66	48	885
146	12	7926	7636	gnl pid d101140	transposase [Synecocystis sp.]	66	42	291
147	6	7137	6154	gi 472326	TPP-dependent acetoin dehydrogenase alpha-subunit [Clostridium magnum]	66	48	984
149	6	4435	5430	gnl pid d101887	pentose-5-phosphate-3-epimerase [Synecocystis sp.]	66	46	996
149	13	10756	11575	gi 42371	pyruvate formate-lyase activating enzyme (AA 1-246) [Escherichia coli]	66	42	822
186	4	2578	2270	gnl pid d101199	ORF11 [Enterococcus faecalis]	66	41	309
207	2	2340	2597	gnl pid e321893	envelope glycoprotein gp160 (Human immunodeficiency virus type 1)	66	46	258
210	7	3358	3678	gi 49318	ORF4 gene product [Bacillus subtilis]	66	46	321
217	8	5143	5355	gi 49538	thrombin receptor [Oricetulus longicaudatus]	66	38	213
220	4	3875	3642	gi 466648	alternate name ORF2 of L23635 [Escherichia coli]	66	33	234

TABLE 2

S. pneumoniae - Putative coding regions of novel proteins similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)	match accession	match gene name	% sim	% ident	length (nt)
223	1	1070	138	gnl pid e247187	zinc finger protein [Bacteriophage phigle]	66	45	933
224	2	1864	2640	gi 1176399	putative ABC transporter subunit [Staphylococcus epidermidis]	66	41	777
243	1	3	872	dbj AB000617.2	[AB000617] YcdH [Bacillus subtilis]	66	45	870
268	2	891	568	gi 517210	putative transposase [Streptococcus pyogenes]	66	60	324
322	1	2	643	gi 1499836	Zn protease [Methanococcus jannaschii]	66	40	642
5	10	13909	13178	gi 1574292	hypothetical [Haemophilus influenzae]	65	34	732
6	11	10465	11190	gi 142854	homologous to E. coli radC gene product and to unidentified protein from Staphylococcus aureus [Bacillus subtilis]	65	48	726
7	2	647	405	pir C64146 C641	hypothetical protein HI0259 - Haemophilus influenzae (strain Rd KW20)	65	42	243
7	7	6246	6821	gnl pid d101323	YqhU [Bacillus subtilis]	65	50	576
10	2	1873	1397	gi 1163111	ORF-1 [Streptococcus pneumoniae]	65	54	477
16	3	1428	2222	gnl pid e325010	hypothetical protein [Bacillus subtilis]	65	45	795
21	4	3815	3357	gnl pid e314910	hypothetical protein [Staphylococcus sciuri]	65	40	459
22	34	25776	26384	gi 1123030	CpxA [Actinobacillus pleuropneumoniae]	65	42	609
43	2	1648	290	gi 1044826	P1485.1 [Caenorhabditis elegans]	65	38	1359
48	13	10062	10856	gi 1573390	hypothetical [Haemophilus influenzae]	65	45	795
48	22	17521	16883	gi 1573391	hypothetical [Haemophilus influenzae]	65	37	639
48	25	19027	18533	gnl pid e264484	YCR020c, len:215 [Saccharomyces cerevisiae]	65	38	495
49	3	3856	5334	gi 1480429	putative transcriptional regulator [Bacillus stearothermophilus]	65	32	1479
50	6	5337	4519	gi 171963	tRNA isopentenyl transferase [Saccharomyces cerevisiae]	65	42	819
52	15	14728	15588	gi 1499745	M. jannaschii predicted coding region M30912 [Methanococcus jannaschii]	65	46	861
59	7	3963	4745	gi 496514	orf zeta [Streptococcus pyogenes]	65	42	783
68	3	2500	3483	gi 1887824	ORF.0310 [Escherichia coli]	65	46	984
69	3	2171	1077	gnl pid e311453	unknown [Bacillus subtilis]	65	42	1095
69	7	6029	5325	gi 809660	deoxyribose-phosphate aldolase [Bacillus subtilis]	65	55	705
71	5	8536	9783	gi 1573224	glycosyl transferase lgtC (GP:U14554.4) [Haemophilus influenzae]	65	42	1248
72	8	7664	8527	gnl pid e267589	unknown, highly similar to several spermidine synthases [Bacillus subtilis]	65	39	864

TABLE 2

S. pneumoniae - Putative coding regions of novel proteins similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)	match accession	match gene name	% sim	% ident	length (nt)
76	5	5773	4097	gml PID d101723	DNA REPAIR PROTEIN REC (RECOMBINATION PROTEIN N). [Escherichia coli]	65	44	1677
76	9	8099	7875	gml 1574276	exodeoxyribonuclease, small subunit (xseB) [Haemophilus influenzae]	65	38	225
84	2	2870	2352	gml 2313188	[AE000532] conserved hypothetical protein [Helicobacter pylori]	65	41	519
86	15	14495	13407	gml PID d101880	3-dehydroquinase synthase (Synecocystis sp.)	65	44	1089
87	3	3706	2423	gml 151259	HMG-CoA reductase (EC 1.1.1.88) [Pseudomonas mevalonii]	65	51	1284
88	3	2425	2736	gml 1098310	unknown [Lactococcus lactis]	65	30	312
89	2	1627	1007	gml PID d102008	[AB001488] SIMILAR TO ORF14 OF ENTEROCOCCUS FAECALIS TRANSPOSON TN916. [Bacillus subtilis]	65	41	621
111	6	6635	6186	gml PID e246063	NM23/nucleoside diphosphate kinase [Xenopus laevis]	65	50	450
116	1	3	1016	gml PID d101125	queuosine biosynthesis protein QueA [Synecocystis sp.]	65	44	1014
123	1	69	389	gml 498839	[ORF2] [Clostridium perfringens]	65	36	321
123	7	6522	7190	gml 1575577	DNA-binding response regulator [Thermotoga maritima]	65	39	669
125	3	3821	2859	gml PID e257609	sugar-binding transport protein [Anaerocellum thermophilum]	65	47	963
137	12	8015	7818	gml 2182574	[AE000090] Y4pE [Rhizobium sp. NGR234]	65	41	198
147	4	5021	3885	gml 472329	dihydrolipoamide acetyltransferase [Clostridium magnum]	65	47	1137
148	2	1053	1931	gml PID d101319	YqgH [Bacillus subtilis]	65	42	879
151	2	3212	4687	gml 304897	EcoE type I restriction modification enzyme M subunit [Escherichia coli]	65	50	1476
156	2	730	437	gml 310893	membrane protein [Theileria parva]	65	47	294
164	7	4256	4837	gml 410132	ORFX8 [Bacillus subtilis]	65	48	582
169	6	3192	3914	gml 1552737	similar to purine nucleoside phosphorylase [deoD] [Escherichia coli]	65	41	723
176	4	2951	2220	gml PID e339500	foliopoetide binding lipoprotein [Streptococcus pneumoniae]	65	43	732
195	4	4556	3900	gml 1592142	ABC transporter, probable ATP-binding subunit [Methanococcus jannaschii]	65	40	657
196	1	160	1572	gml PID d102004	[AB001488] PROBABLE UDP-N-ACETYLURACIYLALANYL-D-GLUTAMYL-2, 6-DIAMINOLIGASE (EC 6.3.2.15). [Bacillus subtilis]	65	51	1413
204	2	2246	1215	gml 143156	membrane bound protein [Bacillus subtilis]	65	37	1032
210	4	1544	1891	gml 49315	ORF1 gene product [Bacillus subtilis]	65	48	348
242	2	1625	723	gml 1787540	[AE000226] f249; This 249 aa orf is 32 pct identical (8 gaps) to 244 residues of an approx. 272 aa protein AGAR_ECOLI SW: P42902 [Escherichia coli]	65	42	903

TABLE 2

S. pneumoniae - Putative coding regions of novel proteins similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)	match accession	match gene name	% sim	% ident	length (nt)
284	1	1	900	gi 559861	clm [Plasmid PAD1]	65	36	900
304	1	2	574	gnl pid e290934	unknown [Mycobacterium tuberculosis]	65	52	573
315	1	2	1483	gi 790694	mammalian C-5-epimerase [Asotobacter vinelandii]	65	57	1482
320	1	3	569	gnl pid d102048	K. aerogenes, histidine utilization repressor; p1380 (199) DNA binding [Bacillus subtilis]	65	46	567
358	1	1	309	gnl pid e323508	YloS protein [Bacillus subtilis]	65	55	309
2	7	7571	6896	gi 1498753	nicotinate-nucleotide pyrophosphorylase [Rhodospirillum rubrum]	64	47	876
6	6	5924	6802	gnl pid d101111	methionine aminopeptidase [Synecocystis sp.]	64	52	879
8	4	3417	3686	gi 1045935	DNA helicase II [Mycoplasma genitalium]	64	58	270
11	4	3249	2689	gnl pid e265529	orfB [Streptococcus pneumoniae]	64	46	561
15	7	6504	7145	gi 1762328	Ycr59c/Yig2 homolog [Bacillus subtilis]	64	45	642
22	11	9548	9895	gnl pid d100581	unknown [Bacillus subtilis]	64	38	348
22	30	22503	23174	gi 289260	comE ORF1 [Bacillus subtilis]	64	44	672
26	7	14375	14199	gi 409286	bmrU [Bacillus subtilis]	64	30	177
27	2	1510	1334	gi 40795	ddai methylase [Desulfovibrio vulgaris]	64	51	177
29	2	614	297	gi 2326168	type VII collagen [Mus musculus]	64	50	318
35	2	368	721	pir JC1151 JC11	hypothetical 20.3K protein (insertion sequence IS1131) - Agrobacterium tumefaciens (strain P02) plasmid Ti	64	50	354
40	1	3	449	gi 46970	epid gene product [Staphylococcus epidermidis]	64	41	447
40	7	4683	4976	gnl pid e325792	(AJ000005) glucose kinase [Bacillus megaterium]	64	45	294
45	7	8068	6920	gnl pid d102036	subunit of ADP-glucose pyrophosphorylase [Bacillus stearothermophilus]	64	40	1149
51	2	301	1059	gi 43985	nifs-like gene [Lactobacillus delbrueckii]	64	54	759
51	13	15251	18397	gi 2293260	(AF008220) DNA-polymerase III alpha-chain [Bacillus subtilis]	64	46	3147
53	3	1157	555	gi 1574292	hypothetical [Haemophilus influenzae]	64	47	603
58	2	4236	1606	gi 1573826	alanine-tRNA synthetase (alaS) [Haemophilus influenzae]	64	51	2631
66	1	3	1259	gi 895749	putative cellobiose phosphotransferase enzyme II' [Bacillus subtilis]	64	42	1257
68	5	5213	6556	gi 436965	(aalA) gene product [Bacillus stearothermophilus]	64	47	1344
69	6	5356	4949	gnl pid d101316	cds [Bacillus subtilis]	64	52	408

TABLE 2  
S. pneumoniae - Putative coding regions of novel proteins similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)	match accession	match gene name	% sim	% ident	length (nt)
74	4	6948	5038	gi 726480	L-glutamine-D-fructose-6-phosphate amidotransferase [Bacillus subtilis]	64	50	1911
75	3	1283	1465	bbs 133379	TLS-CHOP-fusion protein (CHOP-C/BBP transcription factor, TLS=nuclear RNA-binding protein) [human, myxoid liposarcoma cells, Peptide Mutant, 462 aa] [Homo sapiens]	64	57	183
81	13	14016	14231	gi 143175	methanol dehydrogenase alpha-10 subunit [Bacillus sp.]	64	35	216
83	22	21851	22090	gnl PID d101315	YnfA [Bacillus subtilis]	64	44	240
87	11	10046	9300	gnl PID e323505	putative PteI protein [Bacillus subtilis]	64	43	747
98	7	5032	5706	gnl PID e233880	hypothetical protein [Bacillus subtilis]	64	38	675
105	1	2	1276	gi 1657503	[similar to S. aureus mercury(II) reductase [Escherichia coli]]	64	45	1275
113	7	5136	6410	gnl PID d101119	Wfs [Synecocystis sp.]	64	50	1275
119	1	2	1297	gnl PID e320520	hypothetical protein [Natronobacterium pharaonis]	64	37	1296
123	3	1125	2156	gnl PID e251284	ORF YDL244w [Saccharomyces cerevisiae]	64	40	1032
124	5	2331	1780	gnl PID d101884	hypothetical protein [Synecocystis sp.]	64	50	552
129	4	3467	2709	gnl PID d101314	YnfU [Bacillus subtilis]	64	52	759
131	1	152	3	gi 1377841	unknown [Bacillus subtilis]	64	42	150
137	11	7196	7549	pir JC1151 JC11	hypothetical 20.3K protein (insertion sequence IS1131) - Agrobacterium tumefaciens (strain P022) plasmid T1	64	50	354
139	3	3226	2851	gi 2293301	[AF008220] YnfB [Bacillus subtilis]	64	44	576
146	10	6730	5648	gi 1322245	mevalonate pyrophosphate decarboxylase [Rattus norvegicus]	64	45	1083
147	1	2	1018	gnl PID e137033	unknown gene product [Lactobacillus leichmannii]	64	46	1017
148	11	8430	8783	gi 2130630	[AF000430] dynamin-like protein [Homo sapiens]	64	28	354
156	7	4313	3612	gnl PID d102050	transmembrane [Bacillus subtilis]	64	31	702
157	4	1299	2114	gnl PID d100892	homologous to Gln transport system permease proteins [Bacillus subtilis]	64	43	816
162	6	5880	6362	gi 517204	ORF1, putative 42 kDa protein [Streptococcus pyogenes]	64	58	483
164	13	9707	8769	gnl PID d100964	homologue of ferric anguipactin transport system permease protein PatD of V. anguillarum [Bacillus subtilis]	64	40	939
175	5	3906	4598	gi 534045	antiterminator [Bacillus subtilis]	64	39	693
189	10	6154	6507	gi 581307	response regulator [Lactobacillus plantarum]	64	33	354
191	4	3519	2863	gi 149520	phosphoribosyl anthranilate isomerase [Lactococcus lactis]	64	46	657



TABLE 2

S. pneumoniae - Putative coding regions of novel proteins Vfa1 to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)	match accession	match gene name	% sim	% ident	length (nt)
202	1	76	1140	gnl PID e293806	O-acetylhomoserine sulphydrolase [Leptospira meyeri]	64	47	1065
224	1	234	1571	gi 1573393	collagenase (prtC) [Haemophilus influenzae]	64	42	1338
231	3	291	647	gi 40174	ORF X [Bacillus subtilis]	64	43	357
253	3	709	1089	pir JC1151 JC11	hypothetical 20.3K protein (insertion sequence IS1131) - Agrobacterium tumefaciens (strain P022) plasmid Ti	64	50	381
265	1	820	2	gi 1377832	unknown [Bacillus subtilis]	64	31	819
297	1	1	660	gi 1590871	collagenase [Methanococcus jannaschii]	64	48	660
328	1	263	21	gi 992651	Gln4p [Saccharomyces cerevisiae]	64	41	243
5	4	8730	8098	gi 556885	unknown [Bacillus subtilis]	63	48	633
10	6	5178	4483	gi 1573101	hypothetical [Haemophilus influenzae]	63	40	696
12	11	9324	9902	gi 806536	membrane protein [Bacillus acidopulluliticus]	63	42	579
15	10	8897	9187	gi 722339	unknown [Acetobacter xylinum]	63	40	291
17	2	1031	309	gnl PID e217602	PinU [Lactobacillus plantarum]	63	32	723
18	8	7778	6975	gi 1377843	unknown [Bacillus subtilis]	63	45	804
26	4	9780	7078	gi 142440	ATP-dependent nuclease [Bacillus subtilis]	63	46	2703
29	5	3488	4192	gi 1377829	unknown [Bacillus subtilis]	63	35	705
34	11	8830	7988	gnl PID d101198	ORF8 [Enterococcus faecalis]	63	45	843
35	3	1187	876	gi 722339	unknown [Acetobacter xylinum]	63	39	312
48	15	12509	11691	gi 1573389	hypothetical [Haemophilus influenzae]	63	41	819
51	11	12719	12189	gi 142450	ahrC protein [Bacillus subtilis]	63	35	531
55	4	3579	5022	gi 1708640	YeaB [Bacillus subtilis]	63	41	1044
55	15	13669	14670	gnl PID e311502	thioredoxine reductase [Bacillus subtilis]	63	44	1002
68	10	9242	8919	sp P37686 YIAY_	HYPOTHETICAL 40.2 KD PROTEIN IN AVTA-SELB INTERGENIC REGION (F382)	63	40	324
86	7	6554	5685	gi 1574382	lic-1 operon protein (licD) [Haemophilus influenzae]	63	41	870
88	8	6085	5180	gi 2098719	putative fibrillar-associated protein [Actinomyces naeslundii]	63	43	906
96	8	3858	6484	gi 1052803	orf197b gene product [Streptococcus pneumoniae]	63	38	627
100	1	240	1940	gi 7171	fucosidase [Dictyostellium discoideum]	63	36	1701

TABLE 2

S. pneumoniae - Putative coding regions of novel proteins similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)	match accession	match gene name	% sim	% ident	length (nt)
104	4	3063	5765	gi 144985	phosphoenolpyruvate carboxylase [Corynebacterium glutamicum]	63	46	2703
106	8	9189	8554	gi 533099	endonuclease III [Bacillus subtilis]	63	45	636
122	6	4704	4886	gnl PID d101139	transposase [Synechocystis sp.]	63	39	183
128	7	4517	5203	gnl PID d101434	orf2 [Methanobacterium thermoautotrophicum]	63	50	687
137	4	963	1547	gi 472920	v-type Na-ATPase [Enterococcus hirae]	63	27	585
142	7	4100	4585	gnl PID e313025	hypothetical protein [Bacillus subtilis]	63	44	486
159	5	1741	2571	gi 1787043	(AE000184) f271, This 271 aa orf is 24 pct identical (16 gaps) to 265 residues of an approx. 272 aa protein YIDA_ECOLI SW: P09997 [Escherichia coli]	63	39	831
171	12	8803	14406	gnl PID e324918	IgA1 protease [Streptococcus sanguis]	63	48	5604
177	1	3	347	gi 1773150	hypothetical 14.8kd protein [Escherichia coli]	63	34	345
178	2	423	917	gi 722339	unknown [Acetobacter xylinum]	63	41	495
178	3	794	1012	gi 1591582	cobalamin biosynthesis protein N [Methanococcus jannaschii]	63	36	219
195	1	1377	175	gnl PID e324217	fteQ [Enterococcus hirae]	63	33	1203
234	5	1739	1527	gi 1591582	cobalamin biosynthesis protein N [Methanococcus jannaschii]	63	36	213
249	1	81	257	gi 1000453	TreR [Bacillus subtilis]	63	41	177
283	1	127	1347	gi 396486	ORF8 [Bacillus subtilis]	63	44	1221
293	3	2804	3466	gi 722339	unknown [Acetobacter xylinum]	63	37	663
311	1	905	486	gi 1877424	UDP-galactose 4-epimerase [Streptococcus mutans]	63	46	420
324	1	2	556	gi 1477741	histidine periplasmic binding protein P29 [Campylobacter jejuni]	63	36	555
365	1	219	13	gi 2252843	(AF013293) No definition line found [Arabidopsis thaliana]	63	33	207
382	1	88	378	gi 722339	unknown [Acetobacter xylinum]	63	40	291
385	3	364	158	gi 2252843	(AF013293) No definition line found [Arabidopsis thaliana]	63	33	207
2	1	2495	288	gnl PID e325007	penicillin-binding protein [Bacillus subtilis]	62	42	2208
3	23	23374	24231	gnl PID e354993	hypothetical protein [Bacillus subtilis]	62	35	858
6	16	14320	13193	gnl PID e349614	nit5-like protein [Mycobacterium leprae]	62	37	1128
7	8	6819	7232	gnl PID d101324	YqhY [Bacillus subtilis]	62	32	414
7	19	15466	14207	gnl PID d101804	beta ketoacyl-acyl carrier protein synthase [Synechocystis sp.]	62	43	1260

**TABLE 2**  
S. pneumoniae - Putative coding regions of novel proteins similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)	match accession	match gene name	% sim	% ident	length (nt)
7	21	17155	16229	gnl pid e323514	putative FabD protein [Bacillus subtilis]	62	46	927
7	24	19526	18519	gi 1276434	beta-ketoacyl-ACP synthase III [Cuphea wrightii]	62	37	1008
12	7	5904	4702	gi 1573768	A/G-specific adenine glycosylase (mutY) [Haemophilus influenzae]	62	43	1203
12	9	8032	8793	gi 1591587	pantothenate metabolism flavoprotein [Methanococcus jannaschii]	62	33	762
15	11	9678	9328	pir JC1151 JC11	hypothetical 20.3K protein (insertion sequence IS1131) - Agrobacterium tumefaciens (strain P022) plasmid T1	62	43	351
17	4	2609	2442	gi 1591081	M. jannaschii predicted coding region M30174 [Methanococcus jannaschii]	62	43	168
17	5	3053	2835	gi 149570	role in the expression of lactacin F, part of the laf operon [Lactobacillus sp.]	62	44	219
22	10	8627	9538	gnl pid d100580	similar to B. subtilis DnaH [Bacillus subtilis]	62	43	912
30	3	865	2043	gi 2314379	(AE000627) ABC transporter, ATP-binding protein (yhcg) [Helicobacter pylori]	62	43	1179
33	5	2235	1636	gi 413976	lipa-52r gene product [Bacillus subtilis]	62	44	600
38	11	5689	6123	gi 148231	o251 [Escherichia coli]	62	34	435
40	17	14272	13328	gnl pid d101904	hypothetical protein [Synecocystis sp.]	62	43	945
42	1	3	311	gi 1146182	putative [Bacillus subtilis]	62	41	309
44	2	1267	4005	gi 1786952	(AE000176) o877; 100 pct identical to the first 86 residues of the 100 aa hypothetical protein fragment Y8CB_ECOLI SW: P54746 [Escherichia coli]	62	43	2739
48	12	9712	9304	gi 662920	repressor protein [Enterococcus hirae]	62	32	429
51	8	5664	7181	gnl pid e301153	StySKI methylase [Salmonella enterica]	62	44	1518
52	3	2791	2099	gi 1183886	integral membrane protein [Bacillus subtilis]	62	41	693
55	16	15702	14704	gnl pid e313028	hypothetical protein [Bacillus subtilis]	62	40	999
59	6	3418	3984	gi 2065483	unknown [Lactococcus lactis lactis]	62	32	567
63	5	4997	4809	gi 149771	pilin gene inverting protein (PivML) [Moraxella lacunata]	62	28	189
70	14	10002	10739	gi 992977	bplG gene product [Bordetella pertussis]	62	45	738
71	13	18790	20382	gi 1280135	coded for by C. elegans cDNA cm21e6; coded for by C. elegans cDNA cm01e2; similar to melibiose carrier protein (Chlomethylgalactoside permease II) [Caenorhabditis elegans]	62	62	1593
71	28	32217	32768	gnl pid d101312	YqeG [Bacillus subtilis]	62	35	552
74	7	11666	10383	gi 1552753	hypothetical [Escherichia coli]	62	38	1284

TABLE 2

S. pneumoniae - Putative coding regions of novel proteins similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)	match accession	match gene name	% sim	% ident	length (nt)
80	8	9370	9609	gnl PID d102002	(AB001488) FUNCTION UNKNOWN. [Bacillus subtilis]	62	46	240
97	10	9068	7041	gi 1822463	protein-N(pil)-phosphotransferase [Escherichia coli]	62	42	2028
98	4	2306	3288	gnl PID d101496	BraE (integral membrane protein) [Pseudomonas aeruginosa]	62	42	963
102	3	2823	3539	gnl PID e313010	hypothetical protein [Bacillus subtilis]	62	24	717
103	3	2795	1242	gnl PID d102049	H. influenzae hypothetical ABC transporter; P44808 (974) [Bacillus subtilis]	62	41	1554
111	2	2035	3462	gi 1581297	NISP [Lactococcus lactis]	62	44	1428
112	4	3154	4080	gi 1574379	luc-1 operon protein (lucA) [Haemophilus influenzae]	62	39	927
112	6	4939	5649	gi 1574381	luc-1 operon protein (lucC) [Haemophilus influenzae]	62	39	711
124	3	1137	721	gi 1573024	anaerobic ribonucleoside-triphosphate reductase (nrdB) [Haemophilus influenzae]	62	45	417
124	6	3162	2329	gi 609076	leucyl aminopeptidase [Lactobacillus delbrueckii]	62	40	834
126	7	11073	7516	gnl PID d101163	ORF4 [Bacillus subtilis]	62	38	3558
129	6	4983	4340	pir S41509 S415	zinc finger protein EFG - Chilo iridescent virus	62	48	444
131	7	4510	4103	gi 1857245	unknown [Lactococcus lactis]	62	42	408
149	2	1923	2579	gi 1592142	ABC transporter, probable ATP-binding subunit [Methanococcus jannaschii]	62	41	657
149	7	5360	6055	gnl PID e323508	YLOS protein [Bacillus subtilis]	62	40	696
156	1	450	238	gnl PID e254644	membrane protein [Streptococcus pneumoniae]	62	40	213
156	6	3606	2935	gnl PID d102050	transmembrane [Bacillus subtilis]	62	37	672
171	2	1779	2291	gi 43941	EHII-B Sor PTS [Klebsiella pneumoniae]	62	35	513
172	2	385	723	gi 1895750	putative cellobiose phosphotransferase enzyme III [Bacillus subtilis]	62	39	339
173	3	2599	893	gi 1591732	cobalt transport ATP-binding protein O [Methanococcus jannaschii]	62	42	1707
179	2	492	1754	gi 1574071	H. influenzae predicted coding region H11038 [Haemophilus influenzae]	62	38	1263
181	6	2856	3707	gi 1777435	Lact [Lactobacillus casei]	62	42	852
185	2	2074	311	gi 2182397	(AE000073) Y46N [Rhizobium sp. NGR234]	62	41	1764
200	2	1061	1984	gi 450566	transmembrane protein [Bacillus subtilis]	62	37	924
202	3	2583	3473	gi 422219	P35 gene product (AA 1 - 314) [Escherichia coli]	62	41	891
210	3	1374	1565	gi 49315	ORF1 gene product [Bacillus subtilis]	62	45	192

TABLE 2

S. pneumoniae - Putative coding regions of novel proteins similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)	match accession	match gene name	% sim	% ident	length (nt)
211	1	3	971	gi 147402	mannose permease subunit III-Man (Escherichia coli)	62	43	969
223	2	1495	1034	gnl PID d101190	ORF2 (Streptococcus mutans)	62	41	462
228	1	34	909	gi 530063	glycerol uptake facilitator (Streptococcus pneumoniae)	62	44	876
234	2	90	917	gi 2293259	(AF008220) YtqI (Bacillus subtilis)	62	38	828
282	5	1765	1487	gnl PID e276475	galactokinase (Arabidopsis thaliana)	62	33	279
375	1	1	159	gi 1674231	(AE000052) Mycoplasma pneumoniae, hypothetical protein homolog; similar to Swiss-Prot Accession Number P31515, from B. subtilis (Mycoplasma pneumoniae)	62	40	159
385	5	584	357	gi 1573353	outer membrane integrity protein (tolA) (Haemophilus influenzae)	62	47	228
3	19	18550	19269	gi 606162	ORF_229 (Escherichia coli)	61	41	720
7	4	2725	3225	gi 2114425	similar to Synchocystis sp. hypothetical protein, encoded by GenBank Accession Number D64006 (Bacillus subtilis)	61	42	501
17	6	3326	3054	gi 149569	lactacin P (Lactobacillus sp.)	61	43	273
44	3	4061	4957	gnl PID d101068	xylose repressor (Synchocystis sp.)	61	38	897
54	11	8388	7234	gnl PID d101329	YqjH (Bacillus subtilis)	61	42	1155
57	6	3974	6037	gnl PID d101316	YqfK (Bacillus subtilis)	61	42	2064
58	5	7356	6565	sp P45169 POTC_	SPERMIDINE/PUTRESCINE TRANSPORT SYSTEM PERMEASE PROTEIN POTC	61	34	792
67	1	3	692	gi 537108	ORF_254 (Escherichia coli)	61	46	690
68	9	8816	7890	gi 19501	pPU212 gene product (AA 1-184) (Lupinus polyphyllus)	61	41	927
70	15	10737	12008	gi 992976	bplP gene product (Bordetella pertussis)	61	44	1272
72	11	9759	10202	gnl PID d101833	carboxynorspermidine decarboxylase (Synchocystis sp.)	61	36	444
76	8	7881	7003	gnl PID d100305	farnesyl diphosphate synthase (Bacillus stearothermophilus)	61	45	879
87	4	4914	3697	gi 528991	unknown (Bacillus subtilis)	61	42	1218
87	13	12311	11361	gi 1789683	(AE000407) methionyl-tRNA formyltransferase (Escherichia coli)	61	44	951
91	2	731	2989	gi 537080	ribonucleoside triphosphate reductase (Escherichia coli)	61	45	2259
105	3	2711	3499	gnl PID d101851	hypothetical protein (Synchocystis sp.)	61	44	789
115	6	7968	6478	gi 895747	putative cel operon regulator (Bacillus subtilis)	61	36	1491
123	8	7181	8518	gi 1209527	protein histidine kinase (Enterococcus faecalis)	61	40	1338

TABLE 2

S. pneumoniae - Putative coding regions of novel proteins similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)	match accession	match gene name	% sim	% ident	length (nt)
126	6	7525	6725	gi 1787043	(AE000184) f271; this 271 aa orf is 24 pct identical (16 gaps) to 265 residues of an approx. 272 aa protein YIDA_ECOLI SW: P09997 [Escherichia coli]	61	38	801
128	1	1	639	gnl pid d101328	YqjY [Bacillus subtilis]			
139	7	4794	5054	gi 1022726	unknown [Staphylococcus haemolyticus]	61	41	639
139	9	12632	5913	gnl pid e270014	beta-galactosidase [Thermotoga ethanolicus]	61	41	261
143	1	2552	42	gi 520341	penicillin-binding proteins 1A and 1B [Bacillus subtilis]	61	41	6720
148	16	12125	11424	gi 1552743	tetrahydrodipicolinate N-succinyltransferase [Escherichia coli]	61	42	2511
162	3	4112	3456	gnl pid d101829	phosphoglycolate phosphatase [Synecocystis sp.]	61	42	702
172	3	727	1077	gnl pid d102048	B. subtilis, cellobiose phosphotransferase system, celsA; P46318 (220) [Bacillus subtilis]	61	30	657
177	3	1101	1772	gnl pid d100574	unknown [Bacillus subtilis]	61	44	351
202	2	1278	2585	gi 1045831	hypothetical protein (GB:L18965_6) [Mycoplasma genitalium]	61	43	672
224	3	2782	3144	gi 1591144	M. jannaschii predicted coding region MJO440 [Methanococcus jannaschii]	61	36	1308
225	4	3395	3766	gi 1552774	hypothetical [Escherichia coli]	61	30	363
249	2	212	802	gi 1000453	Trer [Bacillus subtilis]	61	40	372
254	2	843	484	gnl pid d100417	ORF120 [Escherichia coli]	61	42	591
257	1	3	350	gnl pid e255315	unknown [Mycobacterium tuberculosis]	61	36	360
293	4	3971	3657	pir JC1151 JC11	hypothetical 20.3K protein (insertion sequence IS1131) - Agrobacterium tumefaciens (strain P022) plasmid T1	61	42	348
301	1	949	17	gi 2291209	(AF016424) contains similarity to acyltransferases [Caenorhabditis elegans]	61	45	315
373	1	1066	287	gi 393396	Tb-292 membrane associated protein [Trypanosoma brucei subgroup]	61	33	933
3	24	24473	24955	gi 537093	ORF_0153b [Escherichia coli]	61	38	780
6	5	4636	5739	gi 2293258	(AF008220) YcoI [Bacillus subtilis]	60	27	483
6	12	11936	11187	gi 293017	ORF3 (put.); putative [Lactococcus lactis]	60	35	1104
17	13	6708	6484	gi 149569	lactacin F [Lactobacillus sp.]	60	44	750
18	7	6977	5670	gi 1788140	(AE000378) o481; This 481 aa orf is 35 pct identical (19 gaps) to 309 residues of an approx. 856 aa protein NOB1_HUMAN SW: P46087 [Escherichia coli]	60	32	225
20	15	15878	17167	gnl pid d100584	unknown [Bacillus subtilis]	60	43	1308
						60	44	1290

TABLE 2

S. pneumoniae - Putative coding regions of novel proteins similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)	match accession	match gene name	% sim	% ident	length (nt)
22	1	1	243	gnl pid d102050	transmembrane (Bacillus subtilis)	60	36	243
32	10	8296	8964	gi 2293275	[AF008220] YtaG (Bacillus subtilis)	60	37	669
38	15	8837	9697	gi 40023	[B. subtilis genes rpmA, rpmA, 50kd, gldA and gldB (Bacillus subtilis)]	60	35	861
43	6	8610	5944	gi 171787	protein kinase 1 (Saccharomyces cerevisiae)	60	36	2667
44	1	1	1269	gnl pid e235823	unknown [Schizosaccharomyces pombe]	60	44	1269
45	10	11138	10368	gi 397488	[1,4-alpha-glucan branching enzyme (Bacillus subtilis)]	60	43	771
48	19	15766	14378	gnl pid e205173	orf1 (Lactobacillus helveticus)	60	39	1389
48	21	16727	16951	gnl pid d102041	[AB002668] unnamed protein product (Haemophilus actinomycetemcomitans)	60	32	225
50	1	2	898	gnl pid e246537	[ORF286 protein (Pseudomonas stutzeri)]	60	31	897
62	2	638	1177	gnl pid d100587	unknown (Bacillus subtilis)	60	42	540
68	4	3590	5203	gi 1573583	[H. influenzae predicted coding region H10594 (Haemophilus influenzae)]	60	36	1614
70	11	5781	6182	gnl pid d102014	[AB001488] SIMILAR TO YDFR GENE PRODUCT OF THIS ENTRY (YDFR_BACSU)	60	33	402
70	12	6343	8133	gnl pid e24970	hypothetical protein (Bacillus subtilis)	60	38	1791
71	8	11701	14157	gi 580866	[ipe-12d gene product (Bacillus subtilis)]	60	33	2457
74	8	12509	11664	gnl pid d101832	phosphatidate cytidyltransferase (Synecocystis sp.)	60	45	846
76	4	4116	3367	gi 2352096	orf; similar to serine/threonine protein phosphatase (Fervidobacterium islandicum)	60	39	750
80	4	7372	7665	gi 1786420	[AE000131] f86; 100 pct identical to GB: ECODINJ_6 ACCESSION: D38582 (Escherichia coli)	60	30	294
81	6	4073	4522	gi 147402	[mannose permease subunit III-Man (Escherichia coli)]	60	35	450
86	1	940	155	gi 143177	[putative (Bacillus subtilis)]	60	26	786
92	1	1	192	gi 396348	[homoserine transuccinylase (Escherichia coli)]	60	45	192
93	14	10619	9384	gi 1780389	[AE000297] o464; This 464 aa orf is 33 pct identical (9 gaps) to 331 residues of an approx. 416 aa protein MTRC_NE100 SW: P43505 (Escherichia coli)	60	27	1236
94	5	5548	8121	gnl pid e229895	[AJ000496] cyclic nucleotide-gated channel beta subunit (Rattus norvegicus)	60	50	2574
97	7	5396	4533	gi 1591396	[transketolase] (Methanococcus jannaschii)	60	43	864
102	2	2081	2833	gnl pid e220929	hypothetical protein (Mycobacterium tuberculosis)	60	43	753

TABLE 2

S. pneumoniae - Putative coding regions of novel proteins 418 similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)	match accession	match gene name	% sim	% ident	length (nt)
106	9	9773	9183	gnl PID e334782	Y18N protein [Bacillus subtilis]	60	31	591
113	8	6361	6837	gi 466875	infU; B1496_C1_157 (Mycobacterium leprae)	60	43	477
115	2	2755	524	gnl PID e328143	(AJ000332) Glucosidase II (Homo sapiens)	60	32	2232
122	7	4763	5068	gnl PID d101876	transposase [Synecocystis sp.]	60	39	306
127	8	4510	5283	gi 1777938	Pgm [Treponema pallidum]	60	38	774
138	4	3082	2672	gnl PID e325196	hypothetical protein [Bacillus subtilis]	60	36	411
139	1	177	4	gnl PID d100680	ORF [Thermus thermophilus]	60	39	174
139	11	14520	13009	gi 537145	ORF_437 [Escherichia coli]	60	30	1512
140	2	2592	1249	gi 1209527	protein histidine kinase [Enterococcus faecalis]	60	37	1344
141	1	210	1049	gi 463181	E5 ORF from bp 3842 to 4081; putative [human papillomavirus type 33]	60	34	840
141	5	5368	6405	gi 145362	tyrosine-sensitive DHP synthase (arop) [Escherichia coli]	60	41	1038
142	6	3558	4049	gi 600711	putative [Bacillus subtilis]	60	37	492
148	10	7742	8713	gnl PID e313022	hypothetical protein [Bacillus subtilis]	60	27	972
153	5	3667	4278	gi 2293322	(AF08220) branch-chain amino acid transporter [Bacillus subtilis]	60	42	612
155	1	1413	748	gi 2104504	putative UDP-glucose dehydrogenase [Escherichia coli]	60	40	666
158	3	3116	2472	gnl PID d100872	a negative regulator of pho regulon [Pseudomonas aeruginosa]	60	37	645
159	3	778	1386	gnl PID e308090	product highly similar to Bacillus anthracis CapA protein [Bacillus subtilis]	60	48	609
163	7	8049	8488	gnl PID d101313	YqeN [Bacillus subtilis]	60	38	420
170	3	4130	2688	gi 1574179	H. Influenzae predicted coding region HI1244 [Haemophilus influenzae]	60	39	1443
171	7	4717	5901	gi 606076	ORF_0384 [Escherichia coli]	60	44	1185
183	3	2460	2135	gi 1877427	repressor [Streptococcus pyogenes phage T12]	60	38	306
191	10	9444	8428	gi 415664	catabolite control protein [Bacillus megaterium]	60	42	1017
200	1	139	1083	gi 438462	transmembrane protein [Bacillus subtilis]	60	37	945
201	3	3895	1928	gi 475112	enzyme Iabc [Pedococcus pentosaceus]	60	39	1968
214	15	10930	10439	gi 1573407	hypothetical [Haemophilus influenzae]	60	39	492
218	4	2145	2363	gi 608520	myosin heavy chain kinase A [Dictyostelium discoideum]	60	31	219



TABLE 2

S. pneumoniae - Putative coding regions of novel proteins similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)	match accession	match gene name	% sim	% ident	length (nt)
226	4	2518	2351	gi 437705	hyaluronidase [Streptococcus pneumoniae]	60	53	168
242	1	725	3	gi 43938	Sor regulator [Klebsiella pneumoniae]	60	41	723
245	1	1	288	gi 304897	EcoE type I restriction modification enzyme M subunit [Escherichia coli]	60	56	288
251	1	905	45	gi 671632	unknown [Staphylococcus aureus]	60	36	861
259	1	969	82	gi 153794	egg [Streptococcus gordonii]	60	32	888
260	2	1492	1662	pir 531840/S318	probable transposase - Bacillus stearothermophilus	60	26	171
274	1	836	96	gi 1592173	N-ethylmaleine chlorohydrolase [Methanococcus jannaschii]	60	40	741
308	1	463	2	gi 1787397	[AE000214] o157 [Escherichia coli]	60	43	462
318	1	3	308	gnl pid e137594	xerC recombinase [Lactobacillus leichmannii]	60	42	306
344	1	73	522	gi 509672	repressor protein [Bacteriophage Tuc2009]	60	32	450
5	1	576	4	gi 2293147	[AF008220] YtKM [Bacillus subtilis]	59	31	573
7	22	18140	17142	gnl pid e280724	unknown [Mycobacterium tuberculosis]	59	39	999
10	1	1413	4	gi 1353880	isialidase L [Macrobactella decora]	59	41	1410
15	6	6463	5156	gi 580841	F1 [Bacillus subtilis]	59	35	1308
22	2	479	1393	gi 142469	als operon regulatory protein [Bacillus subtilis]	59	34	915
22	5	2698	4614	gnl pid e280623	PCPA [Streptococcus pneumoniae]	59	44	1917
30	1	208	558	gnl pid e233868	hypothetical protein [Bacillus subtilis]	59	37	351
30	4	3678	2455	gnl pid e202290	unknown [Lactobacillus sake]	59	33	1224
35	13	12201	11071	gnl pid e238664	hypothetical protein [Bacillus subtilis]	59	35	1131
35	14	13288	12182	gi 1657647	Cap8M [Staphylococcus aureus]	59	39	1107
36	18	18076	17897	gi 1500535	M. jannaschii predicted coding region MJ1635 [Methanococcus jannaschii]	59	33	180
38	12	6172	7137	gi 2293239	[AF008220] YtAK [Bacillus subtilis]	59	34	966
42	3	1952	3361	gi 1684845	pinin [Canis familiaris]	59	40	1410
50	3	2678	1728	gnl pid d101329	YqJK [Bacillus subtilis]	59	41	951
56	5	1870	2388	gnl pid e137594	xerC recombinase [Lactobacillus leichmannii]	59	41	519
61	6	6812	5626	gnl pid e311516	aminotransferase [Bacillus subtilis]	59	40	1185
67	5	2382	3023	gi 1146190	2-keto-3-deoxy-6-phosphogluconate aldolase [Bacillus subtilis]	59	36	642

TABLE 2

S. pneumoniae - Putative coding regions of novel proteins similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)	match accession	match gene name	% sim	% ident	length (nt)
69	10	8567	8899	gi11573628	anthothenate kinase (coaA) [Haemophilus influenzae]	59	38	333
87	12	11383	10055	gnl PID e323504	putative Fmu protein [Bacillus subtilis]	59	44	1329
113	14	11397	15894	gi11673731	[AE000010] Mycoplasma pneumoniae, fructose-permease IIBC component; similar to Swiss-Prot Accession Number P20966, from E. coli [Mycoplasma pneumoniae]	59	43	1968
115	8	8766	8521	gi11590886	M. jannaachii predicted coding region MJ0110 [Methanococcus jannaachii]	59	38	246
119	2	1966	1526	gnl PID e209005	homologous to ORF2 in nrDEP operons of E. coli and S. typhimurium [Lactococcus lactis]	59	43	441
128	17	13438	13178	gnl PID e279632	unknown [Mycobacterium tuberculosis]	59	38	261
140	22	23303	23388	gi1482922	protein with homology to pail repressor of B. subtilis [Lactobacillus delbrueckii]	59	40	516
148	13	9697	9014	gnl PID d102005	[AB001488] FUNCTION UNKNOWN, SIMILAR PRODUCT IN H. INFLUENZAE AND SYNECHOCYSTIS. [Bacillus subtilis]	59	32	684
149	10	7213	8244	gi1710422	cmp-binding-factor 1 [Staphylococcus aureus]	59	40	1032
164	9	6993	6013	gnl PID d100965	ferric anguibactin-binding protein precursor FatB of V. anguillarum [Bacillus subtilis]	59	41	981
164	12	8836	7823	gnl PID d100964	homologue of ferric anguibactin transport system permease protein FatC of V. anguillarum [Bacillus subtilis]	59	35	1014
177	2	401	1072	gi1289759	coded for by C. elegans cDNA CE263 (GenBank:Z14728); putative [Caenorhabditis elegans]	59	40	672
177	7	3841	4200	gi12313445	[AE000551] H. pylori predicted coding region HP0342 [Helicobacter pylori]	59	38	360
183	4	2768	2508	gi1509672	repressor protein [Bacteriophage Tuc2009]	59	50	261
186	6	3398	2820	gi1606080	ORF_c290; Geneplot suggests frameshift linking to o267, not found [Escherichia coli]	59	38	579
190	3	3120	1711	gi11613768	histidine protein kinase [Streptococcus pneumoniae]	59	32	1410
194	2	1621	1019	gnl PID d100579	unknown [Bacillus subtilis]	59	40	603
198	7	5205	4306	gnl PID e313073	hypothetical protein [Bacillus subtilis]	59	38	900
220	5	4362	3958	gnl PID d101322	YqkL [Bacillus subtilis]	59	46	405
242	3	1573	2367	gi11787045	[AE000184] f308; This 308 aa orf is 35 pct identical (35 gaps) to 305 residues of an approx. 296 aa protein PFIC_ECOLI SW: P32675 [Escherichia coli]	59	42	795
247	2	1154	1480	gi140073	ORF107 [Bacillus subtilis]	59	39	327

TABLE 2  
S. pneumoniae - Putative coding regions of novel proteins similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)	match accession	match gene name	% sim	% ident	length (nt)
256	1	868	2	gml PID d101924	hemolysin [Synecocystis sp.]	59	39	867
258	1	65	820	g1 2246532	ORF 73, contains large complex repeat CR 73 (Kaposi's sarcoma-associated herpesvirus)	59	20	756
270	1	386	1126	gml PID d102092	YnfB [Bacillus subtilis]	59	40	741
281	1	552	166	g1 666062	putative [Lactococcus lactis]	59	31	387
309	1	3	479	g1 405879	yaiH [Escherichia coli]	59	38	477
363	1	2	1894	g1 915208	gastric mucin [Sus scrofa]	59	31	1893
387	2	425	84	g1 160671	S antigen precursor [Plasmodium falciparum]	59	44	342
5	6	1123	10465	gml PID d101812	LumQ [Synecocystis sp.]	58	29	759
29	4	2098	3513	gml PID d100479	Na <sup>+</sup> -ATPase subunit J [Enterococcus hirae]	58	39	1416
30	5	4058	3651	g1 39478	ATP binding protein of transport ATPases [Bacillus firmus]	58	34	408
33	6	2983	2210	gml PID d101164	unknown [Bacillus subtilis]	58	45	774
36	8	5316	6179	g1 1318679	orf [Bacillus subtilis]	58	32	864
43	5	5926	3971	g1 1788150	(AE000278) protease II [Escherichia coli]	58	37	1956
46	5	3704	5221	gml PID e267329	Unknown [Bacillus subtilis]	58	42	1518
48	14	11722	11066	gml PID d101771	thiamin biosynthetic bifunctional enzyme [Synecocystis sp.]	58	34	657
52	1	1229	3	gml PID d101291	reductase [Pseudomonas aeruginosa]	58	35	1227
53	2	702	412	g1 2313357	(AE000345) cytochrome c biogenesis protein (ccda) [Helicobacter pylori]	58	25	291
58	4	6586	5498	g1 147329	transport protein [Escherichia coli]	58	41	1089
69	5	4934	3807	gml PID e311492	unknown [Bacillus subtilis]	58	41	1128
71	27	31357	32277	g1 2408014	hypothetical protein [Schizosaccharomyces pombe]	58	33	921
72	4	3586	2882	g1 18694	nodulin-21 (AA 1-201) [Glycine max]	58	34	705
74	3	4937	4230	g1 2291252	(AF008320) YnfO [Bacillus subtilis]	58	33	708
79	4	4594	3422	g1 1217989	ORF3 [Streptococcus pneumoniae]	58	44	1173
82	8	10585	8171	g1 882711	exonuclease V alpha-subunit [Escherichia coli]	58	38	2415
86	17	16017	15337	g1 47642	5-dehydroquinase hydrolyase (3-dehydroquinase) [Salmonella typhi]	58	32	681
97	2	931	560	g1 153794	egg [Streptococcus gordonii]	58	32	372

TABLE 2

S. pneumoniae - Putative coding regions of novel proteins similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)	match accession	match gene name	% sim	% ident	length (nt)
108	2	358	2724	gi 537020	vacB gene product [Escherichia coli]	58	37	2367
111	5	4593	5240	gi 1592142	ABC transporter, probable ATP-binding subunit [Methanococcus jannaschii]	58	36	648
120	3	4421	5110	gnl pid d101320	yggX [Bacillus subtilis]	58	47	690
128	16	13131	12673	gi 662919	ORF U [Enterococcus hirae]	58	42	459
132	3	6174	4939	gi 1800301	macrolide-efflux determinant [Streptococcus pneumoniae]	58	35	1236
133	1	111	890	gnl pid e269488	Unknown [Bacillus subtilis]	58	36	780
160	11	8615	9865	gi 473901	ORF1 [Lactococcus lactis]	58	39	1251
161	6	6268	6849	gnl pid d101024	DJ-1 protein [Homo sapiens]	58	32	582
169	1	214	2	gnl pid d100447	translation elongation factor-3 [Chlorella virus]	58	31	213
187	1	487	2	gi 475114	regulatory protein [Pedococcus pentosaceus]	58	38	486
187	6	4384	4620	gi 167475	deacetylation-related protein [Craterostigma plantagineum]	58	55	237
190	2	1464	1640	gnl pid e246727	competence pheromone [Streptococcus gordonii]	58	38	177
192	2	2012	1344	gnl pid d100556	rat CCP360 [Rattus rattus]	58	44	669
206	1	1292	696	gnl pid e202579	product similar to MrBA [Lactobacillus sakei]	58	35	597
216	2	2333	555	gnl pid e325036	hypothetical protein [Bacillus subtilis]	58	33	1779
217	5	5250	4321	gi 466474	cellobiose phosphorylase enzyme II'' [Bacillus stearothermophilus]	58	38	930
217	7	5636	5106	gnl pid d102048	B. subtilis cellobiose phosphorylase system celB; P46317 (1998)	58	44	531
232	1	2	811	gi 1573777	cell division ATP-binding protein (ftsE) [Haemophilus influenzae]	58	39	810
264	1	2	715	gi 973330	NetA [Bacillus subtilis]	58	32	714
280	1	33	767	gi 1786187	(AE000111) hypothetical 29.6 kD protein in thrC-talB intergenic region [Escherichia coli]	58	31	735
306	1	845	3	gnl pid e314780	YibL protein [Bacillus subtilis]	58	47	843
360	3	1556	1092	sp P46351 Y2GD_	HYPOTHETICAL 45.4 KD PROTEIN IN THIAMINASE 1 5' REGION.	58	32	465
363	5	2160	1867	gi 160871	S antigen precursor (Plasmodium falciparum)	58	51	294
372	1	806	3	gi 393394	Tb-291 membrane associated protein [Trypanosoma brucei subgroup]	58	37	804
382	2	749	519	pir JC1151 JC11'	hypothetical 20.3K protein (insertion sequence IS111) - Agrobacterium tumefaciens (strain P022) plasmid Ti	58	41	231

**TABLE 2**  
S. pneumoniae - Putative coding regions of novel proteins similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)	match accession	match gene name	% sim	% ident	length (nt)
3	9	8409	7471	gi 1499745	M. jannaschii predicted coding region MJ0912 [Methanococcus jannaschii]	57	38	939
10	10	7674	7507	gi 1737169	homologue to SKP1 [Arabidopsis thaliana]	57	30	168
11	1	2	412	gnl PID d100139	ORF [Acetobacter pasteurianus]	57	42	411
31	4	2032	1388	gi 3293213	[AF008220] YtpR [Bacillus subtilis]	57	37	645
33	11	6931	6449	gnl PID a324949	hypothetical protein [Bacillus subtilis]	57	36	483
45	5	5446	5060	gi 1592204	phosphoserine phosphatase [Methanococcus jannaschii]	57	44	387
49	7	6523	7632	gi 155369	PTS enzyme-II fructose [Xanthomonas campestris]	57	35	1110
52	6	4520	6850	gi 1574144	single-stranded-DNA-specific exonuclease [recJ] [Haemophilus influenzae]	57	35	2331
53	5	2079	1795	gi 1843580	replicase-associated polypeptide [oat blue dwarf virus]	57	46	285
63	6	5312	4995	gi 2182608	[AE000094] Y4rJ [Rhizobium sp. NGR234]	57	39	318
72	15	13883	13059	gnl PID d100892	homologous to SwissProt:VIDA_ECOLI hypothetical protein [Bacillus subtilis]	57	40	825
79	2	2561	1815	gnl PID d100965	homologue of NADPH-flavin oxidoreductase Pp of V. harveyi [Bacillus subtilis]	57	44	747
82	9	9596	9763	gi 1206045	short region of similarity to glycerophosphoryl diester phosphodiesterases [Caenorhabditis elegans]	57	35	168
86	16	15371	14493	gi 1787983	[AE000264] o288; 92 pct identical (1 gaps) to 222 residues of fragment YDIB_ECOLI SM: P28244 (223 aa) [Escherichia coli]	57	34	879
93	3	1695	1177	gi 1500003	mutator mutR protein [Methanococcus jannaschii]	57	33	519
96	6	3026	4519	gi 1559882	threonine synthase [Arabidopsis thaliana]	57	43	1494
99	14	17211	18212	gi 773349	BirA protein [Bacillus subtilis]	57	44	1002
112	8	7448	7903	gi 1591393	M. jannaschii predicted coding region MJ0678 [Methanococcus jannaschii]	57	30	456
113	16	18627	18328	pir A45605 A456	mature-parasite-infected erythrocyte surface antigen MESA - Plasmodium falciparum	57	22	300
123	2	343	1110	gi 1766149 F641	hypothetical protein H10355 - Haemophilus influenzae (strain Rd KW20)	57	38	768
123	4	2108	2884	gnl PID d102148	[AB001684] sulfate transport system permease protein [Chlorella vulgaris]	57	39	777
127	10	6477	5587	gi 1573082	nitrogenase C (nifC) [Haemophilus influenzae]	57	35	891
128	13	9251	9790	gi 153692	pneumolysin [Streptococcus pneumoniae]	57	38	540
131	4	2139	1363	gi 42081	nagD gene product (AA 1-250) [Escherichia coli]	57	36	777

TABLE 2

S. pneumoniae - Putative coding regions of novel proteins similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)	match accession	match gene name	% sim	% ident	length (nt)
136	1	214	1221	bbs1148453	Spae-endocarditis immunodominant antigen [Streptococcus sobrinus, MUCOB 263, Peptide, 1566 aa] (Streptococcus sobrinus)	57	44	1008
140	25	28701	26851	gi1505576	beta-glucoside permease [Bacillus subtilis]			
141	6	6395	7438	gi1995560	unknown [Schizosaccharomyces pombe]	57	38	1851
144	3	3231	2785	gnl PID d100139	ORF (Acetobacter pasteurianus)	57	41	1044
155	4	5454	4564	gi1600431	glycosyl transferase [Erwinia amylovora]	57	42	447
159	9	4877	5854	gi1290509	fo307 [Escherichia coli]	57	34	891
167	11	9710	9249	gnl PID d100139	ORF (Acetobacter pasteurianus)	57	35	978
171	6	4023	4436	gi1147402	mannose permease subunit III-Man [Escherichia coli]	57	42	462
178	4	2170	1076	gnl PID d102004	(AB001488) ATP-DEPENDENT RNA HELICASE DEAD HOMOLOG. [Bacillus subtilis]	57	29	414
190	1	145	1455	gi1149420	export/processing protein [Lactococcus lactis]	57	39	1095
198	1	298	95	gi1522268	unidentified ORF22 [Bacteriophage bIL67]	57	30	1311
203	2	3195	2110	gnl PID e283915	orf_c01003 [Sulfolobus solfataricus]	57	36	204
205	1	40	507	gi11439527	ELIA-man [Lactobacillus curvatus]	57	41	1086
214	7	4243	3797	gnl PID d102049	H. influenzae, ribosomal protein alanine acetyltransferase; P44305 (189) [Bacillus subtilis]	57	28	468
268	3	1767	1276	gi143979	L. curvatus small cryptic plasmid gene for rep protein [Lactobacillus curvatus]	57	48	447
351	1	324	34	gnl PID e275871	T03F6.b [Caenorhabditis elegans]	57	36	492
386	1	226	2	gi1160671	S antigen precursor [Plasmodium falciparum]	57	31	291
5	5	10486	8777	gi1405857	yehU [Escherichia coli]	57	45	225
8	5	3674	3910	gi1467199	phsC; L518_F1_2 [Mycobacterium leprae]	56	33	1710
10	3	3442	1874	gnl PID d101907	sodium-coupled permease [Synchocystis sp.]	56	39	237
21	1	1860	333	gi12313949	(AE000593) osmoprotection protein (proWX) [Helicobacter pylori]	56	36	1569
22	29	21968	22456	gnl PID d102001	(AB001488) PROBABLE ACETYLTRANSFERASE. [Bacillus subtilis]	56	33	1348
27	1	1361	3	gi1215132	lea59 (525) [Bacteriophage lambda]	56	37	489
28	9	4667	4278	gi11592090	DNA repair protein RAD2 [Methanococcus jannaschii]	56	30	1359
33	1	3	386	gnl PID d100139	ORF (Acetobacter pasteurianus)	56	29	390
						56	41	384

TABLE 2

S. pneumoniae - Putative coding regions of novel proteins similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)	match accession	match gene name	% sim	% ident	length (nt)
36	7	5122	5397	pir PQ0053 PQ00	hypothetical protein (proc 3' region) - <i>Pseudomonas aeruginosa</i> (strain PAO) (fragment)	56	28	276
40	4	3137	4318	gi 1800301	macrolide-efflux determinant ( <i>Streptococcus pneumoniae</i> )	56	27	1182
40	16	12511	13191	gnl PID e217602	plnU ( <i>Lactobacillus plantarum</i> )	56	38	681
48	17	13775	13023	gi 143729	transcription activator ( <i>Bacillus subtilis</i> )	56	35	753
75	4	1674	2594	gnl PID d102036	membrane protein ( <i>Bacillus stearotherophilus</i> )	56	25	921
85	3	1842	1459	gnl PID d100139	ORF ( <i>Acetobacter pasteurianus</i> )	56	41	384
89	7	5815	4940	gi 853777	product similar to E. coli PRF2 protein ( <i>Bacillus subtilis</i> )	56	42	876
105	2	1360	2718	gnl PID d101913	hypothetical protein ( <i>Synechocystis</i> sp.)	56	37	1359
112	3	2151	3194	gi 537201	ORF_0345 ( <i>Escherichia coli</i> )	56	31	1044
113	4	2754	2963	gnl PID d100340	ORF (plum pox virus)	56	28	210
122	3	1203	2054	gi 1649035	high-affinity periplasmic glutamine binding protein ( <i>Salmonella typhimurium</i> )	56	30	852
124	8	3939	3694	gnl PID e248893	unknown ( <i>Mycobacterium tuberculosis</i> )	56	27	246
125	4	4403	4107	gnl PID d100247	human non-muscle myosin heavy chain (Homo sapiens)	56	32	297
127	11	6608	6405	gi 2182397	(AE000073) Y4fN ( <i>Rhizobium</i> sp. NGR234)	56	35	204
134	5	4769	3849	gnl PID d101870	hypothetical protein ( <i>Synechocystis</i> sp.)	56	39	921
137	10	6814	7245	gi 1592011	sulfate permease (CysA) ( <i>Methanococcus jannaschii</i> )	56	34	432
142	8	5019	4582	pir A47071 A470	orf1 immediately 5' of nifs - <i>Bacillus subtilis</i>	56	29	438
146	8	4676	3650	gnl PID d101911	hypothetical protein ( <i>Synechocystis</i> sp.)	56	32	1017
148	3	1906	2739	gnl PID d101099	phosphate transport system permease protein PatA ( <i>Synechocystis</i> sp.)	56	36	834
150	4	4449	2743	gnl PID e304628	probably site-specific recombinase of the resolvase family of enzymes ( <i>Bacteriophage TP21</i> )	56	27	1707
172	1	2	208	gi 1787791	(AE000249) f317; This 317 aa orf is 27 pct identical (16 gaps) to 301 residues of an approx. 320 aa protein YXX-BACSU SW: P39140 ( <i>Escherichia coli</i> )	56	34	207
172	7	4979	5668	gi 396293	similar to <i>Bacillus subtilis</i> hypoth. 20 kDa protein, in tsr 3' region ( <i>Escherichia coli</i> )	56	40	690
186	7	3732	3367	gi 1732200	PTS permease for mannose subunit IIPan ( <i>Vibrio furnissii</i> )	56	36	366
187	2	2402	819	pir S57904 S579	virR49 protein - <i>Streptococcus pyogenes</i> (strain CS101, serotype M49)	56	35	1584

TABLE 2

S. pneumoniae - Putative coding regions of novel proteins similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)	match accession	match gene name	% sim	% ident	length (nt)
204	3	2772	2239	gi 606376	ORF_0162 (Escherichia coli)	56	35	534
206	2	3342	1633	gi 559861	clpM (Plasmid pAD1)	56	38	1710
219	3	1689	1096	gi 1146197	putative (Bacillus subtilis)	56	27	594
230	2	409	1485	pir C60328 C603	hypothetical protein 2 (ser 5' region) - Streptococcus mutans (strain OH2175, serotype 1)	56	40	1077
233	4	2930	3268	gi 1041785	rhoprY protein (Plasmodium yoelii)	56	24	339
273	2	1543	2724	gi 143089	lep protein (Bacillus subtilis)	56	32	1182
353	1	1	516	gnl PID e325000	hypothetical protein (Bacillus subtilis)	56	41	516
359	1	87	641	gi 1786952	(AE000176) o877; 100 pct identical to the first 86 residues of the 100 aa hypothetical protein fragment Y8G8_ECOLI SM: P54746 (Escherichia coli)	56	46	555
363	7	4482	4198	gi 1573353	outer membrane integrity protein (tolA) (Haemophilus influenzae)	56	38	285
376	1	2	508	gnl PID e325031	hypothetical protein (Bacillus subtilis)	56	33	507
18	1	836	177	gnl PID d100872	a negative regulator of pho regulon (Pseudomonas aeruginosa)	55	31	660
28	4	1824	1618	gnl PID e316518	SPAT protein (Dictyostelium discoideum)	55	40	207
29	6	4496	5041	gi 1088261	unknown protein (Anabaena sp.)	55	31	546
38	16	9695	10702	gi 580905	B. subtilis genes rpmI, rnpA, 50kd, gida and gidB (Bacillus subtilis)	55	31	1008
49	5	5727	6182	gi 1786951	(AE000176) heat-responsive regulatory protein (Escherichia coli)	55	29	456
51	4	2381	3241	gnl PID d101293	ybbA (Bacillus subtilis)	55	42	861
52	9	9640	10866	gi 153016	ORF 419 protein (Staphylococcus aureus)	55	23	1227
53	4	1813	1349	gi 896042	ospP (Borrelia burgdorferi)	55	30	465
60	5	4794	5756	gi 1499876	magnesium and cobalt transport protein (Methanococcus jannaschii)	55	38	963
71	9	14176	15408	gi 1857120	glycoyl transferase (Neisseria meningitidis)	55	41	1233
75	6	3189	4229	gnl PID e209890	NAD alcohol dehydrogenase (Bacillus subtilis)	55	44	1041
108	10	10488	9820	gnl PID e324997	hypothetical protein (Bacillus subtilis)	55	36	669
113	12	12273	13037	gnl PID e311496	unknown (Bacillus subtilis)	55	34	765
113	13	13007	13945	gi 1573423	1-phosphofructokinase (fruk) (Haemophilus influenzae)	55	39	939
126	5	6764	5907	gi 1790131	(AE000446) hypothetical 29.7 kD protein in bpa-gyrB intergenic region (Escherichia coli)	55	37	858



TABLE 2

S. pneumoniae - Putative coding regions of novel proteins similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)	match accession	match gene name	% sim	% ident	length (nt)
129	3	2719	902	gnl PID d101425	Pr-peptidase [Bacillus licheniformis]	55	35	1818
138	3	2593	1610	gi 142833	ORF2 [Bacillus subtilis]	55	37	984
140	6	6916	5633	gnl PID d100964	homologue of hypothetical protein in a rapamycin synthesis gene cluster of Streptomyces hygroscopicus [Bacillus subtilis]	55	26	1284
147	3	3854	2136	gi 472330	dihydrolipoamide dehydrogenase [Clostridium magnum]	55	39	1719
147	10	10204	8921	gnl PID e73078	dihydroorotase [Lactobacillus leichmannii]	55	38	1284
148	5	3430	4119	gi 290572	peripheral membrane protein U [Escherichia coli]	55	29	690
148	6	4171	4650	gi 695769	transposase [Xanthobacter autotrophicus]	55	37	480
149	14	12564	11650	gnl PID d101329	YqjG [Bacillus subtilis]	55	32	915
156	3	1113	550	gi 2314496	(AE000634) conserved hypothetical integral membrane protein [Helicobacter pylori]	55	34	564
159	10	6625	5897	gi 290533	similar to E. coli ORF adjacent to suc operon; similar to gntR class of regulatory proteins [Escherichia coli]	55	29	729
164	3	1784	2332	gnl PID e255118	hypothetical protein [Bacillus subtilis]	55	37	549
166	5	2772	3521	gi 40348	put. resolvase Tnp I (AA 1 - 284) [Bacillus thuringiensis]	55	35	750
164	11	7428	7216	gnl PID e249407	unknown [Mycobacterium tuberculosis]	55	38	213
167	5	3860	3345	gi 535052	involved in protein secretion [Bacillus subtilis]	55	28	516
186	5	2880	2563	gi 606080	ORF_0290: Geneplot suggests frameshift linking to o267, not found [Escherichia coli]	55	35	318
189	8	4311	5396	gnl PID e183450	hypothetical EcsB protein [Bacillus subtilis]	55	32	1086
192	5	3270	3079	gi 1196504	vitellogenin convertase [Aedes aegypti]	55	38	192
195	2	2454	1384	gi 1574693	transferase, peptidoglycan synthesis (murG) [Haemophilus influenzae]	55	33	1071
198	4	3013	2471	gnl PID e13074	hypothetical protein [Bacillus subtilis]	55	29	543
214	1	373	744	gnl PID d101741	transposase [Synechocystis sp.]	55	33	372
219	2	1115	456	gi 288301	ORF2 gene product [Bacillus megaterium]	55	30	660
263	7	3742	3443	gi 18137	ecgr-4 product [Chlamydomonas reinhardtii]	55	48	300
285	1	2	829	gnl PID d100974	unknown [Bacillus subtilis]	55	40	828
286	1	650	249	gi 396844	ORF (18 kDa) [Vibrio cholerae]	55	31	402
297	2	1329	1696	gi 150848	prtc [Porphyromonas gingivalis]	55	39	468

TABLE 2

S. pneumoniae - Putative coding regions of novel proteins similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)	match accession	match gene name	% sim	% ident	length (nt)
309	2	218	982	gi 1574491	hypothetical [Haemophilus influenzae]	55	35	765
328	2	646	224	gi 571500	prohibitin [Saccharomyces cerevisiae]	55	27	423
330	1	1340	474	gi 396397	soxS [Escherichia coli]	55	29	867
364	3	2538	1546	gi 393394	Tb-291 membrane associated protein [Trypanosoma brucei subgroup]	55	36	993
368	3	941	105	gi 160671	S antigen precursor [Plasmodium falciparum]	55	40	837
3	5	4604	3624	gi 2293176	(AF008220) signal transduction protein kinase [Bacillus subtilis]	54	26	981
9	11	7746	7246	gi 1146245	putative [Bacillus subtilis]	54	38	501
38	24	16213	17937	gi 1480429	putative transcriptional regulator [Bacillus stearothermophilus]	54	27	1725
40	8	5076	4882	gi 39989	methionyl-tRNA synthetase [Bacillus stearothermophilus]	54	35	195
43	4	3980	2367	gnl PID el48611	ABC transporter [Lactobacillus helveticus]	54	25	1614
52	10	10844	12103	gi 1762962	FemA [Staphylococcus simulans]	54	29	1260
57	1	3	512	gi 558177	endo-1,4-beta-xylanase [Cellulomonas fimi]	54	36	510
58	3	4749	4246	gnl PID d101237	hypothetical [Bacillus subtilis]	54	29	504
71	7	10684	11703	gi 510255	orf3 [Escherichia coli]	54	31	1020
71	20	27546	27737	gi 202543	serotonin receptor [Rattus norvegicus]	54	31	192
72	2	844	1098	gi 148613	srnB gene product [Plasmid F]	54	37	255
72	7	7438	6695	gi 1196496	recombinase [Moraxella bovis]	54	38	744
74	10	14043	13465	gi 1200342	ORF 3 gene product [Bradyrhizobium japonicum]	54	32	579
74	12	16483	15995	gi 2317798	maturase-related protein [Pseudomonas alcaligenes]	54	30	489
86	3	2877	2155	gi 46988	orf9.6 possibly encodes the O unit polymerase [Salmonella enterica]	54	34	723
89	5	4433	3921	gi 147211	phnO protein [Escherichia coli]	54	41	513
90	1	3	464	gi 2317798	maturase-related protein [Pseudomonas alcaligenes]	54	30	462
96	10	8058	8510	gnl PID d102015	(AB001488) SIMILAR TO SALMONELLA TYPHIMURUM SLTY GENE REQUIRED FOR SURVIVAL IN MACROPHAGE. [Bacillus subtilis]	54	32	453
97	6	4662	3604	gi 1591394	transketolase [Methanococcus jannaschii]	54	30	1059
106	11	10406	12010	gi 606286	ORF_o637 [Escherichia coli]	54	32	1605
147	8	8663	7404	gnl PID d101615	ORF_ID:o31987; similar to [SwissProt Accession Number P37340] [Escherichia coli]	54	35	1260

TABLE 2  
S. pneumoniae - Putative coding regions of novel proteins similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)	match accession	match gene name	% sim	% ident	length (nt)
171	4	2477	3223	gi 1439528	EIIC-man [Lactobacillus curvatus]	54	36	747
174	2	2068	1787	gnl PID d100518	motor protein [Homo sapiens]	54	35	282
188	1	526	1188	gnl PID e250352	unknown [Mycobacterium tuberculosis]	54	31	663
198	5	3582	2884	gnl PID e313074	hypothetical protein [Bacillus subtilis]	54	33	699
207	1	1	1641	gnl PID d101813	hypothetical protein [Synecocystis sp.]	54	24	1641
210	1	2	655	gi 2293206	[AF008220] Ymp [Bacillus subtilis]	54	29	654
225	2	966	2357	gnl PID e330194	R1186.1 [Caenorhabditis elegans]	54	39	1392
241	1	1681	347	gnl PID d101813	hypothetical protein [Synecocystis sp.]	54	26	1335
263	2	907	1395	gnl PID d101886	transposase [Synecocystis sp.]	54	30	489
263	6	3450	2977	gi 160671	S antigen precursor [Plasmodium falciparum]	54	47	474
277	3	2517	1363	gi 1196926	unknown protein [Streptococcus mutans]	54	30	1155
307	1	828	4	gi 2293198	[AF008220] Ytp [Bacillus subtilis]	54	28	825
325	1	19	768	gi 2182507	[AE000083] Y4IH [Rhizobium sp. NCR234]	54	37	750
332	2	898	590	gi 1591815	ADP-ribosylglycohydrolase (drac) [Methanococcus jannaschii]	54	32	309
385	4	240	479	gi 530878	amino acid feature: N-glycosylation sites, aa 41...43, 46...48, 51...53, 72...74, 107...109, 128...130, 132...134, 158...160, 163...165; amino acid feature: Rod protein domain, aa 169...340; amino acid feature: globular protein domain	54	49	240
7	25	19702	19493	gnl PID e255111	hypothetical protein [Bacillus subtilis]	53	32	210
23	3	2497	2033	gnl PID d102015	[AB001488] SIMILAR TO SALMONELLA TYPHIMURUM SLVY GENE REQUIRED FOR SURVIVAL IN MACROPHAGE. [Bacillus subtilis]	53	25	465
29	11	9042	10121	gi 143331	alkaline phosphatase regulatory protein [Bacillus subtilis]	53	31	1080
33	3	1479	1009	pir S10655 S106	hypothetical protein X - Pyrococcus woesei (fragment)	53	33	471
36	6	4583	5134	gnl PID e316029	unknown [Mycobacterium tuberculosis]	53	30	552
38	14	8521	8898	gi 580904	homologous to E. coli rnpA [Bacillus subtilis]	53	30	378
52	7	7007	8686	gi 1377831	unknown [Bacillus subtilis]	53	29	1680
54	17	17555	19564	gi 666069	orf2 gene product [Lactobacillus leichmannii]	53	36	2010
56	1	1	681	gi 1592266	restriction modification system S subunit [Methanococcus jannaschii]	53	32	681

TABLE 2

S. pneumoniae - Putative coding regions of novel proteins similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)	match accession	match gene name	% sim	% ident	length (nt)
57	10	9431	8487	gi 1788543	(AE000310) f351: Residues 1-121 are 100 pct identical to YJUL_ECOLI SW: P33944 (122 aa) and aa 152-351 are 100 pct identical to YJUL_ECOLI SW: P33943 [Escherichia coli]	53	31	945
61	1	429	4	gnl PID e236467	B0024.12 [Caenorhabditis elegans]			
71	1	5772	4	gi 393394	7B-291 membrane associated protein [Trypanosoma brucei subgroup]	53	33	426
72	3	894	2840	gi 2293178	(AF008220) YtaD [Bacillus subtilis]	53	33	5769
73	14	9793	9212	gi 1778556	putative cobalamin synthesis protein [Escherichia coli]	53	27	1947
88	7	5217	4342	gi 2098719	putative fimbrial-associated protein [Actinomyces naeslundii]	53	32	582
93	5	2395	1688	gi 563366	glucuronate oxidoreductase [Gluconobacter oxydans]	53	38	876
96	9	6632	7762	gi 517204	ORF1, putative 42 kDa protein [Streptococcus pyogenes]	53	33	708
108	8	7629	8600	gi 149581	maturation protein [Lactobacillus paracasei]	53	42	1131
128	9	6412	6972	gnl PID e317237	unknown [Mycobacterium tuberculosis]	53	32	972
128	12	8429	9253	gi 311070	pentraxin fusion protein [Xenopus laevis]	53	36	561
148	1	3	950	pir A61607 A616	probable hemolysin precursor - Streptococcus agalactiae (strain 74-360)	53	31	825
163	2	2162	3022	gi 1755150	nocturnin [Xenopus laevis]	53	36	948
171	3	2304	2624	gi 1732200	PTS permease for mannose subunit IIPMan [Vibrio furnissii]	53	30	861
182	5	3785	3051	gnl PID d100572	unknown [Bacillus subtilis]	53	32	321
209	3	2948	1935	gi 1778505	ferric enterobactin transport protein [Escherichia coli]	53	35	735
218	5	3884	2406	gi 40162	murE gene product [Bacillus subtilis]	53	28	1014
250	3	473	790	gnl PID e334776	YlbH protein [Bacillus subtilis]	53	34	1479
275	1	1	1611	gnl PID d101314	Yqew [Bacillus subtilis]	53	30	318
332	1	544	2	gi 409286	barU [Bacillus subtilis]	53	35	1611
3	2	2543	3445	gnl PID e233879	hypothetical protein [Bacillus subtilis]	53	31	543
3	22	22402	23376	gi 38969	lacP gene product [Agrobacterium radiobacter]	52	39	903
5	3	8094	2356	gnl PID e324915	IgaI protease [Streptococcus sanguis]	52	36	975
22	26	19961	20212	gi 152901	ORF 3 [Spirochaeta aurantia]	52	32	5739
22	31	23140	24666	gi 289262	comE ORF3 [Bacillus subtilis]	52	35	252
27	6	5397	4801	gi 39573	P20 (AA 1-178) [Bacillus licheniformis]	52	32	1527
						52	35	597

TABLE 2

S. pneumoniae - Putative coding regions of novel proteins<sup>a</sup> similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)	match accession	match gene name	% sim	% ident	length (nt)
35	10	8604	7357	gi 508241	putative O-antigen transporter [Escherichia coli]	52	27	1248
45	4	4801	3662	gnl PID d102243	(AB005534) homologs are found in E. coli and H. influenzae; see SWISS_PROT ACC# P42100 [Bacillus subtilis]	52	36	1140
48	18	14385	13726	gnl PID e205174	orf2 [Lactobacillus helveticus]	52	25	660
49	4	5321	5755	gi 2317740	(AF013987) nitrogen regulatory IIA protein (Vibrio cholerae)	52	19	435
54	4	2773	4668	gi 1500472	M. jannaschii predicted coding region MJ1577 [Methanococcus jannaschii]	52	36	1896
54	6	5250	4969	gi 2182453	(AB000079) Y410 [Rhizobium sp. NGR234]	52	40	282
66	6	8400	6955	gi 43140	TrkO protein [Escherichia coli]	52	30	1446
71	26	30659	31312	gnl PID e314993	unknown [Mycobacterium tuberculosis]	52	23	654
75	2	1673	1035	gnl PID d102271	(AB001683) Para [Streptomyces sp.]	52	27	639
81	3	1439	2893	gnl PID e311458	rhamnose kinase [Bacillus subtilis]	52	32	1455
81	8	4987	5781	gi 147403	mannose permease subunit II-P-Man [Escherichia coli]	52	37	795
83	21	20687	21853	gi 143365	phosphoribosyl aminimidazole carboxylase II (PUR-K; ttg start codon) [Bacillus subtilis]	52	37	1167
86	6	5785	4592	gi 1276879	EpsF [Streptococcus thermophilus]	52	26	1194
86	120	19390	17861	gi 454844	ORF 3 [Schistosoma mansoni]	52	26	1530
96	13	10540	9659	gi 288299	ORF1 gene product [Bacillus megaterium]	52	33	882
111	1	2	2026	gi 148309	cytolysin B transport protein [Enterococcus faecalis]	52	27	2025
112	2	1457	2167	gi 471234	orf1 [Haemophilus influenzae]	52	33	711
118	3	2931	2365	bbs 151233	Hip-24 kDa macrophage infectivity potentiator protein [Legionella pneumophila, Philadelphia-1, Peptide, 184 aa] [Legionella pneumophila]	52	33	567
122	9	5846	5951	gi 8214	myosin heavy chain [Drosophila melanogaster]	52	36	306
122	11	6159	6374	gi 434025	dihydrolysoamide acetyltransferase [Pelobacter carbinolicus]	52	52	216
134	6	4880	6313	gi 153733	M protein trans-acting positive regulator [Streptococcus pyogenes]	52	43	1434
135	3	1238	2716	gnl PID e245024	unknown [Mycobacterium tuberculosis]	52	35	1479
141	3	1681	2319	gnl PID d100573	unknown [Bacillus subtilis]	52	32	639
161	4	2562	5024	gi 1146243	22.4% identity with Escherichia coli DNA-damage inducible protein ...; putative [Bacillus subtilis]	52	36	2463
173	2	968	183	gi 1215693	putative orf; GT9 orf434 [Mycoplasma pneumoniae]	52	30	786

TABLE 2  
S. pneumoniae - Putative coding regions of novel proteins similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)	match accession	match gene name	% sim	% ident	length (nt)
198	6	4400	3567	gnl PID e313010	hypothetical protein [Bacillus subtilis]	52	26	834
210	12	8844	9107	gi 497647	DNA gyrase subunit B [Mycoplasma genitalium]	52	38	264
214	10	5264	5431	gi 550697	envelope protein [human immunodeficiency virus type 1]	52	36	168
225	1	15	884	gi 1552773	hypothetical [Escherichia coli]	52	34	870
230	1	39	362	gnl PID d100582	unknown [Bacillus subtilis]	52	28	324
287	1	871	2	gnl PID e335028	protease/peptidase [Mycobacterium leprae]	52	29	870
363	2	1305	4	gi 3931394	TB-291 membrane associated protein [Trypanosoma brucei subgroup]	52	32	1302
23	2	2048	1173	gnl PID e254943	unknown [Mycobacterium tuberculosis]	51	30	876
29	3	742	1521	gi 929900	5'-methylthioadenosine phosphorylase [Sulfolobus solfataricus]	51	31	780
45	1	410	1597	gi 1877429	integrase [Streptococcus pyogenes phage T12]	51	32	1188
48	26	19227	18946	gi 2314455	[AE000633] transcriptional regulator (tena) [Helicobacter pylori]	51	33	282
73	5	4276	4016	gi 474177	alpha-D-1,4-glucosidase [Staphylococcus xylosum]	51	31	261
81	11	8935	12057	gi 311070	pentraxin fusion protein [Xenopus laevis]	51	31	3123
83	5	1195	1986	gnl PID d101316	Qqf1 [Bacillus subtilis]	51	33	792
98	10	7531	8538	gi 41500	ORF 3 (AA 1-352); 38 kD (put. ftsX) [Escherichia coli]	51	28	1008
113	6	3908	5173	gi 466882	pps1; B1496_C2_189 [Mycobacterium leprae]	51	27	1266
124	1	326	57	gi 2191168	[AF007270] contains similarity to myosin heavy chain [Arabidopsis thaliana]	51	32	270
129	10	7286	6816	gi 1046241	orf14 [Bacteriophage HP1]	51	30	471
143	3	4963	3983	gi 1354935	probable copper-transporting atpase [Escherichia coli]	51	26	981
148	15	11359	10226	gi 2293256	[AF008220] putative hippurate hydrolase [Bacillus subtilis]	51	36	1134
149	8	6003	7313	gi 1633572	Herpesvirus saimiri ORF73 homolog [Kaposi's sarcoma-associated herpes-like virus]	51	21	1311
151	9	12092	11550	gnl PID e281580	hypothetical 40.7 kD protein [Bacillus subtilis]	51	34	543
159	6	2555	3208	gi 146944	CMP-N-acetylneuraminic acid synthetase [Escherichia coli]	51	36	654
174	1	1797	4	gi 1773166	probable copper-transporting atpase [Escherichia coli]	51	28	1794
265	4	2231	1773	gnl PID e256400	anti-P.falciparum antigenic polypeptide [Saimiri sciureus]	51	18	459
277	2	643	1311	pir S32915 S329	plid protein - Neisseria gonorrhoeae	51	33	669

TABLE 2  
S. pneumoniae - Putative coding regions of novel proteins similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)	match accession	match gene name	% sim	% ident	length (nt)
350	1	890	3	gi 290509	j0307 [Escherichia coli]	51	30	888
363	4	1228	4885	gi 1707247	partial CDS (Caenorhabditis elegans)	51	23	3258
367	1	1701	4	gi 393394	Tb-291 membrane associated protein (Trypanosoma brucei subgroup)	51	32	1698
15	5	5174	4497	gnl PID e58151	P3 [Bacillus subtilis]	50	38	678
16	4	2220	2582	gnl PID e325010	hypothetical protein [Bacillus subtilis]	50	29	363
19	5	2591	4159	gi 1552733	similar to voltage-gated chloride channel protein (Escherichia coli)	50	30	1569
25	4	2701	1997	gi 887849	ORF_f219 [Escherichia coli]	50	27	705
35	1	211	417	gnl PID e236697	unknown [Saccharomyces cerevisiae]	50	33	207
39	4	3416	5152	gnl PID d100974	unknown [Bacillus subtilis]	50	27	1737
51	7	4000	5181	gi 1592027	carbamoyl-phosphate synthase, pyrimidine-specific, large subunit [Methanococcus jannaschii]	50	27	1182
51	9	7179	8303	gi 1591847	type I restriction-modification enzyme, S subunit [Methanococcus jannaschii]	50	28	1125
52	8	8740	9534	gi 144297	acetyl esterase (XyC) [Caldocellum saccharolyticum]	50	34	795
52	16	16591	15770	gi 2108229	basic surface protein [Lactobacillus fermentum]	50	34	822
57	7	6031	6336	gi 2275264	60S ribosomal protein L78 [Schizosaccharomyces pombe]	50	40	306
71	23	29348	28383	gnl PID d101328	YqjA [Bacillus subtilis]	50	30	966
86	12	11155	10769	gnl PID e324964	hypothetical protein [Bacillus subtilis]	50	24	387
93	2	1205	330	gi 1066016	similar to Escherichia coli pyruvate, water dikinase, Swiss-Prot Accession Number P25538 [Pyrococcus furiosus]	50	24	876
96	5	1673	2959	gnl PID e322433	gamma-glutamylcysteine synthetase [Brassica juncea]	50	29	1287
98	2	218	1171	gi 151110	leucine-, isoleucine-, and valine-binding protein [Pseudomonas aeruginosa]	50	30	954
103	4	3303	2785	gi 154310	O-antigen ligase [Salmonella typhimurium]	50	31	519
115	5	6480	5980	gi 895747	putative cel operon regulator [Bacillus subtilis]	50	26	501
129	11	7559	7305	gi 1216475	skeletal muscle ryanodine receptor (Homo sapiens)	50	32	255
129	13	8192	7965	gi 152271	319-kDa protein [Rhizobium meliloti]	50	30	228
151	5	7634	6819	gi 40348	put. resolvase Tnp I (AA 1 - 284) [Bacillus thuringiensis]	50	35	816
153	1	1	597	gnl PID d102015	(AB001488) SIMILAR TO NITROREDUCTASE, [Bacillus subtilis]	50	29	597

TABLE 2

S. pneumoniae - Putative coding regions of novel proteins similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)	match accession	match gene name	% sim	% ident	length (nt)
155	5	5986	5432	gi 1276880	EpsG (Streptococcus thermophilus)	50	28	555
160	9	7390	6323	gi 1786983	(AE000179) o331, 92 pct identical to the 333 aa hypothetical protein YHE_EC01 SW: P52697; 26 pct identical (7 gaps) to 167 residues of the 373 aa protein MLE_TRICU SW: P46057; SW: P52697 (Escherichia coli)	50	30	1088
163	6	7396	8091	gnl PID d101313	Yqen (Bacillus subtilis)	50	22	696
167	6	5232	3940	gi 413926	ipa-2r gene product (Bacillus subtilis)	50	27	1293
169	2	807	130	gnl PID e304540	endolysin (Bacteriophage Bastille)	50	35	678
171	5	3168	4025	gi 806080	[ORF_0290; Geneplot suggests frameshift linking to o267, not found (Escherichia coli)]	50	27	858
210	11	8151	8414	gi 330038	HRV 2 polyprotein (Human rhinovirus)	50	25	264
364	1	1538	135	gi 393396	Pb-292 membrane associated protein (Trypanosoma brucei subgroup)	50	31	1404
10	7	5911	5090	gi 144859	[ORF B (Clostridium perfringens)]	49	24	822
26	5	10754	9768	gi 142440	ATP-dependent nuclease (Bacillus subtilis)	49	31	987
66	7	9777	8398	gi 414170	[trkA gene product (Methanosarcina mazei)]	49	26	1380
77	6	5364	4648	gnl PID e285322	RecX protein (Mycobacterium smegmatis)	49	28	717
82	13	12689	13249	gnl PID e255091	hypothetical protein (Bacillus subtilis)	49	20	561
93	9	4866	4531	gi 40067	X gene product (Bacillus sphaericus)	49	26	336
112	5	4019	4948	gi 1574380	lhc-1 operon protein (lhcB) (Haemophilus influenzae)	49	27	930
129	7	6058	4949	gnl PID e267587	Unknown (Bacillus subtilis)	49	35	1110
135	5	3875	4438	gi 39573	P20 (AA 1-178) (Bacillus licheniformis)	49	25	564
154	2	1423	1953	gnl PID d101102	regulatory components of sensory transduction system (Synechocystis sp.)	49	29	531
156	5	2878	1637	gnl PID d101732	hypothetical protein (Synechocystis sp.)	49	25	1242
173	5	3500	2940	gi 490324	LORF X gene product (unidentified)	49	30	561
182	1	1057	2	gi 331002	first methionine codon in the ECLF1 ORF (Saimiriine herpesvirus 2)	49	25	1056
192	6	5352	3667	gi 2394472	(AF024499) contains similarity to homeobox domains (Caenorhabditis elegans)	49	23	1686
253	4	1129	1350	gi 531116	SIR4 protein (Saccharomyces cerevisiae)	49	23	222
277	1	600	136	gi 396844	[ORF (18 kDa) (Vibrio cholerae)]	49	32	465
327	3	1435	887	gi 733524	phosphatidylinositol-4,5-diphosphate 3-kinase (Dictyostelium discoideum)	49	24	549



TABLE 2

S. pneumoniae - Putative coding regions of novel proteins similar to known proteins

Config ID	ORF ID	Start (nt)	Stop (nt)	match accession	match gene name	% sim	% ident	length (nt)
365	3	1436	132	gi 393394	Tb-291 membrane associated protein (Trypanosoma brucei subgroup)	49	31	1305
33	7	4461	3277	gi 1145644	codes for a protein of unknown function (Escherichia coli)	48	26	1185
40	2	652	1776	gnl pid e290649	ornithine decarboxylase (Nicotiana tabacum)	48	29	1125
67	4	1377	2384	gi 1772652	2-keto-3-deoxygluconate kinase (Haloferax alicantel)	48	30	1008
74	2	4269	3871	gi 2182678	(AE00101) Y4vJ (Rhizobium sp. NCR234)	48	27	399
81	2	1326	541	gi 153672	lactose repressor (Streptococcus mutans)	48	33	786
81	4	2981	3646	gi 146042	fuculose-1-phosphate aldolase (fucA) (Escherichia coli)	48	30	666
97	1	602	51	gi 153794	rgg (Streptococcus gordonii)	48	29	552
110	1	1	3132	gi 138114	prtB gene product (Lactobacillus delbrueckii)	48	23	3132
131	5	2914	2147	gnl pid e183811	Acyl-ACP thioesterase (Brassica napus)	48	27	768
133	4	3494	2628	gnl pid e261988	putative ORF (Bacillus subtilis)	48	27	867
139	6	4231	4599	gi 1049388	ZK470.1 gene product (Caenorhabditis elegans)	48	23	369
139	8	5036	5665	gi 1022725	unknown (Staphylococcus haemolyticus)	48	29	630
140	12	11936	11007	gnl pid d102049	H. influenzae, ribosomal protein alanine acetyltransferase; P4305 (189) (Bacillus subtilis)	48	27	930
146	9	5670	4654	gi 1591731	melvalonate kinase (Methanococcus jannaschii)	48	24	1017
161	3	1280	2374	gnl pid d101578	Collagenase precursor (EC 3.4.-.-) (Escherichia coli)	48	24	1095
172	11	10581	11048	gnl pid d101132	hypothetical protein (Synecocystis sp.)	48	27	468
182	4	2930	2586	gi 40067	X gene product (Bacillus sphaericus)	48	37	345
210	15	10786	11196	sp p13940 LE29	LATE EMBRYOGENESIS ABUNDANT PROTEIN D-29 (LEA D-29)	48	30	411
214	12	6231	6482	gi 40389	non-toxic components (Clostridium botulinum)	48	26	252
221	1	704	3	gi 1573364	H. influenzae predicted coding region HI0392 (Haemophilus influenzae)	48	27	702
227	2	647	3928	gi 1673693	(AE000005) Mycoplasma pneumoniae, C09_orf718 Protein (Mycoplasma pneumoniae)	48	30	3282
253	2	480	758	gnl pid e236697	unknown (Saccharomyces cerevisiae)	48	31	279
363	3	1874	1122	gi 18137	cgcr-4 product (Chlamydomonas reinhardtii)	48	40	753
389	1	505	2	gi 18137	cgcr-4 product (Chlamydomonas reinhardtii)	48	38	504
3	21	20879	22258	gnl pid e264778	putative maltose-binding protein (Streptomyces coelicolor)	47	33	1380

TABLE 2

S. pneumoniae - Putative coding regions of novel proteins similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)	match accession	match gene name	% sim	% ident	length (nt)
6	4	4089	4658	gi 39573	p20 (AA 1-178) [Bacillus licheniformis]	47	23	570
15	3	3736	1760	gnl PID d100572	unknown [Bacillus subtilis]	47	25	1977
35	15	14516	13263	gi 1773351	Cap5L [Staphylococcus aureus]	47	20	1254
51	6	3547	4002	pir A37024 A370	32K antigen precursor - Mycobacterium tuberculosis	47	38	456
55	8	10154	9273	gi 39848	IJ3 [Bacillus subtilis]	47	26	882
92	4	1753	3276	gnl PID e280611	PCPC (Streptococcus pneumoniae)	47	35	1524
127	9	5589	5386	gi 1786458	(AE000134) f120; This 120 aa orf is 76 pct identical (0 gaps) to 42 residues of an approx. 48 aa protein Y127_HAEIN SW: P43949 [Escherichia coli]	47	32	204
130	2	1232	1759	gnl PID e266555	unknown [Mycobacterium tuberculosis]	47	23	528
140	4	4951	3542	gnl PID d100964	homologue of hypothetical protein in a rapamycin synthesis gene cluster of Streptomyces hygroscopicus [Bacillus subtilis]	47	24	1410
151	4	6814	6200	gi 1522674	M. jannaschii predicted coding region MJEC44 [Methanococcus jannaschii]	47	27	615
157	3	803	1174	gnl PID d101320	Yqg2 [Bacillus subtilis]	47	25	372
178	5	3267	2155	gi 2367190	(AE000390) o334; sequence change joins ORFs yqjR & yqjS from earlier version (YqjR_ECOLI SW: P42599 and YqjS_ECOLI SW: P42600) [Escherichia coli]	47	30	1113
273	1	2	1549	gnl PID e254973	autolysin sensor kinase [Bacillus subtilis]	47	32	1548
300	2	880	644	gi 1835755	zinc finger protein Png-1 [Mus musculus]	47	22	237
54	14	14182	12638	pir S43609 S436	rofa protein - Streptococcus pyogenes	46	24	1545
88	1	2	1018	gnl PID e223891	xylose repressor [Anaerocellum thermophilum]	46	27	1017
96	7	4553	5860	gnl PID d101452	ORF_ID: o34785; similar to [SwissProt Accession Number P45272] [Escherichia coli]	46	23	1308
112	1	1127	3	gi 2209215	(AF004325) putative oligosaccharide repeat unit transporter (Streptococcus pneumoniae)	46	24	1125
122	13	7308	7982	gi 1054776	hr44 gene product (Homo sapiens)	46	34	675
127	14	9198	8125	gi 1469286	afuA gene product [Actinobacillus pleuropneumoniae]	46	28	1074
132	4	7093	6197	gi 153794	egg [Streptococcus gordonii]	46	26	897
140	8	8220	7723	gi 1235795	pullulanase [Thermoanaerobacterium thermosulfurigenes]	46	21	498
140	9	9205	8315	gi 407878	leucine rich protein (Streptococcus equisimilis)	46	27	891

TABLE 2

S. pneumoniae - Putative coding regions of novel proteins similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)	match accession	match gene name	% sim	% ident	length (nt)
162	1	1	1125	gi 1143209	ORF7: Method: conceptual translation supplied by author [Shigella sonnei]	46	25	1125
199	1	1	585	gi 1947171	[AF000299] No definition line found [Caenorhabditis elegans]	46	28	585
223	3	1971	1477	sp P02562 MYSS_	MYOSIN HEAVY CHAIN, SKELETAL MUSCLE (FRAGMENTS)	46	27	495
232	2	760	1608	gi 1016112	ycf38 gene product [Cyanophora paradoxa]	46	28	849
292	1	687	220	gi 1673744	[AE000011] Mycoplasma pneumoniae, cytidine deaminase; similar to GenBank Accession Number C5312, from H. pium [Mycoplasma pneumoniae]	46	29	468
30	8	5843	6472	gi 1798049	[AE000270] o235; This 235 aa orf is 29 pct identical (10 gaps) to 198 residues of an approx. 216 aa protein YTXB_BACSU SN: P06568 [Escherichia coli]	45	24	630
48	6	3461	3868	gi 722339	unknown [Acetobacter xylinum]	45	29	408
60	1	307	2	gi 1699079	coded for by C. elegans cDNA yk41h4.3; coded for by C. elegans cDNA yk148g10.5; coded for by C. elegans cDNA yk152g5.5; coded for by C. elegans cDNA yk59a10.5; coded for by C. elegans cDNA yk41h4.5; coded for by C. elegans cDNA cm20g10; coded	45	36	306
72	16	14371	114874	gi 1321900	NADH dehydrogenase (ubiquinone) [Artemia franciscana]	45	25	504
99	7	9158	7941	gi 152192	mutation causes a succinogluconate-kinase phenotype; ExoQ is a transmembrane protein; third gene of the exoFQ operon; putative [Rhizobium meliloti]	45	28	1218
127	12	7046	6606	bbs 153689	HistB-iron utilization protein [Haemophilus influenzae, type B, DL42, NTHI TN106, Peptide, 506 aa] [Haemophilus influenzae]	45	24	441
137	5	1561	2619	gi 472921	v-type Na-ATPase [Enterococcus hirae]	45	33	1059
209	1	774	364	gi 304141	restriction endonuclease beta subunit [Bacillus coagulans]	45	28	411
314	1	604	2	gi 1480457	latex allergen [Hevea brasiliensis]	45	31	603
20	18	19782	20288	gi 433942	ORF [Lactococcus lactis]	44	26	507
87	8	7030	6452	gi 537207	ORF f277 [Escherichia coli]	44	26	579
166	5	4909	4037	gnl PID a308082	membrane transport protein [Bacillus subtilis]	44	25	873
247	1	818	75	gnl PID d100718	ORF1 [Bacillus sp.]	44	20	744
32	3	1885	3876	gi 2351768	PSPA [Streptococcus pneumoniae]	43	24	1992
36	17	13467	18256	gi 1045739	M. genitalium predicted coding region MG064 [Mycoplasma genitalium]	43	26	2790
54	15	14656	17343	gi 520541	penicillin-binding proteins 1A and 1B [Bacillus subtilis]	43	27	2688
67	2	696	1352	gi 536934	yjca gene product [Escherichia coli]	43	29	657
139	2	2416	338	gi 396400	similar to eukaryotic Na/H+ exchangers [Escherichia coli]	43	24	2079

TABLE 2

S. pneumoniae - Putative coding regions of novel proteins similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)	match accession	match gene name	% sim	% ident	length (nt)
298	1	3	809	gi 413972	ipa-48r gene product (Bacillus subtilis)	43	24	807
387	1	47	427	gi 2315652	(AF016669) No definition line found (Caenorhabditis elegans)	43	30	381
185	4	4221	3127	gi 2182399	(AE000073) Y4fP (Rhizobium sp. NGR234)	41	25	1095
340	1	582	70	gnl PFD e218681	CDP-diacylglycerol synthetase (Arabidopsis thaliana)	41	20	513
363	6	4205	1914	gi 1256742	R27-2 protein (Trypanosoma cruzi)	41	27	2292
368	2	2	943	gi 21783	LMW glutenin (AA 1-356) (Triticum aestivum)	41	34	942
155	3	4489	2861	gi 42023	member of ATP-dependent transport family, very similar to mdr proteins and hemolysin B, export protein (Escherichia coli)	40	18	1629
365	2	95	1438	gi 1633572	Herpesvirus saimiri ORF73 homolog (Kaposi's sarcoma-associated herpes-like virus)	40	21	1344
1	3	2979	3860	gnl PFD d101908	hypothetical protein (Synecocystis sp.)	39	26	882
1	5	3814	4647	gnl PFD d101961	hypothetical protein (Synecocystis sp.)	39	19	834
26	6	14035	10724	gi 142439	ATP-dependent nuclease (Bacillus subtilis)	38	20	3312
47	1	3	4916	gi 632549	NP-180 (Petrotyzon marinus)	36	23	4914

TABLE 3

S. pneumoniae - Putative coding regions of novel proteins not similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)
1	4	3428	3009
1	6	4611	4964
3	2	818	994
3	3	1182	1574
3	7	5382	6497
3	25	25046	25396
3	26	25625	26317
6	2	1519	1689
6	14	12875	12618
6	15	13215	12841
6	18	15977	15390
7	12	9955	9419
7	13	10161	9910
8	6	3915	4280
9	9	6024	5704
10	8	6909	6298
10	9	7136	6888
10	11	7968	7672
12	1	1140	4
12	3	1779	1456
14	2	1913	1434
16	1	1	243
16	5	5675	3087
17	1	324	34
17	3	1451	1050
17	9	4890	4465
20	14	14544	15893

TABLE 3

S. pneumoniae - Putative coding regions of novel proteins not similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)
21	3	3359	2589
21	5	4802	4482
22	21	17099	17362
22	25	19467	19982
22	33	25540	25764
22	35	26388	26218
22	36	26382	27572
23	7	6655	6032
23	8	7132	6653
24	1	36	518
25	5	3009	2641
27	4	4819	4223
27	5	4789	4956
28	5	3017	1797
28	8	4272	3850
28	10	5028	4597
28	11	5746	5072
29	7	5596	4919
29	8	5039	5518
29	9	5595	8207
30	9	6511	6263
31	6	2664	2344
32	5	5203	5538
33	8	5327	4668
34	10	8024	7740
34	12	9360	8641
34	13	9667	9377

**TABLE 3** *S. pneumoniae* - Putative coding regions of novel proteins not similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)
34	18	13104	11902
35	11	9688	8588
35	12	11073	9670
36	2	334	1041
36	12	11120	10893
36	13	10993	11388
36	15	12172	14595
38	7	4269	4577
38	8	4480	5001
38	10	5517	5711
38	17	10732	11376
40	3	1728	3143
43	1	172	5
43	7	8884	8732
43	8	9568	9071
44	4	4831	6811
45	3	3204	3665
46	4	3875	3468
46	7	6074	7081
48	5	3196	3582
48	8	4579	4229
48	11	9323	8922
48	16	13042	12494
48	20	16342	15764
48	24	17971	18351
48	30	21979	21776
49	1	209	3

TABLE 3

S. pneumoniae - Putative coding regions of novel proteins not similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)
50	4	3307	2672
51	5	3239	3598
52	11	12146	12883
54	7	5588	5187
54	8	6013	5459
54	9	6004	6210
54	16	17685	17506
55	9	10515	10123
55	12	11947	12141
56	3	935	1387
56	4	1496	1939
57	3	1624	2130
57	4	2100	2501
58	6	7541	7335
59	1	2	430
59	4	2416	2736
59	5	2734	3063
59	8	4743	5549
59	9	5459	5929
60	6	5741	6451
61	3	2395	1772
61	5	3316	3176
64	1	2722	2
66	2	1180	3147
66	8	9082	9495
67	3	1343	1182
69	2	1165	980



**TABLE 3** *S. pneumoniae* - Putative coding regions of novel proteins not similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)
70	5	4059	3922
70	6	4215	4057
70	9	5268	5504
71	15	20351	21901
71	16	21859	22336
71	19	26204	27556
72	9	8458	8081
73	4	3815	4216
73	6	4214	4582
73	7	4369	4773
73	10	7183	6428
73	15	9462	9668
76	1	524	195
76	2	867	535
76	11	8602	9210
80	6	7924	8109
81	1	244	2
81	10	6631	8931
83	4	1872	1150
83	17	16810	16460
84	3	4464	2929
86	2	2147	1092
86	4	3606	2875
86	19	16767	17114
87	5	5326	5000
87	7	6459	6001
87	9	7224	7006

TABLE 3

S. pneumoniae - Putative coding regions of novel proteins not similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)
87	18	17930	17670
87	19	18275	17928
88	2	1619	1840
88	4	2711	2878
88	9	6252	6016
89	3	2634	1621
89	9	7371	6868
90	2	899	2395
90	3	1143	952
91	3	2959	3141
91	4	3170	3691
91	6	4253	4573
93	1	391	2
93	6	2648	2379
93	8	4533	3712
96	1	3	182
96	2	904	632
96	3	1407	1147
96	4	1250	1420
97	9	7043	6753
99	15	18522	18692
99	17	19717	19541
100	2	4094	1980
103	1	48	299
103	6	4924	4373
104	5	6142	6735
105	7	6098	6517

**TABLE 3** *S. pneumoniae* - Putative coding regions of novel proteins not similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)
106	1	1	363
106	10	9832	10212
108	1	2	268
111	3	3417	3788
111	4	3809	4606
115	10	10854	10438
116	3	2873	2121
118	2	2274	1357
122	4	2698	2333
122	10	5858	6199
122	12	6301	7416
124	2	346	690
128	4	2544	3368
129	1	689	102
129	2	1011	724
129	8	6454	6056
129	9	6540	6277
129	12	7809	7621
131	3	1433	756
131	10	5972	5673
134	11	11838	11209
135	2	625	1140
136	4	2913	3830
137	2	325	134
139	12	14027	14521
139	13	14840	14532
139	14	15363	14875

TABLE 3

S. pneumoniae - Putative coding regions of novel proteins not similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)
140	20	19823	20838
142	1	1	285
146	3	760	479
146	4	1149	778
146	7	3604	2885
146	13	8223	9401
146	14	9399	110676
146	15	10052	9750
147	7	7488	7276
147	9	8913	8647
148	7	5298	4765
149	1	2	1936
149	3	2557	2880
149	9	6258	6070
150	2	1355	579
150	3	2556	1909
153	3	2061	2642
154	3	1953	1741
155	2	2181	1411
156	8	4550	4311
157	1	37	294
159	2	631	780
159	4	1384	1722
159	7	3271	4017
161	2	1332	1018
165	3	5535	4945
166	6	5406	4972

TABLE 3

S. pneumoniae - Putative coding regions of novel proteins not similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)
167	9	6075	6395
169	5	2828	3205
170	7	6485	6243
170	8	5964	6362
170	9	7303	6962
170	11	8790	7906
171	9	7150	7476
172	5	2298	1948
173	4	2913	2677
175	2	559	835
175	3	893	1789
176	2	1487	546
176	3	2200	1466
177	9	4686	4925
177	10	4923	5177
177	11	5111	5347
177	13	7396	8703
178	6	3452	3724
181	5	1853	2473
182	2	2112	1102
182	3	2617	2006
183	2	2126	2320
185	5	4683	4219
185	6	4846	4634
187	4	2940	3557
188	4	3686	4363
188	5	4183	4821

TABLE 3

S. pneumoniae - Putative coding regions of novel proteins not similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)
188	6	5882	6493
189	5	3143	2844
189	9	5956	5564
191	1	618	4
191	11	10357	10001
192	3	2861	2268
192	4	3081	2878
192	7	6800	5331
193	3	997	839
194	4	2315	2127
195	5	6249	4543
195	6	6620	6231
196	2	1553	1849
197	1	1	861
198	9	6844	6644
200	5	5329	5769
200	6	5993	6595
204	5	3914	3276
205	2	447	1709
209	4	2038	2460
209	5	2458	2682
210	10	7370	8230
210	13	9029	10441
210	14	10439	10705
214	5	2581	2330
214	9	5065	5277
214	11	5996	5754

**TABLE 3**  
*S. pneumoniae* - Putative coding regions of novel proteins not similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)
217	2	541	194
218	2	914	1432
218	3	1430	1972
218	6	3639	3821
219	1	458	39
220	1	869	600
223	4	2617	1964
227	1	1	510
234	4	1539	1312
234	6	2116	1838
235	1	52	312
235	2	310	687
238	1	660	64
246	1	1	270
248	1	3	362
248	2	443	1222
254	3	2789	792
258	2	1179	1616
260	3	1770	2123
263	1	653	177
263	4	2244	1900
263	5	3569	2973
266	1	1	342
266	2	177	1022
270	2	1124	1681
272	1	857	186
275	2	1684	2295

**TABLE 3**  
*S. pneumoniae* - Putative coding regions of novel proteins not similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)
278	1	2	406
282	1	714	391
282	4	1463	1134
287	2	1119	826
288	1	540	4
289	1	684	4
291	5	1589	1858
293	2	2539	2925
294	1	21	608
296	2	494	700
296	3	670	843
302	1	261	530
309	3	559	350
310	2	249	1889
316	2	2087	1818
317	2	1048	584
318	2	313	777
319	3	477	133
327	2	912	607
331	1	1	549
333	1	2	535
333	2	465	82
333	3	127	342
341	1	1	705
345	2	895	701
346	2	750	199
349	1	1	198



**TABLE 3** *S. pneumoniae* - Putative coding regions of novel proteins not similar to known proteins

Contig ID	ORF ID	Start (nt)	Stop (nt)
350	2	81	413
355	1	44	973
358	2	636	448
360	2	948	628
364	2	1639	1265
378	1	345	1004
379	2	683	510
381	1	109	693
385	1	150	4
385	2	269	30

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(1) GENERAL INFORMATION:

(i) APPLICANT: Charles Kunsch  
Gil H. Choi  
Patrick S. Dillon  
Craig A. Rosen  
Steven C. Barash  
Michael R. Fannon  
Brian A. Dougherty

(ii) TITLE OF INVENTION: Streptococcus pneumoniae Polynucleotides and Sequences

(iii) NUMBER OF SEQUENCES: 391

(iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: Human Genome Sciences, Inc.  
(B) STREET: 9410 Key West Avenue  
(C) CITY: Rockville  
(D) STATE: Maryland  
(E) COUNTRY: USA  
(F) ZIP: 20850

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage  
(B) COMPUTER: HP Vectra 486/33  
(C) OPERATING SYSTEM: MSDOS version 6.2  
(D) SOFTWARE: ASCII Text

(vi) CURRENT APPLICATION DATA:

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(A) APPLICATION NUMBER:

(B) FILING DATE:

(C) CLASSIFICATION:

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER:

(B) FILING DATE:

(viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: Brookes, A. Anders

(B) REGISTRATION NUMBER: 36,373

(C) REFERENCE/DOCKET NUMBER: PB340P1

(vi) TELECOMMUNICATION INFORMATION:

(A) TELEPHONE: (301) 309-8504

(B) TELEFAX: (301) 309-8512

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## (2) INFORMATION FOR SEQ ID NO: 1:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 5625 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

CCAAGCAAAA CCAGCTACAG CTAAAGGAAC TTACGTAACA AACTTGACTA TCACAACCTAC	60
TCAAGGTGTT GGTATCAAAG TTGACGTAAA CTCACCTTAA TCAGTAGTTA AAGTAATGTA	120
AAAAAGTTGA AGACGCTATG TCTCAACTTT TTTTGATGTA CGACGGGCAT GTTGATAGT	180
AGATGTGTAC TATTCTAGTT TCAATCTACT ATAGTAGCTC AGAAGTCGGT ACTTAAACGT	240
GCTATATCAA AACCAGTCCT TGAAAAACGT GGACTGGTTT CGTGTGTTGA TTATTACCTT	300
GAACGACATG CGTTAAAAGT TAGTTGAACC GCCGTATGCC GAACGGACGT ACGGTGGTGT	360
GAGAGGGGCT AGAGATTATC CCCTACTCGA TTTCGAAATC TAGTGGAATG AATCTGGAAT	420
AGTCCATCGA GCTTCTAAT ACTCTTCGAA AATCTCTTCA AACCACGTCA ACGTCGCCTT	480
GCCGTGCGTA TGGTTACTGA CTTGTCAGT TCTATCCACA ACCTCAAAC AGTGTGTTGA	540
GCTGACTACG TCAGTTCAT CTACAACCTC AAAACAGTGT TTTGAGCAAC CTGCGGCTAG	600
TTTCCTAGTT TGCTCTTGG TTTTCATTGA GTATAACACA TTGTTAGAAG TTGGTTTAAA	660
TTTCCTAATC AGTTTGTCA CATTTACCTT CGATATATTA TATCCCATAG TTAAGGTTGG	720
TCATACAGAT GATTATAGTC ATGGAGCCGT AAAACTTAGT GTTCTTTAG TTGACAAAGA	780
TGCCATGAAA AAAATATTTG TAACTGTAAT AGGATATTTT GAAATAAATA TAGATGAAAA	840
TATCACCGAT ATTCTATACG TAAATGGTAC TGCTATTCTT TATCTTTATT TACGTTCAAT	900
TGTTTCAATA GTTTCGGCAA TTGATAGCAG TGAAGCAATG TTGCTACCTA TCATTAATGT	960
TTTAGAGTTA CTAGATAAAT CTCAACCTTT TGAAGAAGAA TAATTTATTA GCTCACTAAA	1020
TTGAGGGTAA GGAAAAGTAA AAGCAGTAAG AAAAAATGCT TGCATTATAC AGCAACCTTT	1080
TGGGAATGAG TGGATGGATT GAATAAAATT TGATTAAGAG TGGATGATTT ATCTGTAGAT	1140
TATTATTGGA CAGTTAGTCT TGAAGTAGTC TAAGAATTAG GTTATAATCA GTAGAAGCCT	1200
TGCTAATAAT GAGGAGGTTA GTTTATGTAT AGTAGACTGA ATCTAAAATA GTACGAAACA	1260
ATTGCTAAAA CATTATAGA AATTAATTTT ACTTCCCAA TCGATTGTGT CTCATCTTAT	1320
TTCAATCCGC TATATATTAT GGTATCGAAT CTTATCAGA ATGATAAAAT TAATCAATTG	1380
ATATCTGATT ACAAACAGAA TATGAAAGCT TTTTATATCA CTATTGAAAA ATTTATACGA	1440

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GATGATGAAA GCCTTAAGTG TTATTTTATA AAGGTTATTT CAAGTCGTTT CAAGGTAACA	1500
AGTCTAGATC AGATTGAAGC TGATAAAACG ATACAAAGAA AATATTCAAG TGAGCTAAAA	1560
AAATTTATTG GATTTTATAA TGAGATTATT TGTGAGGAAA ATAGTTTCCT ACATGTACGA	1620
AAGAGGTGGT CGAGTTGGTT TAGGTAGTCG ATGCGTGAGT TGATAATTCT CAGGGTATGG	1680
ACTTCTTTTT CATGAATGAG GTAAAAGAGC AGGTATTGTT TAGAGACAAT CATTCCTGAGC	1740
ATATTTTCTG GATAGAGGGA GTATCCGATT TTATGATCAA AGTTAATACC GCCCTCTGGT	1800
GAGAAGATGA GTAGGTTGGT AATTTAACT ATTAACAGA ATTTTGTGATT AAAAGTATTA	1860
TTTCATGAGA GAAATCCTAA TTTCACAATC CATAGGCAAA CGCTTGCAAT TCGTTTTTTA	1920
TTGGACTATA ATAGGTTGGT ATAAAGCCTT CTGTAGTAAT AAAATGTAGA AGGTGTAGAA	1980
AGTAAGGATT TAGAATATTT GTAGTTAAAA ACACAATGTT GCTATTCCTT ACGATAGGGA	2040
GATAGATATG GCAATGATAG AAGTGAACA TCTTCAGAAA AATTTTGTGA AGACTGTAA	2100
GGAACCGGGC TTGAAGGGG CTTTGCGCTC CTTTATTCAT CCTGAAAAGC AGACCTTTGA	2160
AGCGGTCAAG GATTTGACCT TTGAGGTTCC AAAAGGCGAG ATTTTAGGAT TTATCGGGGC	2220
AAATGGTGCT GGGAAATCGA CAACCATTA AATGCTGACA GGAATTTTGA AACCAACATC	2280
TGCTTTTGTG CGGATTAACG GCAAGATTCC CCAGGACAAT CGGCAAGATT ATGTCAAAGA	2340
TATTGGCGTA GTCTTTGGAC AACGCACCCA GCTATGGTGG GATTTGGCTC TGCAAGAGAC	2400
CTACACTGTC TTTAAAGAGA TTTATGATGT GCCAGACTCG CTCTTTCATA AGCGTATGGA	2460
CTTTTGAAT GAAGTCTTGG ATTTGAAGGA CTTTATCAAG GATCCCGTGC GGACTCTTTC	2520
ACTGGGACAA CGGATCGGG CGGATATTGC GGCCTCCTTG CTCCACAATC CCAAGTTCT	2580
TTTTTTAGAT GAGCCGACCA TTGGTTTGA CGTTTCGGTT AAGGATAATA TTCGTCGGGC	2640
AATTACTCAG ATCAATCAAG AGGAAGAAAC TACCATTCTT TTGACCACTC ACGATTTGAG	2700
TGATATTGAG CAATTTGTG ATCGGATTTT CATGATTGAC AAGGGGCAAG AGATTTTGA	2760
TGGAACGGTG AGCCAACCTCA AGGAGACCTT TGGTAAGATG AAGACTCTCT CTTTGAAC	2820
GCTACCAGGT CAAAGTCATC TCGTCTCTCA CTATGACGGT CTGTCTGATA TGACCATTGA	2880
TAGACAAGGA AACAGCCTCA ACATTGAAT TGATAGTTCT CGCTACCAGT CAGCTGACAT	2940
TATCAAGCAA ACCCTGTCTG ATTTTGAAAT CCGCGATTG AAGATGGTGG ATACGGATAT	3000
TGAGGATATT ATCCGTCGCT TCTACCGAAA GGAGCTCTAG GATGATCAAA TTGTGGAGAC	3060
GTTATAAACC CTTTATCAAT GCAGGGGTTT AGGAGTTGAT TACTTACCGA GTCAACTTTA	3120
TTCTCTATCG GATTGGCGAT GTCATGGGG CTTTGTGGC CTTTATCTC TGAAGGCTG	3180

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TCTTTGATTC TTGCAAGAG TCTTTGATTC AGGGCTTCAG TATGGCGGAT ATCACCTCT	3240
ACATCATCAT GAGTTTGTG ACCAATCTTC TGACTIONATC CGATTCTGCC TTTATGATTG	3300
GGGAGGAGGT CAAGGATGGC TCCATTATCA TGCCTTTGTT GCGACCACTG CATTTTGCGG	3360
CCTCCTATCT TTTACCGAG CTTGGTTCCA AGTGGTTGAT TTTTATCAGC GTTGGCCTTC	3420
CATTTTAAAG TGTCATTGTC TTGATGAAAA TCATATCGGG TCAAGGTATT GTAGAGGTGC	3480
TAGGATTAAC TGTCATTAT CTTTTAGCT TAACGCTCGC CTATCTGATT AACTTTTCT	3540
TTAATATTG CTTTGGATTT TCAGCCTTTG TGTTAAAAA TCTTTGGGGT TCCAACCTAC	3600
TTAAGACTTC CATAGTGGCT TTTATGTCGG GGAGTTTGAT TCCCTTGGCA TTTTTCCAA	3660
AGGTGTTTC AGATATTCTC TCCTTTTGC CTTTTTCATC CTTGATTAT ACTCCAGTTA	3720
TGATCATGT TGGAAAATAC GATGCCAGTC AGATTCTTCA GGCACCTCTT TTGCAGTTCT	3780
TCTGGCTCTT AGTGATGGT GGATTGTCTC AGTTAATTG GAAACGGGC CAGTCTTTA	3840
TCACCATTCA AGGAGGTTAG TATGAAAAA TATCAACGAA TGATCTGAT TTTTATCAGA	3900
CAATACATCA AACAATCAT GGAATATAAG GTAGATTTG TGGTTGGTGT CTTGGGAGTC	3960
TTTCTGACTC AAGGCTTGAA TCTCTGTTT CTCAATGTCA TCTTCAACA TATCCATT	4020
CTAGAAGGCT GGACCTTCA AGAGATAGCT TTCATTTATG GATTTTCTT GATTCCCAAG	4080
GGAATGGACC ATCTCTTTT TGACAATCTC TGGGCACTAG GGCAACGCCT AGTCCGAAAA	4140
GGGAGTTTG ACAAGTATCT GACTCGTCCC ATCAATCTC TCTTTCACAT CTTAGTTGAA	4200
ACCTTTCAGA TTGATGCCTT GGGTGAATC TTAGTCGGTG GTATTTTATT GGAACAACA	4260
GTGACCAGCA TTGTTGGAC TCTTCAAAA TTCCTGCTTT TCCTAGTTTG TATTCCTTTT	4320
GCGACCTGA TTTATACTTC TCTTAAATC GCAACAGCCA GTATCGCCTT TTGGACTAAG	4380
CAGTCAGGCG CCATGATTTA CATCTTCTAT ATGTTCAATG ACTTTGCTAA GTATCCGATT	4440
TCTATTTACA ATTCTTCT TCGTTGGTTG ATTAGCTTTA TCGTGCCTTT CGCCTTTACA	4500
GCCTACTATC CAGCTAGCTA TTTCTTACAG GAAAAGGATG TGTCTTTAA CGTAGGAGGT	4560
TTGATGTTGA TTTCTCTGTT TTTCTTTGTT ATTTCCCTTA AACTTTGGGA TAAGGGCTTA	4620
GATTCCTACG AAAGTGGGG TCGTAAAG CTAAAGTAAG ACTAAATCA AGAAAGAAAC	4680
TTATGATGTT TGTAAATGAA GAAGTCAAGG ATGAAAATCA AAAAAAGCA GTTGTCTGCTG	4740
AGGTTTGA GATTTGCCA GAATGGTTG GAATCCCAGA AAGCACACAA GCCTATATAG	4800
AAGGAACCAC GACACTGCAA GTTTGGACCG CCTATCAGGA GAGTGATTG ACTAGATTG	4860
TAAGCTTATC CTATTCGAGT GAAGATTGTG CAGAGATTGA TTGTCTCGGC GTAAAAAGC	4920
TTATCAAGGT AGAAAAATTG GGAGCCAATT GCTTGCTACT TTAGAGAGTG AAGCTCGTAA	4980

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AAAAGTTGGT TATCTGCAGG TCAAAACAGT GGCAGAAGGT TCTAATAAAG ATTATGATCG	5040
AACAAATGAC TTTTATCGAG GTCTTGGCTT TAAAAAGTTA GAGATTTTTC CTCAACTATG	5100
GAATCCGCAA AATCCTTGTC AGATTTTGAT TAAAAAGCTT GAATAATATT ACTTGACATC	5160
TATTCTCAGA GTGCTATACT GTAAGTGTA TCGCCGATTT AGCTTAGTTG GTAGAGCAAG	5220
GCACTCGTAA AGCCTAGGTT ATAGGTAGAT AAACGACTGA GGATTGAAA AAATAGATAG	5280
GTAGAAGATA ACCGTTAAGC CTTACTCTTA GCGGTATTTT ATATTGTTTA ATAGCGCTAA	5340
TATTTTATCA ATTATGCCTG TTTTCGTGTT TCTGGTAGTT GTTCAAGTTT ATTGCTACTA	5400
TTTTTGATGG TATGAATGTG CTTATAATGT ATCCCGGTTA ACGAAAGTTT TGGACTTATA	5460
CTCTTCGAAA ATCTCTTCAA ACCACGTCAA CGTCGCCTTG CCGTGCCTAT GGTATGACT	5520
TCGTCAAGTT TATCCACAAC CTCAAAACAG TGTTTTGAGT GACTACGTCA GTTCCATCTA	5580
CAACCTCAAA ACACTGTTTT GCCCAATCTG CGGCTAGTTT CCTAG	5625

(2) INFORMATION FOR SEQ ID NO: 2:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 7571 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

CTCTCCAGCT TTCCCTGCGA GTTGCCCATG TTGTGTCTTT AAGAAGTCTA AAAATATCTC	60
CAATAAAACG CATCGCTCTC TCCTATCTCG TTTCTCTGTG TGTAAGTGTAC TTGCCACAAT	120
GCTTACAAAA TTTATTTACT TCTAGTCGTG TAGGCTTGAG GTTTCGCTG ATCTTGATTG	180
AATAGTTTCT CGAACCACAA ACCGCACAAG CTAGGCTTGC TTTTTTTAGT GCCATAACGC	240
CTCCATCTTA TCCATTATAA CAAGAAAGCT AGGCTTTGAC AAGCATCTTA GCGAAATAGA	300
TTGACTATCG AATCCCATAT TGTTTGAGCC TTTTCCTTAA TCTTCGCATC TGAGATAGCC	360
CGGCTAGCCT CATCTACTAG ACTTTGCGCA CGCCCTCGAA TATCAGACAA ATTATCATCT	420
GTCTGGCTAT TATCATTTGG TTGTACTTGT CTTTTGTAT TGGCTGGTGC AATTCCATTT	480
TGCTTATAAG CATTTTCAAC CGTAAAGGTA CTTCTGGCG TATAAGGTAA AATGGTATTG	540
GCAATGTTTC TAAAGACATG AGCTGCACCG TTTGAAGTAG AGCCAGCTAG ATAGTGGTTT	600
TCATCAGTGG TCGGAAAGCC AAGCCAGTGG CTAATCACTA CATCCGGAGT ATAACCAATT	660
ACCCACTGGT CACTTGTGTA CTCGGGATTG AAAACTGCTT CAGTTGTTC AGTTTTCCTT	720

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GCCATGACAT AGTCTGCAGG CGATGAACTA ATACCGGTAC CGTTGGTGAA AGTCCCCAAC	780
ATCATACTGG TCATCTTGTC AGCTACAGAC TTATCAATCA CCCGTTTTTG TGAATTTT	840
TGACTCGCAA TAACCTTGCC ACTAGCATTT TCAATTCTAC TAATAAAATG AGCTTCAGGC	900
ATTAAACCTT CATTTGCAAA GGCGGCGTAT GCTTGAGCCA TTTGAAGAGG GTTGGTTTCA	960
ACACCGCTTC CCAAGGCGAC ACCAAGAACA CGGTGCACCT TTTCCATGTT GAGTCCGAAT	1020
TTTTCGCCTG CCTCAAAAGC CTTGTGACA CCCAAATCAT TAACAGTGGC AACAGCAGGT	1080
AGATTAAGCG ATTCTGCCAA GGCTTGATAC ATAGGAACCT CTCGACTCGT TTTGATCCCT	1140
GCATAGTTAT CAACCTTATA GCTGTCATAC TGCATGGTAT GGTATCCAA CTGCTTATTC	1200
AAAGCCCAGC TTGCTTCAAC TGCTGGCGTA TAAACAACTA AAGGCTTAAT TGTAGAACCA	1260
GGACTACGCT TTGATTGGGT TGCATAGTTG AAATTCGGA ATCCAGTTTT ATCATGTGCA	1320
GCAACTGAC CGACAACTCC ACGAACTCCC CCTGTTTTCG GTTCGAGGGC TACACTTCCT	1380
GATTGAGCAA ACGTTCCATC CTCTGCCCTC GGAAATAGCG ATGTGTTTTC ATAAACAATC	1440
TGCATATTTG CTTGGTAGTT TTGGTCCAGC TCTGTGTAAG TCGGTAGCC ATTATTGACA	1500
ATCTCTTCCT CTGTTAGATT ATACTTGAA ACAGCTTCAT TAACCACCGC ATCAAAATAA	1560
GAGGGGTAAC GGTAATCTGA GATTTTTCCT TCATACTTAT CGTGCAATTG CGAAGTCATA	1620
TCAACTTCAG CAGCTTTGGT TTCTTGGTTT TTATCAATAT ATCCTGCTGC AACCATATTC	1680
TGCAAGACAG TATCGCGCCG ATTAGTAGAA TCTTCTACGG AATTCAAGGG ATTATACAGT	1740
TCCGGCCCCT TGAGCATCCC TGCCAGAGTC GCAGCTTGAT CCAGACTCAC TTCTGATGCA	1800
GAAACTCCAA AGTATTTCTT ACTCGCATCT TCTACACCCC ACACACCATT TCCAAAATAA	1860
GCGTTGTTAA GGTACATGGT TAGAATTTGC TCCTTACTAT ATTTTTTGCT TAATTCTAAG	1920
GCAAGGAAAA ATTCTTTCGC TTTTCTCTCA ACAGTTTGAT CCTGCGATAA ATAGGCGTTT	1980
TTAGCCAGCT GTTGGTAAT GGTAGAGCCA CCACCTGAAC GTCCAGCAGT GACAATAGCC	2040
AAGAAAAAAC GGCCATAGTT AATCCCGTCA TTTTATAGA AAGAACGGTC TTCTGTGCA	2100
ATAACAGCAT TCTGCAAGTT TTTACTGATG TCAGTCAGCT CAACATAGGT TCCCTTTTGA	2160
CCAGACAAGG CACCAGCCTC TTTTCTTCA CGGTCAAAAA TAAGAGTCCG AGTTTCAAG	2220
GCATTTTGCA AATCATTGAC ATTGGTCGAC TTGGCTACAG CAAACAAATA GATTCCAAC	2280
AGCAAGCCTG CACTCAAACC TAGTATAAGG ATAATCTTTG TTAGATGATA ACGACGCCAG	2340
AATTTTCGAA TCGGACCTAC TTGGGCTAAT TTTTTCGAT CACTACGAGA GCGACGTAAG	2400
ATAGTAGAAT CAGAGTCTC TAGTTCACTT GTTCTTTTT TAAAAAGAGA AAGAAATTC	2460
TCAATAAATT TATCTAATTT CATGCGTTA TTTTATCATC TTCATCATAG GAAGACAAGA	2520



ATTTAGCTAT TTCCTATCCA AATAGGGCTT TTTTGTGTAC AATATCTGTA TGCAATTCAC	2580
ATTTACATTA CCCGCCTCTC TACCTCAAAT GACAGTAAAG CAATTACTTG AGGAACAAC	2640
CCTCATCCCT AGAAAAATCC GTCATTTTTT GAGAATCAAG AAACATATTT TGATAAATCA	2700
AGAAGAAGTC CACTGGAAGG AAATCGTAAA TCCTGGAGAT GTTGCCAGT TGACTTTTGA	2760
CGAGGAAGAT TATTTCCAAA AGACGATCCC TTGGGGCAAC CCAGACTTAG TGCAGGAAGT	2820
TTATCAAGAT CAACACTTGA TTATTGTAAA CAAACCAGAG GGGATGAAAA CGCATGGTAA	2880
TCAACCAAAC GAAATTGCCC TTCTTAACCA TGTCAGTACC TATGTTGGCC AAACCTGCTA	2940
TGTCGTTTAT CGTCTGGACA TGGAAACCAG TGGCTTAGTT CTCTTTGCCA AAAATCCTTT	3000
TATCCTGCCC ATTCTCAATC GCTTATTGGA GAAAAAGAG ATTTCTAGAG AATATTGGGC	3060
TCTAGTTGAT GGAAATATCA ACAGAAAAGA ACTTGTTTTC AGAGACAAAA TTGGACGTGA	3120
TGCGCATGAT CGTAGAAAA GAATAGTTGA TGCAAAAAAT GGGCAATATG CTGAAACGCA	3180
TGTAAGCAGA TTAAAGCAAT TCTCAAACAA GACTTCCTTG GCTCATTGCA AGCTAAAGAC	3240
AGGGCGAACC CATCAGATTC GTGTGCACCT TTCGCATCAT AATCTTCCTA TCCTGGGAGA	3300
CCCTCTCTAT AATAGTAAAT CAAAGACAAG CCGGCTTATG CTTTCATGCCT TCCGACTTTC	3360
CTTTACCCAC CCACTTACTT TAGAGAAGCT AACTTTCACT ACCCTTTCAA ATACATTGTA	3420
AAAAGAATTA AAAAAGAATG GATGATCGTG TCATCCATTT TTCCATATAA AAAAGCAAGA	3480
CCACAAAGCC TTGCTTTCTA TCAACTCAAG AATTATTTAG CAATTTTTCG GAAGTATPCA	3540
AGAGTACGAA CAAGTTGTGC AGTGTATGAC ATTTGTTGT CGTACCATGA TACAACTTTA	3600
ACCAATTGTT TACCGTCAAC GTCAAGAACT TTAGTTTGAG TTGCGTCAA CAATGAACCG	3660
TAAGACATAC CTACGATATC TGAAGATACG ATTGGATCTT CTGTGTAACC GTATGATTCG	3720
TTTGAAGCTG CTTTCATAGC TGCCTTCACT TCATCAACAG TAACGTTCTT TTCAAGAACT	3780
GCTACCAATT CAGTAACTGA TCCAGTTGGA GTTGGAAACG GTTGTGCAGA TCCGTCAAGT	3840
TTACCATTCA ATTCTGGGAT TACAAGACCG ATAGCTTTTG CAGCACCAGT TGAGTTAGGA	3900
ACGATGTTTG CAGCACCAGC GCGAGCACGG CGAAGGTCAC CACCACGGTG TGGTCCGTCA	3960
AGGATCATTT GGTCAACAGT GTAAGCGTGG ATAGTAGTCA TCAATCCTTC AACAACACCA	4020
AAGTTGTCTT GAAGAGCTTT AGCCATTGGA GCCAAGCAGT TTGTAGTACA TGAAGCACCT	4080
GAGATAACTG TTTCAGTACC GTCAAGAACG TCGTGGTTAG TGTGAATAC AACTGTTTTA	4140
ACGTCGTTTC CACCAGGAGC AGTGATAACA ACTTTTTTAG CTCCACCTTT AAGGTGTTTT	4200
TCAGCTGCTT CTTTCTTAGC AAAGAAACCA GTAGCTTCAA GAACGATTTT TACACCGTCA	4260

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GTAGCCAGT CGATTGTTC TGGATCACGT TCAGCAGAAA CTTTGATGAA TTTACCGTTA	4320
ACTTCAAATC CACCTTCTTT AACTTCAACA GTACCGTCGA AACGACCTTG AGTTGTGTCG	4380
TATTTCAACA AGTGTGCAAG CATAACTGGA TCTGTAAGGT CGTTGATGCG TGTAACCTCA	4440
ACACCTTCTA CGTTTGGAT ACGACGAAA GCAAGACGAC CGATACGTCC GAAACCGTTA	4500
ATACCAACTT TAACTACCAT TAGTGATTTC CTCCTTATGA AAATCATGAA ATTTTATTG	4560
TGAAAAGAGT AACTTGAATC ACTACAAATC ACCTTCAAC AAACCTATTA TACAACCTATT	4620
TGAGTTGAAT TGCAAGTATG GCCATTGTTT TTCTATGTTA GTTCTTTTTT AAGACTGTAA	4680
ACCAAGGAAT CCCTTACTAT TCATAGCATA ACGATTCTAT AGGATCCATT TTACTAATCT	4740
TACGCGCCGG GAAGTAGGCT GAGACATAAC CAAGTAATAG AGCGAAAAC AGAGTTCCTA	4800
AAACAGATAA AAGATTTAAT TTA AAAACCT TAGTGATGGA TGGGTAAAAG TGACTTACAA	4860
TCGCATTGCG CAAACTTCCC ACCCCTTGTG CAACCAAAAA TGCCAGCAGC AAGGCGATGC	4920
CTACAATCCA GATAGCCTCG TAAATAAAAA TTCCTTTGAC ATCAGGATTC TGATAACCAA	4980
CTGCTTTCAT GACACCTATT TCCTTGGAAC GTTGCATGAT ATTGATGTAA ATAATGATAC	5040
CAATCATAAC CGCTGCTACC ACAATAGCTT GTGATGAAAG CACAATCAAT AATCCCTGAA	5100
TAACACGAAT AAAGGTAATC ACAATATCAA GAACTCTCTG TTGAGAAAGC ACAGTATACT	5160
TCTTATTTTT CTGTAATTCT TCTGTACTA CTTTTGTCTG TGATGGATCT TTGAGTTCCA	5220
AGATAAAATA AGATACAGCT TTCGTAAATC CAGCCTCTTT CAAAATCGTT TCCATTTGAT	5280
GAGACAGCAT GAAACTGTTG CTGTCCTCCA TGTCATCTTC ATCATTGATT ACACGTACAA	5340
TCTTCGTTTG AAATTGAGCA ATCTTACTAG TTTCGGCAGC ACTTCTACA ATGCTGGCTG	5400
AGACTGATTT GCCAATAAGA TCATTAGCTG TCAAATTTTT TCCTGTCTGT TCATTCCAAT	5460
TTTTTAGTAA ACTGCTTGGA ATCGTTAATC CCTGTTCAAT TGTATCAGTA TAGAGGGATC	5520
CAGCCAAAC TTTGTCCGTC TCATTATTAC TAACAGAGAT ACTTGTATCA TCATAAAGAC	5580
TCACTACTTG AGCATAAGAA GGCATCGTTT GACTCAGATC CATTTCTTGC CCATCTATAG	5640
TAATATTTGA CATGTTTCATC CAAAAGGAC TCTCCAAATA TTTAATAGCT TCTTTCCCAA	5700
CTGTATCCGT GATATATACT CAATTGAAAC AAGAGCAGGA TAAAAAGCC TCGTAAAAGG	5760
TATTGCAACT TGGTAATACC TTTTGTAGGT GCTTTTGTAT ATGAGCCCAT GTTTTCTCAA	5820
TAGGATTGTA CTCAGGCGAG TAGGGAGGAA GAGGTAAAAG TTTATGCCCA AACTCTTCGC	5880
ATAAAAGTTC TAGCTTCCCC ATTCTATGGA ATCTTACATT ATCCATAATA ATAACCGATG	5940
GTGTGTTTAA TGTGGTAAG AGAAAATCT GAAACCAAGC TTCAAAAAG TCGCTCGTCA	6000
TCGTCTCTTC GTAAGTCATT GGAGCGATTA ATTCACCATT TGTAGACCT GCAACCAAAG	6060

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AAATCCTCTG ATATCTTCTT CCAGATACTT TGCCTCTTAT TAATTGACCT TTTAATGAGC	6120
GACCATATTC TCGATAAAAA TAAGTATCGA ATCCTGTTTC GTCAATCTAA ACAGGTGCTA	6180
GGTGCTTTAA ACTATTAAAA TTCTTAAGAA ATAAGGCTAC TTTTCTGGG TCTTGTTCAT	6240
AGTAGGTGTG GTTCTTTTTT CGAGTGTAGC CCATAGCTTT GAGCGTATAG TGGATGGTAG	6300
TTGGATGACA GCCAAATTCA GAAGCTATTT CAGTCAAATA AGCGTCTGGA TTGTCACTAA	6360
GATAGTTTTT AAGTCTATCT CTATCAACCT TTCTTGGTTT TATTCCTTTT ACTTGGTGGT	6420
TTAGCTCTCC TGTCTTCTCT TTTAGCTTTA ACCAGCCATA AATGGTATTA CGTGAGATTT	6480
GGAAAACTGT TGATGCTTCT GTTATACTAC CTGTTTCGCTC ACAATAAGAG AGAACTTTTT	6540
TACGAAATC TATTGAATAT GCCATAAAAA GATTATACCA CATTGTGTAC TATTTTGGT	6600
TCATTTTACT ATATTGAAG AGGCGTTTAA ACTATCTGAC ATAAAACTCG TTCTAGAGGA	6660
AAGACATCCT TTAATAAGTT AGTTTATTTT ACAACTTAGA CATCAAGGTA GGTAAACCCC	6720
TTCATGGAAT AATCAAGACT CTTAGCACTA TGGGTAAAC TACCACTGGA GACGTAATCA	6780
ATCGCTAAAC CACGAAAACG GCTAATAGTG GTCATATCAA TATTTCCAGA ACATCAATC	6840
CGAGAACGTC CTGCAATTAG GGTAATGGCC TGTTCATCT GTTCCAATGA CATATTATCC	6900
AACATGATAA TATCAGCACC CGCCGCCGCA GCTTCTTCGG CAGCAGCAAG GCTTCCACT	6960
TCCACCTCGA CCATTTTCAC AAAAGGGGCA TAGGCACGCG CTTGAGCAAT TGCCTTTTGA	7020
ACACTACCTA CTGCCGCAAT GTGATTGTCT TTTAGCAGGA TAGCATCTGA TAAATTAAAG	7080
CGATGATTAT AGCCACCGCC AACTCTCAGC GCATATTTCT CAAAAAGACG TAAATTAGGA	7140
GTAGTTTTTC GAGTATCAAA TACCTTAATG CAATCATCGC CTAAGGCTTC TACATAAGCA	7200
GCTGTCATCG AAGCAATCCC TGATAAATGT TGTAATAAAT TCAAGGCAAC GCGTTCACAT	7260
GTTAAGAGAC TTCTCACCGA GCCTATGATT TCTAAAACCA AATCGCCACT AGTCAAACGA	7320
TCCCCATCCT TAAATTGATG AGGATTCTGG AAGGTCACCT CGGCATCAAA TAGGGTAAAA	7380
ACCCTTTGAA AAACGGTTAG CCCCGCTAAA ACACCAGCTT CCTTGGCAAA AAGCGACACC	7440
TTGGCTTGGC CATGATGATC AAAAATGGCA TTGGTACTGT AATCTTCGGA ATGAACATCT	7500
TCTCGCAAGG CTGCTTTCAA TGTATCATCT ATTTGAAAAG GGGTTAAATC AGTTGAAATG	7560
ATTGACATCA C	7571

(2) INFORMATION FOR SEQ ID NO: 3:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 26385 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double

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(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:

TTTGCTAGTG GCTTAAATTC TTCAGGAAAA TCAGGCGTAT CTAAAAGTCG TGTCGTTTTT	60
GTTTCATCTA TATAAAGACT TCCTGCTCCC CCTACAATA GAAAACGTGT CTGTGTTCCA	120
GCAAGAAGCT GATTAAATAG TTCGATTGAT TTGCTGTGGA GCGGTAGCGT ATCTGGTGTA	180
TAAGCACCAA ACGCTGAAAT AACAGCATCA AATCCAGTAA GATCATCTTT TGTCAACTCA	240
AATAAATCTT TTTTAATAAT AGACTCAGCT TGACTTTTGT TTTCAGAACG AACAATAGCC	300
GTTACTTCAT GTCCTCGTTT GACTGCTTCT TCAACAATTG CTTTCCCCGC TTGTCCATTT	360
GCTGCAATAA CTGCTAGTTT CATTTTTAT ACCTCTCTTG TTGTAATTAT TTTAGTTACA	420
GAAATTGTGA CACTCTTAAT AATCAATGTC AATAGTCTTG CTTAATTATT ATCAAAATAT	480
TTCTACCAAG AAAACTAACC ATGATTCTAG TGAAAAAAA TCTTCTTTGT CAACAAATTT	540
ACTTTCTTGT TTAAACATG CTATAATAAT CATAGCAAGA GATCTAAGTT GTCTGTTTTT	600
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ACTCAAGGGA CTCTATATAA ACAATCTTCT CTTCTTTACA CCTCTGGTAA TCTTGATTGT	780
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GCTCTTTTAC TTTACTATCA TAACCTTTGG TGAGTTTATA CTAATTTACT TGCTAATCTA	900
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TATTGCCTTC TCTTGGCAGT GGATTCTAAA CGGGGTTTAT GGCTACTTAC CTAATCTAAT	13860
CGTAAATTA GGTTTAATGG AACATACACC TGCATTTTGT ACAGATAGTA CATGGGCATT	13920
CCTATGTTTG GTGTTTATCA ACATTTGGTT TGGAGCACCA ATGATTATGG TTAATGTGCT	13980

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TTTCAGCTTTG CAAACAGTAC CAGAAGAACA ATTTGAGGCT GCTAAGATAG ATGGTGCTTC	14040
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AGTTGTTTTG AGAACTGTAT GGATCTTTAA TAACTTTGAC ATTATCTACC TCATTACTGG	14160
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TCAAAGGCTC CAAACGCTAT TCTATAAGCG AGAACTAAA ATCGG	26385

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## (2) INFORMATION FOR SEQ ID NO: 4:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 2716 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:

CCTGCCCGCA TTGCCCTAGG CATTAAGTAA ACATATAAAA GCATGTGAGA GACTGTTGGA	60
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AAAGAAAATG ATATAAGT AGTTATGGAG AAAAAGAAAT TACGCATCAA TATGTTGAGT	180
TCAAGTGAGA AAGTAGCAGG ACAGGGAGTT TCAGGTGCTT ACCGTGAATT AGTTCGTCTT	240
CTTCACCGTG TGCCAAGGA CCAATTGATT GTTACAGAAA ATCTTCCAAT CGAGGCAGAT	300
GTGACTCACT TTCATACGAT TGATTTTCCC TATTATTAT CAACCTTCCA AAAGAAACGC	360
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CCTTTCCTTTG CTTTAAAGGA TCGTCGCTTT GCCTACCGAG GTTTTAGCAA GGCACCTGAA	1440
ATTGCTAAAC AGTATCAGCT AGATATTATC CATACTCAGA CAGAATTTTC TCTTGGCCTG	1500
TTGGGGATTT GGATTGCGCG TGAATTGAAA ATTCCAGTCA TCCATACCTA TCACACCCAG	1560
TATGAAGACT ATGTCCATTA TATTGCTAAG GGGATGTTGA TCCGGCCGAG TATGGTCAAG	1620
TATCTGGTTA GAGGTTTCCT GCATGATGTG GATGGGGTTA TTTGCCCTAG TGAGATTGTC	1680
CGTGACTTGC TATCTGATTA TAAGGTCAAG GTTGAAAAAC GGGTCATTCC TACTGGGATT	1740
GAATTAGCCA AGTTTGAGCG TCCGGAATC AAGCAGGAAA ATTTGAAAGA ACTGCGTAGT	1800
AAACTAGGGA TTCAAGATGG TGAAAAGACG TTGCTTAGTC TTTCGAGAAT CTCCTATGAA	1860
AAAAATATTC AAGCAGTTTT AGCAGCCTTT GCTGATGTTT TGAAAGAGGA AGACAAGGTT	1920
AAACTGGTAG TAGCTGGGA TGCCCTTAT CTGAATGACC TCAAAGAGCA AGCCCAGAAC	1980
CTAGAGATTC AAGACTCAGT CATCTTTACA GGGATGATTG CTCCTAGTGA GACGGCTCTT	2040
TACTATAAAG CGGCGGATTT CTTCAATTCG GCATCGACAA GCGAAACGCA AGGTTTGACC	2100
TACTTGGAAG GCTTAGCCAG TGGAACACCT GTCATTGCTC ACGGAAATCC TTATTGAAC	2160
AACCTCATCA GTGATAAAAT GTTTGGAACC TTGTAATATG GAGAACATGA TTTGGCTGGT	2220
GCTATTTTGG AAGCCCTGAT TGCAACACCA GACATGAACG AGCATACCTT ATCAGAGAAA	2280
TTGTATGAGA TTTCAGCTGA GAACTTTGGG AAACGAGTGC ATGAGTTTGA TCTGGATGCC	2340
ATTATTTCAA ATAACCTCCA GAAAGATTG GCTAAAGATG ATACGGTCAG TCAGCGTATC	2400
TTTAAGACAG TTTTGTATCT TCAGCAACAG GTGGTTGCTG TACCTGTAAA AGGATCTAGA	2460
CGCATGTTGA AGGCTTCAAA AACACAGTTG ATCAGTATGA GAGACTATTG GAAAGACCAT	2520
GAAGAATAGA AAGAGGAACA GCTATGAAAA AAACAATTAA TGAGAAGCGG TCGTGATAAA	2580
AAGATTGCGG GTGTTTGTGC TGGGTGGGCC CATTATCTGG ATATGGATCC GACTATCGTT	2640
CAAGTCATTT GGGGTGTTCT TACTTGCTGT TACGGAGCTG GAATTGTAGC TTACATTATT	2700
TTATGGATTA TCGCGA	2716

## (2) INFORMATION FOR SEQ ID NO: 5:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 13926 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:

CTTTGGTTTT GCCTATTCA AGACATGAGG GCCATCAGGA ATGATCTGAA ACTGCGAATC 60

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TGTTAACAGT CTATGGAGAG CTTTCATAGA ACTAAGATTC GGTTTATCTT TGCTGCCACA	120
AATTAGTAAG GTTGGATAAG GGTAAGTTCC TGCTATATCC GTTAAATCAA GTGTCTTCAA	180
CTCCTCAGAA ACTCCGACCA TAAGAGTCTT GTCTGCTCCC TGTTTTTCAA ATACTCTTTT	240
GGGAAGTAGT TTA AAAATCA GCAATTGAAG ATAAAATAGG ATATTCCCTG CTAATTTAAG	300
CGGGCATCCT GACAGAATCA AAGCTCGAAG ATTTGGTAAA TCGTAACTGG AAAGTTCTAG	360
TGTCAGGGCA GCACCTAAGG ACAATCCAAT CAAAACAAA GGTTCGTCT CTTGAGCTAG	420
GTGCTGATAA ACTCGCTCTT TAGCTTGTTG ATAGTTACTA ACTCCAGAAG GAAATAACTC	480
GATAGCCTCA GAAGGATAAT CTGTCACTAG ATTCCGAAGT TCTTTCCAAG ACTCTGCTGA	540
CTGCCCTAAC CCATGCAAAA ATATTAATTT CATCTAGTTC TCCTCAAGGC TTAATTCATA	600
CAAGCCTCTC ACTGCATTAC AGCCGTAAAT AGCTTCTGCT TGGGTAAAT CTGCCAAGGT	660
CAAGACTTTC TCTTCTACCT GTCTGTGTT TAGCAAATGC TGACGGTAAA TTCTGGCAA	720
GATTCCAAGT CGGATAGGCG GTGTGTAGAG TTTTCCAGCG ATTTTCAGAA CCAAATTTCC	780
TATAGAGGTT TCAAGCAGTT CTCCTGACTT ATTGTGGTAA ATCTTCTCTT GTTCTCCTAG	840
GCTCAAATGC GGTGGGTGAG TGGTTTTAAA GTAGGTAAAG GATTGATTCA AAGCAGCTTC	900
CTGAAGACAG ACTTGGGCCT GACAAAAGCT TGTACTGAGA GGGGTAAATA CTTGACGATT	960
GACTTCTATC TCTCCAGATT TGCTAAGGCT GATTCGCAAG CGGTAATCTC GATTAGCTTC	1020
ACAACTCTGA CACTCTTCTT CAATCTTGTTG TCCCAAGTCT TCTGCATCAA AAGGAAAAGC	1080
AAAATAACGA CTAGCTTTTC TCAGCCTTTC CAGATGTTGT TCTTCAAACA TCAGTTGTTT	1140
TTGGCTGATT TTTCCAGTTG TAATTAATTG GAAGCGAGCT TGTTTACGAT AGAGAACTGC	1200
TGCCTTTTGA TGAACCTCTC GGTATTCAGA TTCCCATGTG CTATCCAAG TAATCCCTCC	1260
GCCAACTCCA TAAATGGCTT GACCTTTGTG AAGTTGAATG GTACGAATGG CCACATTAAA	1320
AATCCGTCGT CCATTTGGAA GCAAGAGACC AATCGTTCCA CAGTAGACTC CACGCGGTTG	1380
AGGCTCCAAG TCCTTGATAA TCTCCATTGT CGCAATTTTC GGTGCACCCG TTATGGAACC	1440
ACAAGGAAAG AGTGAGCGGA AGATTTC AACGTCCACA TCCTCTCGCA ACTGACTCTT	1500
GATGGTCGAA GTCATCTGCC AAACAGTTGA ATACTGCTCT ACCTGACACA GACGCTCCAC	1560
GTGCTCGCTC CCAACTTCAG AAATACGGTT CATATCATTC CGCAAGAGGT CCACAATCAT	1620
CATATTTTCA GAGCGATTTT TGGGATCCTG TTCCAACCAA CTGGCCTGTT CAAGATCTTC	1680
TTGGTCAGTT ACCCCACGCT GAGTCGTCCT CTTCATTGGT CGTGTGTGCA ACTCGCGATC	1740
ATTTTGCTCA AAAAAGAGCT CTGGGCTCAT GGAAATCACT GTCATCTCGT CATGTTCCAC	1800

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ATAGGCATTG TAGCCCGCCT CCTGCTCTAC CACCATACGA TTGTAGATGG CAAAAGGATT	1860
GGCATTTAAC TTTTGCTTAA GTTGGACGGT GTAGTTGACC TGATAGGTAT CTCCCTGCCG	1920
TAAATGATGG TGAATTTGGG CAATGGCCTT TTCATAGTCT GCTGCAGACG TTAATTCTCTG	1980
CCAATTTGAG GGCAAATCAA TATCCTCATA AGTCAGAGGA ATAGGGGAAG TTTCTACGAT	2040
ATCATGAACA GTAAAGTAAA GCAGGTACTC TCCCAGTAGG GGATCCTTGT GAACTGCTAA	2100
TTTTTCCTCA AAAGCAGGTG CAGCCTCGTA GCTGACATAC CCCACCACAT AATAACCTTG	2160
CTCTTGGTAG CTTTCCACTT GTGCCAGCAA ATCTGCCACT TCTTCTACAT TTCTCGTTTT	2220
CAACTCTTTA ATAGGCTGGG TAAAGGTATA TCTCTCCCC AAAGTCCTAA AATCAATCAC	2280
TGTTTTTCTA TGCATACCTT AAGTATAGCA TAAAATAAGA AAACCCCTCAT CCGCAAAGCA	2340
GATGAGAGAT TTCAATTATT TAAAGATTGA AGTTTTAAAG CTATTTGTTT GTTGAAGAAG	2400
TTTCTTATAA ACAGCTTCTT TTAATTTAAC TGTATTATTC ATAGATACTG TTTTATTACC	2460
GTTTGCTTCT TGTTTAAGAG TTTCCGCATC TTTTTTAACA GCTTCTTTAA ACAATGTCAG	2520
TAAATCATCG TATGATGAAA CGGAAGAACC ATTTACTTCG AATGTTGTTA ATCCTTTCGT	2580
TGCTTTATCT TTAACCTCTT TGAAGTAAGC TTTTTTAAAT TCTTCAATAG TATTAAATGT	2640
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ACCCATAAT CTAAAAGCAT TATGTTTGAA TGAAACAGCT CCAGGAGCAC CTTTACTAGT	2820
ATTACCTCCG TAGATACCGG TCATCATCTC AACACCTACA TAAGGTGATT GATCGTTATA	2880
GCTAATTGCT TCGGGTTTAT AGATACCATT ACCTGGATTG CGATTAGTCA TTAATTGTTG	2940
ATCAACTAAA TCATTAACAG ATTGAATATT TAATTCATTT TTCTCTTCTT GACTTAGATT	3000
TCGAATTTTA TCCCATTGAT TTAATTTATT GTTATCACGG TATCTCTAT CTATTTTTTT	3060
GAACCATGCA CTATTTAAAT CTTTATTTTG TTGAGAAATC ACAGATTCAG CCTCAATTC	3120
ATCAAGAAGA GTTAAAGTGT CATTATAACC CTTCATATAT CTATTAATAT CTTCTCGTGT	3180
TTTTAGAGTT TTTGGATCTG TAATATACCA CTGATTCCCA TCATTTTTCG GTTTAAATAC	3240
CATATTAATA CCTAAGAAC CAACTCATC AAATCCACTA CCAGTAACAG GAGTTTGTAG	3300
CATACCCTGA GCATATGCTT CAGCATCAGT ACCTTCACGG TGTCCAAAGC CACCTAAGTA	3360
AATCGCACGG TCGTTGACGT GTGTTGTTTC ATGTGTGTAA ACTGAAATAC CGTATTCACC	3420
AACCATTTCT AAATGAACAT ATTTTACATC AGTTCTAATA TCATCAGAGT TAGGATATAT	3480
AGCAGCATAA GCTCCTGTTT CATTATAATT ATAATACTTA TCCATAGGAC CAAAGAATTC	3540
TCTAAGAGGA GTATATACCT TGTCCGTATT ATAGCGGCCA TATTTTTCAA CCCATCCACC	3600

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GTATACAGAC GCTAGACGAT ACCAGAAATC ATAATAGTTT CTATAACCAT CTGCAGCTTT	3720
GTAAACGATA TCTTTAATAT CTTCTAATGA TTTTMTACCT AATCGCTCTG CACTACCAAA	3780
GGCAATTGCA TTATAATTTG AAATTAAATA AAGATGTGCT TTATCAATAT TCAGTAGTGG	3840
GAGTATAGTA TTTCTAAGGT GACTTCGTTT TAAATTATCG AATGCACGAT GTTTAGAATT	3900
TTTAATTTCT TCGACCTCAG AAGCGCGTTC TCGATGTAG ACATGGTCTT CTGTAGCATC	3960
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TGCATCTAAA TTACCTGATT TAGTATATTT AGCCAATACT TGACCGAATG CGTCGAATGT	4080
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AACTTTTTCA CCATAGAAAT CTGGTTTGAA TAGCATTAA TCTTTAATAT TAACATCACC	4200
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TTGTTTTGA ACTAATTTTG TGATTAGGTT TGTAAAGTTT TCTTTAACAT CTGTGAAGCT	4380
TTCTCTAAA TATAATCTT TGATTGCATT AACTCTATAG TCACCTAATC GATTTAGATG	4440
CTGATACATC GTTTGAGACT GAAGCTCTAC TGATTCTAAA ATAGATTTTA TATCATTAAC	4500
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AGTATATTCT TTTACATTAC TTAAACCTTC ACTGCTAGAA GACAAGTTAA AGTAATCTTT	4620
TGTACCGTCC GCATAGTGAA CAATAATTTT ATTAGCTTCA TCTAGGTTTG TGATAAACTC	4680
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AAATGATCTA TTACCTGACG AATATCCCTC TACCGCATAT AAATCTTTTA TATGAGCACT	5040
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TTTTGTACCA ATAAGATGGT CTAGAGTTAA TCCATAATCT ACTTTAGGAA CTAACAAGCT	5280
GGCGCGTGT TTGTTTCCTG TAATAGTAGC ATCAACATAT GCTTTTCTAA CAATTCCTCT	5340

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ATAGTTTGTA CCTGCAATTC CCCCTGTATG AGAGCCATTT CCACTTGTAG AGTGTAGTTT	5400
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TTCAAAATTC ACATTATTTA TCGTTGCGTT TGTATCACA TTAATAATG GATGTTCCAA	5640
TTCAGTAATA GCAAATGTT TTCCTTCAGA ACTTAAAAGT TTTCTGTGA ATTCCTTAGT	5700
GATATATGAT TTTCCATTAG GAACAACATT TCTAGCGCTC ATTGATTGTC CCAGACGATA	5760
TTCTTTTGAA GGATCGTTTT GAATAGCTTC CACTAATTCT TTGAAATTAT AATATACATT	5820
ATCTTCGTGG ACTTTAGGTT TTTCAATATA GTGAACGTAT TCTTCTTCAA ATTTATTATC	5880
AGCAGTTCTA GAGACTAAAT TGTCTGCGAT TGCTGTAAC TTATATACAG GTGTTCCGTT	5940
AACCGTAGTT TCTTCTATAT TTTTAACAGC TAGTAATGTA GTTTCTGAT TATTTGAACT	6000
TATTTTAAAA TAATAATTGC TCTTATCATC AGGAATAGTT GTTATCAGTG ATTCATTAGT	6060
TTCTTTTCCA TTTTCGTATT TGATTAAATC TGTACGTTTA ATATTTTAA GCTCAACTTT	6120
TTTAAGATCT AATTGAATAT TTTGATTTTC TAGAGTTTCA GTTCTCTCAC CGTTACCTCT	6180
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TACTTTAGGA AGGGTGTCTG CAGTAGGTTT TACCTCCGAT TTTGGTTCTT CCTTTGGACT	7440
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CTCTCCAGGT TTTGCTGAGG TTTCTTCTAA AACAGTGTCC AAGCCAAGCG TTTTGAGGAT	7620
GTCACCTGAT AGATAACCAA CATAGCGATA GCCCTCCATT TCAACAACAC CCTCTCGACT	7680
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CTTTTGGGG TCTAGAATCA ATCTTCATAT GGTAATTGGC TCCAAAATGA AGTTTGAGCC	8880

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CACCAACTTC CTTGGCACGA AGATTTTGAG CACCAGAAGC AATTTCCAAC ATGGTTTCTC	9540	
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CCTCGACCTT GTCTTGACTG GGATTCTCAG CATAGGCCAG AACATCCGTC TGCTGGGTCA	10260	
AACCAGTCGA GGTGGTTTCT AGTTTMTTGA TATAAGACTG AATAAAGTGG CTAGTCTGGC	10320	
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ATAATGCGGA AATAGTGAAG	CAGGATTTCC	TTGAGAGAAA	TTTGCTTGGC	ATCATAGGTG		12240
ACATGGACGG TTTCTGCATG	ACCTGTTTGG	TTAATCAATT	CGTACTTGGT	TGTTTCTCCT		12300
CTACCATTG CATAGCCTGA	AACGGCATCC	GTCACCCCGG	GAACACGTGA	GAAATATTTCC		12360
TCCACTCCCC AGAAACAACC	TCCAGCTAGA	TAAATTTCTG	GCAAGTCTGC	GTCTTTACTA		12420

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ATTTCTGTTT TTTTCACTGC TTTTCCTCCT TGGCTAACTG CCGCCTTTTC AATTTGCGAG	12480
GCATCTGTCT GCCCTGCATT TCGTATCAAT AGAACATAGA AACCGGTTAT GGCTAGAAAA	12540
AATACTCCTA GCAACAAGAA GATTTTAAAC TTATCATTTA TAAGACGCCT CCTAGGCTAA	12600
TTCCCTTCAA GTTTGCAAAA TIGCATCTTT TTCCATGAAT CCTGGATGTG TTTTGACCAG	12660
CTTGCCCTCT TGTCTATAA AGGCTTGGGT TGGGTAAGAA CGGACACCAT AAGTTTCCAA	12720
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ATTCCTAAAG TCCGCTTCAG ATTGCTCTCC CTTATGTCCT GGTGACACTA CTGTCAAGAC	12840
CACATAGTCA TCACCAGCTT CTTTAGCAAT CTCATCCGTA TCTGGAAGAC TAGCCAGACA	12900
GATGGAACAC CAAGAAGCCC AGAATTTGAG ATAGACTTTC TTGCCCTTGT AATCAGATAA	12960
ACGGTAGGTC TTGCCATCTA CTCCCATCAA TTCAAATCA GCCACCTCTT TCCCTTTAGC	13020
TGCGCTTGTT TTAGTAGCTG TCTGCTCCGT CTTTATTTC TCTTTCGTTT GGTGTTCACT	13080
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CTCCCTGCCA AGCTCCTGAA CCACCTGAAG CCGCCAAGGC CAAAACAGAC CCCAGAACCG	13440
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TAAATATAAA GGAAATTCCT GCTATAAAGG CCAGAGTTCG TAATAAACTA GTAACGTAGA	13740
TTGAAAATTT GCCGCTAGAA GCCTGAGCAC CATCCTTATC ATCTAGTAAC ACTCCTGTAT	13800
AGACCGGTAA CAAAGGTAAG ATACAAGGAG AAAAGAAGGA TAGAATCCCT GCCAAAAAGA	13860
CACTTAGAAA AAAGAAAATA TGACCCATAA AGTTCCTCCT ATCATTATAT TGATAGATT	13920
ATTATA	13926

(2) INFORMATION FOR SEQ ID NO: 6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20199 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:

CCCAGCAGAA AAATGGCATT TGGAGATAAT GGAAATCGTA AAAAACTAT GTTTGAGAAA	60
ATAACCTTGT TTATCGTGAT TATCATGCTA GTAGCAAGTT TATTGGGAAT TTTTGCAACT	120
GCAATTGGTG CCCTCAGTAA TCTATAAAAT AGATTCAAGA AAATTTAGTG ACTGGGATTT	180
CCCAGCCCTT TTTTAAAGTG AGAAGAAATA ATGAGTATGT TTTTAGATAC AGCTAAGATT	240
AAGGTCAAGG CTGGTAATGG TGGCGATGGT ATGGTTGCCT TTCGTCGTGA AAAATATGTC	300
CCTAATGGAG GCCCTTGGGG TGGTGATGGT GGTCTGGAG GCAATGTGGT CTTCTGTGTA	360
GACGAAGGAC TACGTACCTT GATGGATTTC CGCTACAATC GTCATTTCAA GGCTGATTCT	420
GGTGAAGAAG GGATGACCAA AGGGATGCAT GGTCTGGTG CTGAGGACCT TAGAGTTGCA	480
GTACCACAAG GTACGACTGT TCGTGATGCG GAGACTGGCA AGGTTTAAAC AGATTTGATT	540
GAACATGGGC AAGAATTTAT CGTTGCCAC GGTGGTCGTG GTGGACGTGG AAATATTCGT	600
TTCCGCGAC CAAAAATCC TGCACCGAA ATCTCTGAAA ATGGAGAACC AGGTCAGGAA	660
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GTAGGGAAGT CAACACTTTT AAGTGTTATT ACCTCAGCTA AGCCTAAAT TGGTGCCTAC	780
CACTTTACCA CTATTGTACC AAATTTAGGT ATGGTTGCGA CCCAATCAGG TGAATCCTTT	840
GCAGTAGCCG ACTTGCCAGG TTTGATTGAA GGGGCTAGTC AAGGTGTGG TTTGGGAACT	900
CAGTTCTCC GTCACATCGA GCGTACCGT GTTATCCTTC ACATCATTGA TATGTCAGCT	960
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GATGAAGCCC TTCGTGCGCG TGGAGCTAAA GATGGGATT TGGTCCGCAT TGGTAAATTT	1500
GAGTTTGAAT TTGTAGACTA GGAGACTGGT ATGGGAGATA AACCGATATC TTTCCGAGAT	1560
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CAAAATTAAA TTGTTTGATT CTTATTTCAA TTTGTTATAG TATATCTGAT GTCAAAGTTC	1980
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AATCGGCAAA	AAATGTCATT	AGTTTTTTGA	CATCATAGCC	AAAACCACGA	CGACCAAGTT	12360
CACCAAAATA	GGAAAAATCA	CGACGTACGG	TCGCTGAATC	AATACCGATA	GCCTCTGCAA	12420
TTTGCTTAGA	GTTGGCACGT	TCAATCTTTT	CTGCATGAAA	TCTCTTAAAA	ATTCGATAGT	12480
AGAGAGAGAG	TCTTTTGGCT	GTAGCTTTTG	GAATAGCAAA	CTGTTTATCT	TTCACAAAAT	12540
CACAACCTTT	CTATTCTTCT	ATTTTATAGA	AACATTGTGA	AAAAATCAAC	AAAAATAAGA	12600
AAAAACTAAG	AAAAATCTTA	GTTTTGATGT	AAAAATCTG	CATGAGATAG	AAAACGGTAG	12660
AGGTCTCCGA	CCAGCCCCTG	ATAAATCTTT	TTGCCCTTAA	AAGTCAGAGA	AGTCACATAA	12720
AGTGATCTCG	GTAAGGTAC	ACATCCTGAC	AAAGTCAACA	TGAGAGCCTC	ATGATCCTCA	12780
TACTTGAGAG	TACGCTCTAC	ATGATAGCAG	TCCTTATAGG	TCAGTTCAAA	CATTTTGGCT	12840
CTATCTTTCC	GATTTTGTA	AGACACCACG	TTCTACCAAG	CTATCCATGA	GGAAGTAGAA	12900
TTTTTCCTGA	TGAATATGGT	GGTCTTCTGA	TTTGAAAATA	TCAACTAGAC	GAAGGCCAAA	12960
CTTGTCAGTG	ATATTGATTT	TAGCCCCTGT	AAGTTCCTTG	TTAATGATGA	TTTTGAGTTG	13020
GAAGCCTTCA	CCGCTGTTTG	GCACCTTTTC	CAAAAGGCGA	GTGAGTTTCT	AGTTACCAAC	13080
CTTAGTTTCA	AAAAAGGTGT	TATCTTTGAG	GGTGAATTTT	TTAACAGAAG	GGCTAAGAGT	13140
GTAATCGTAA	CGACAATTTT	TTAACTGAAT	GATTTTTTCA	AATGCCATAT	GGCTAACCTC	13200
CGATAATTTT	TTTTAAGGTT	TTTGCGAGGG	TTTGTAGGTC	TTCAACGGTA	TTTTGTGGCG	13260
ACAACTGAT	GCGAAGGGAT	TCCTTCAAGC	GTTCTGAATT	TGCGCCATAC	ATGGCTTCAA	13320
GAACATGGCT	GGATTGGACA	ACGCCTGCAG	TACAGGCTGA	GCCAGTAGAG	ATTGAAATTC	13380
CAGCTAAATC	TAGCCGAAGG	AGTAAGAGGT	CATTTTCTTG	ACCAGGAAAT	CCAATATTGA	13440
GAACATAAGG	GAGATGATGT	TTTCCTCTAT	TCAGGTAATA	CTGAATGCCC	TCCAGCTCTG	13500
CCAGAAAGGC	AGTTTCTAGA	TTTTGTACAT	GTTGAAAATG	TTCTTCTTGT	TTTTCTAGGT	13560
CTTCTTTTAG	GGCTGCAACC	ATGCCTACAA	TGGCAGGCAG	ATTTTCAGTT	CCTGCACGTT	13620
TTTTCTGTTC	CTGGTCTCCG	CCATGTAGAT	AGGAATCAAA	GTCCATGCTA	GATGCGTAGA	13680
GAAAACCGAT	TCCCTTAGGA	CCATGGAATT	TGTGGGCAGA	AGCAGTGAGA	AAATCAATGC	13740
CCAATCTTTC	TGAATGAATT	GGGATTTTAC	CAATAGCCTG	AACTGCATCA	ACATGATAGG	13800
CAGCAGGGTG	TTGCTTGAGT	ATTTGGCCAA	TTTCAGCGAT	GGGCAGTAGG	TTTCCTGTCT	13860
CATTATGAC	AAACATGGTA	GAAACCAAAA	TCGTATCGTC	ACGTAAAGCC	TTTTGAATTT	13920
GCTGGGCTGT	GATTTCTTGA	TTTTCTGGCT	GGATAATGGT	TGCTTCAAAC	CCAAAGTGTT	13980
GAACCAAGTA	ATCAATTGTT	TCAAGGACAG	CATGGTGCTC	GATGGCAGTT	GTGATGATAT	14040

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GTTCCTCTTG TTCTTGGTGA CGAAGACAGT AGCCAATGAT GGTAGTATTA TTGCCTTCAG	14100
TCCCACCAGA AGTGAAAAAG ATATGTTGAG GTTTTGTCTT TAGTAAGTGG GCTAGTTCCT	14160
GACGGGCTTC TCGCAAGAGT TTGCCAGCTT GACGACCATG ACCATGAATA CTAGAAGGAT	14220
TTCCGTGGGT TTCTTGCATA ACCTTGGTCA TAGCTGAAAT AGCAACTGCT GACATAGGAG	14280
TCGTTGCAGC ATTGTCCAAA TAAATCAAAG AATCACCTTA TTTCTTTTTA TTGTAGGCAA	14340
AGAGTGGGCT GACTGGTTTT CTTTCGTGAA TACGGACGAT AGCATCACCA ATTAACCTAC	14400
TAGCAGTGAT GTAGCATACA TTTTTAGGAG TTTTTCCTTT TGTGCTACT GAATCAGTCA	14460
CAAGAAATTC TTTAATATTA GTATTGTCAA GAAGCTCAGC AGCTCCCTCG ACGAAGAGAC	14520
CGTGGCTAGA AACAGCATAA ATTTCTGTAG CTCCTTCACG TTCAACGATT TTAGAAGCTT	14580
CAGAGAAGGT ACGTCTCTGA TTTAAATAT CATCAATCAA GATAGCTTTC TTACCTTCAA	14640
CATCACCAAT AATATAACCT TCGTTACGAG TTGCATCGTC TTGAGGGTAG TCGATAATGG	14700
CGATAGGAGC ATCAAGATAT TCAGCCAGGC TACGCGCACG TTTGACACCT GAATTTTTAG	14760
GGCTAACGAC AACAACTCT GAACCAAGCA ATCCTTTATC GCAGTAATGT TTTGCGAATA	14820
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TATAAATCCT AGTTATATTT ACCTTACATA TATGAACTGG GATTTGTGTA TTTTATCTT	15360
TTCTATTTTA CCAAAAAATG GAGATTATTT CAGCTATTTT TCATACTTTT GACAAATCGA	15420
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TCCTGTTTGC CTGCTCATG ATTTTCCACT TCAAGCTCCA ATTCGTAATC TGTATATCA	15540
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TCCAGTACTA GCCCTTGAGG AAGTTCTTCC TTACTIONAGT AGTTCTCAGC ATCTTTTAGT	15720
TGCAATTTTT GGTGTATTC CATGTTTCCA AACTCTGCG GGACTTTGAG TGTCAACTCA	15780

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GCCCAGTCTT CAAAGGTTTCG AATGCGCATA GCGACTTTCT TTTCTCGCAG TTCAAAATCA	15840
GGCGTGTCGA TG TAGTAATT TGTTTGAAGA ACAGGAGTGA CACCTGTGAA CTGGTCTTTT	15900
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TTTCTTACCT TTTTTTATCG TTGAAAGCGG ATTTATGGTA TAATAAGCAT TGTATTTATT	16020
GTATATGAAT CTGGAGAAAA AATCAAAGAT ATTTTGTACG GATAATATGA GAACAAGGGA	16080
GAATATATGA CCTTAGAATG GGAAGAATTT CTAGATCCTT ACATTCAAGC TGTGGTGAG	16140
TTAAAGATTA AACTTCGTGG TATTCGTAAG CAATATCGTA AGCAAAATAA GCATTCTCCA	16200
ATTGAGTTTG TGACCGGTCG AGTCAAGCCA ATTGAGAGCA TCAAAGAAAA AATGGCTCGT	16260
CGTGGCATT CTTATGCGAC CTTGGAACAC GATTTCGAGG ATATTGCTGG CTTACGTGTG	16320
ATGGTTCAGT TTGTAGATGA CGTCAAGGAA GTAGTGGATA TTTTGCACAA GCGTCAGGAT	16380
ATGCCAATCA TACAGGAGCG AGATTACATT ACTCATAGAA AAGCATCAGG CTATCGTTCC	16440
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AAGATTAAAGT TTCGAGGTGG AGCTATTCTG GTCAATAATC AACCGCAAAA TGCAACGTAT	17700
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AATAAACCCCT ATGGAGTGGC TTCTATTCCCT AGTGTCAATC ACTCTAATAC CATTGCCAAT	17880
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CGATTAGACA AGCAGTTGCA GAAGAAATCT ATCGAGAAAC GCTACTTTGC TTTGGTTAAG	18060
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TTAAAGGAGA AACTCATGG AAGTTTTTGA AAGTCTCAA GCCAACCTTG TTGGTAAAAA	18540
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TCTTGAAATT GAAGGAATCA TGGATGGTTA TGAGGTCAAC GACCCCTAAC ATTATCCTCA	18720
ATTTGAAGAA ATGGTTTCTG CCTTGGTGGA GCGTCGCAAG GGCAAAATGA CTGAAGAAGA	18780
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CTTGGTTGAT GGAATGGTGT CAGGAGCGAT TCACTCAACA GCTTCAACAG TTCGCCCAGC	18900
TCTACAAATC ATCAAACTC GTCCAAATGT AACTCGTACT TCAGGAGCCT TCCTCATGGT	18960
TCGTGGTACG GAACGTTACC TATTTGGAGA CTGTGCCATT AACATCAATC CAGATGCAGA	19020
AGCCTTGGCT GAAATTGCCA TCAACTCAGC AATCACAGCT AAGATGTTG GCATCGAACC	19080
TAAAAATGCC ATGTTGAGCT ATTCTACTAA AGGTTTCAGG TTTGGTGAAA GCGTTGATAA	19140
GGTCGTTGAA GCAACTAAAA TTGCTCACGA CTGCGTCCT GACCTTGAAA TCGATGGTGA	19200
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GGTAGCTGGT CAAGCAAATG TCTTCATCTT CCCAGGTATC GAGGCAGGAA ATATTGGTTA	19320

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CAAGATGGCT GAACGCCTGG GTGGCTTTGC GGCTGTAGGA CCTGTTTGC AAGGTTTAAA	19380
CAAGCCAGTT AATGATCTTT CTCGTGGATG TAATGCAGAT GATGTTTACA AGTTGACCCT	19440
CATCACAGCA GCTCAAGCAG TTCATCAATA GTGAAACTA TAAAGTGATA TACTATGCTA	19500
TACTGTAGTT ATGAAACTAT GTACGAAAAG CACTGCCATT AATTCCTGAG AACTAAATTA	19560
CTGATTGGTG TCAAAAAGGA AAACCTCCAA GCGATGATAT CCTGTCTATA CACGACCTAT	19620
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TGGTCGCTTC CAGTTTGGCG TTAGAATAGT GTAGTTGAAG GCGTTGATA ATCTTTTCTT	19920
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CCTCAATAAG TCCGAAAAAT TTCTCTGTTT CCTTATTCTG GAAGTGAAGA AGCAAGAGTT	20040
GATAGAGCTG ATAGTGGTGT TTCAAGTCTT CCGAATAGCT CAAAAGCTTG TTTAAAATCT	20100
CTTTATTGGT TAAGTGCATA CGAAAAATAG GACGATAAAA TCGCTTATCA CTCAGTTTAC	20160
GGCTATCCTG TTGAATGAGT TTCCAGTAGC GCTTGATAG	20199

## (2) INFORMATION FOR SEQ ID NO: 7:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 19702 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7:

ACCCGATGTA TCAGCGGATA TTTACTCTAT TTTTCAAACG ATGTTATACC CACAATAAAA	60
GAAAAAAGAC CCTAAGGTCT CCTTTGCTTT TATTATTAAA CGCGTTCAAC TTTACCTGAT	120
TTCAAAGCAC GAGCTGAAGC CCAAACCTTT TTAGGTTTAC CATCGATAAG AACAGTAACT	180
TTTTGAAGGT TTGGTTTTAC GGCACGTTTT GTTTGGTTCA TCGCGTGTGA ACGGTTGTTT	240
CCTGATACAG TCTTACGACC TGTAAGTAA CATACTTTAG CCATTGTGTT TTCCTCCTAT	300
TAGATCTAAT ATAGCGGATG TGCTAGCACC ACATACCGTA CTATGTTATC ACATTTTCTT	360
GTTTTTTGCA AGGGAATTGG AAGATTTTTT ATTTGTGTCT TAAATCAGGT CTGCGTGAC	420
ATTTCTGCTC TCCACATGCC ATCGTTGATT AACAGAACAC CAGAATTAAA ATTATGTGTA	480
TAAAAATCAT CTCTAACTGC AGCTAAGGGT ATAGCCGTCA AGTCCAAATC CCACAGCTCA	540



TCTATCGATT TTCTTACAAC AATATCTGAA TCCAAATACA GTACACGAGA CTCGCTTACA	600
TACTTTGGAA TAAAATACCT AAAAAAGCCG CATATGAAAG TCCCTCAAAG GGGAGACGAT	660
AACCTTTCAG AATATTACTG TCAATCTAAA CATTCACAAT CTCACTATTTC AAAGTCTCTA	720
GTCTTTTTC CATCAATTGG AACCATTC TC GCGAAGGTC ATCATTA AAA ACATAAACT	780
TAAGATTATA ATGATGAACA CAAAGAGATT TTATTGTTGT TTCAACTTTA TCCATATAAG	840
CATTATCTGC ACCTAAGACA ATCGCTTTTT TCTCTTCTTT CACTTTTTAT CTCATTTCTT	900
TTTATTCCTCA TCATATTATT CCCATCATAT GTTCCCATC ATATGTTTCT ACGTAACCAT	960
TATTTTCGCC TATTCGTTTC TAAACCATA CCAGTGGAGA TTTTAGATGA AGTCCCATTA	1020
CGGTTTACAA TTTTACATT ACGACACGGA GTTTTACAAA TCGATTTCAT TTGCCAAACG	1080
TAGTTAGTGA GGCAGTTAGC TAGTTCGCCA AATAGCGACT AGCGTCCAAC AATTGGAAC	1140
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CCATGCGGTG TTTAAAGACT TCAAACCTGA GTTGACCTAC AGCGCCTAGC ATGTACTCAC	1440
CTGTTTGSTA ATTCTTATAA AGCTGAACGG CTCCTTCTTG CACCAATTGC TCAATCCCCT	1500
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CCTGATAAGT ACCGGTATCG TAAACCCGA TAATATCACC TGCCACGGCA TTGGTCACAT	1680
TCTCAGGACT CTCGCCATA AACTGGGTAA CATTAGATAG TTTAGCCCC TTACCAGTAC	1740
GAGGGAGATT GACACTCATG CCGCGCTCAA ATTCGCCAGA TACGATACGG ACAAGGCAA	1800
TACGTCACG GTGACGAGG TCCATGTTGG CTTGGATTTT AAAGACAAAG CCTGAGAAAT	1860
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CAAACCTGAG GAAGGTTCA AGGAAGGTCT GCACACCAA GTTGTTCAGG GCTGAACCGA	1980
AAAAGACAGG CGTCAATTCT CCAGCCAGAA TAGCTTCCTC TGAAACTCA TTCCCGCTT	2040
CATTAAAAAG CTCAATGTCA TCCTTGACTT GCTCGTAGAA AGGATTGCTA CCAAAGATT	2100
TGTCCCGTC TTCTAGACTG GCAAAACGCT CATCCCCTTT GTAAAGCTCT AAACGTTGGT	2160
TATAGAGGTC ATACAAGCCC TCAAAGGCTT TCCCCATCCC GATAGGCCAG TTCATAGGGT	2220
AGCTAGCAAT GCCCAAGATT TCTTCCAATT CTTGCAAGAG ATCCAAAGGC TCACGACCGT	2280

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CACGGTCCAG CTTGTTTCATA AAGGTAAAGA CTGGAATGCC ACGATGTTTC ACAACCTCAA	2340
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CCACCGCCAT CAAGGTACGA TAGGTATCTT CTGAGAAGTC CTCGTGCCCT GGCCTGTCTA	2460
AGATATTAC GCGCTTGCCG TCGTAGTCAA ATTGCATAAC AGATGAAGTA ACAGAAATCC	2520
CACGTGTCTT CTCGATATCC ATCCAGTCAG ATTTAGCAAA AGTCCCTGTT TTCTTCCCTT	2580
TTACCGTACC AGCCTCACGA ATCTCACCCC CAAAGTAGAG TAACTGCTCA GTGATGGTTG	2640
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ATAGAACAGA CTA AAAATCA TCATTTACG AAAGGATGCA AGATGAAAAT TACGCAAGAA	2940
GAGGTAACAC ACGTTGCCAA TCTTTCAAAA TTAAGATTCT CTGAAGAAGA AACTGCTGCC	3000
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TCGTTGGTCT CAAACCAACC TACGGAACAG TTTCACGTTT CGGTCTCATT GCCTTTGGTA	3840
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TGATGCCAAA CAAGTCTCTA ACTGGCTCCA AGGGGAAGTC GCTCAGTTCT TGAATGCTGA	5760
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CATCGAAGAC GGTACTATTT CATCTAAGAT TGCCAAGAAA GTCTTTGTCC ATCTAGCTAA	5880
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AGCTATCTTG ATCCCAATCA TCCACCAAGT CTTTGCCGAT AACGAAGCTG CTGTTGCCGA	6000
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AAAGAAAAC AGACAGAACA AAACCAGCCC TAAGGTTGGT TTTTCTTCT CTACCAACTC	6180
CCAATAACTA TTTTGGCTT ATTTCCAGAG TATTTTATGG TAAATGAAG AGTAATAATA	6240
TTTATTAAAG AGGTAAAAAC ATGATTGAAG CAAGTACCTT AAAAGCTGGT ATGACCTTG	6300
AAACAGCTGA CGCAAATTG ATTCGCGTTT TGAAGCTAG TCACCACAAA CCAGGTAAAG	6360
GAAACACGAT CATGCGTATG AAATTGCGTG ATGTCCGTAC TGGTTCTACA TTTGACACAA	6420
GCTACCGTCC AGAGGAAAAA TTTGAACAAG CTATTATCGA GACTGTCCCA GCTCAATACT	6480
TGTACAAAAT GGATGACACA GCATACTTCA TGAATACAGA AACTTATGAC CAATACGAAA	6540
TCCCTGTAGT CAATGTTGAA AACGAATTGC TTTACATCCT TGAAAACTCT GATGTGAAAA	6600
TCCAATTCTA CGGAACGTAA GTGATCGGTG TCACCGTTCC TACTACTGTT GAGTTGACAG	6660
TTGTGTAAC TCAACCATCT ATCAAAGGTG CTACTGTTAC AGGTTCTGGT AAACCAGCAA	6720
CGATGGAAC TGGACTTGTC GTAACGTTT CAGACTTCAT CGAAGCAGGA CAAAACTCG	6780
TTATCAACAC TGCAGAAGGA ACTTACGTTT CTCGTGCCTA ATCTCTAGAA AGAGGTCATT	6840
CTATGGGAAT TGAAGAACA CTTGGCGAAA TCGTTATCGC CCCACGTGTA CTTGAAAAAA	6900
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AACTCACAGC AGATATCTAT CTCTACCTTG AGTACGGAGT AAAAGTTCCT AAGGTAGCGG	7080
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TGTCGTTTCG CCTATCTCA TGATCGTGAA GATACGGATG TACAACCTCC AGCCTTTTGT	7380
ATAGACCTCG TTTCTGGTGT TCAAGCTAAA AAGGAAGAAC TAGATAAGCA AATCACTCAG	7440
CATTTAAAG CAGGTTGGAC CATTGAACGC TTAACGCTCG TGGAGAGAAA CCTCCTTCGC	7500
TTGGGAGTCT TTGAAATCAC TTCATTGAC ACTCCTCAGC TGGTTGCTGT TAATGAAGCT	7560
ATCGAGCTTG CAAAGGACTT CTCCGATCAA AAATCTGCC GTTTTATCAA TGGACTGCTC	7620

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GCATGAGACT CATGATTCCT TCCTGCATAC GGGCTCCACC AGAGGCTGTG AATAGGACAA	11400
CTGGCAATTT TTCGACAGTC GCATACTCAA ACAAACGAGT GATTTTTTCA CCTACAACCG	11460
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GATTTACAGC CTCTGGGCT GCATACAAGG CATATAAAGA ATAGTTATCA AAACGGTTGG	15240
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TCCTTTCAAA ACTTCTACTT ATTTTAGTCT ATTTTCTAA AAGTGCTACT AAACCTGCTT	16260
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CCTCCAACCT TCCTTGCTTA CGTAATAGTT CGATTTCAAC ATAATTTGAC AGTCAAACTA	18180
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TGCTTGCTCT TCAACGTAAG CAACCAAGTC ACCAACTGTT TTCAAGTCAT TTTCTGCTTC	18300
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ACCACTTGCT CTGGCACATA ATGAGCAACC TGACTTATTT TTGCAAAAGC CATTATTTCA	19500
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CGCTCATGCC ATCAATAATT TTTTCTACCA TGGCCTTGTG GAAGCGTTTA TGCAGTCTAT	19620
GAATCAAGCG ACCCTTCTTT GTCAAATGCA GATGCACCAC ACGACGATCC TGTCTGACC	19680
GAACCTGCTC AATGTAGCCC GG	19702

(2) INFORMATION FOR SEQ ID NO: 8:

- (1) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 6211 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 8:

GAAAATTTC TCTCTCTCT TGAATAATTT TGAATAATG GTATGATAGT AACAAGTTAT	60
TTTAAAGAGG AAAGAAAGGG GAATAATGGA GAAATCAGT TTAGAATCTC CTAAGACGGG	120
GTCGGACCTA GTTTTGAAA CACTTCGTGA TTTAGGAGTT GATACCATCT TTGGTTATCC	180
TGGTGGTGCG GTTTTGCCTT TTTATGATGC GATATATAAT TTAAAGGCA TTCGCCACAT	240
TCTAGGGCGC CATGAGCAAG GTTGTGTCGA TGAAGCTGAA GGTATGCCA AATCAACTGG	300
AAAGTTGGGT GTTGCCGTCG TCACTAGTGG ACCAGGAGCA ACAAATGCCA TTACAGGGAT	360
TGCGGATGCC ATGAGCGATA GCGTCCCCT TTTGGTCTTT ACAGGTCAGG TGGCGCGAGC	420
AGGGATTGGG AAGGATGCCT TTCAGGAGGC AGACATCGTG GGAATTACCA TGCCAATCAC	480
TAAGTACAAT TACCAAGTTC GTGAGACAGC TGATATTCGG CGTATCATTA CGGAAGCTGT	540
CCATATCGCA ACTACAGGCC GTCCAGGGCC AGTTGTAATT GACCTACCAA AAGACATATC	600
TGCTTTAGAA ACAGACTTCA TTTATTCACC AGAAGTGAAT TTACCAAGTT ATCAGCCGAC	660
TCTTGAGCCG AATGATATGC AAATCAAGAA AATCTTGAAG CAATTGTCCA AGGCTAAAAA	720
GCCAGTCTTG TTAGCTGGTG GTGGAATTAG TTATGCTGAG GCTGCTACGG AACTAAATGA	780
ATTTGCAGAA CGCTATCAAA TTCCAGTGGT AACCAGTCTT TTGGGACAAG GAACGATTGC	840
AACGATGCAC CCACTCTTTC TTGGAATGGG AGGCATGCAC GGGTCATTCG CAGCAAATAT	900
TGCTATGACG GAAGCGGACT TTATGATTAG TATTGGTTCT CGTTTCGATG ACCGTTTGAC	960
GGGGAATCCT AAGACTTTCG CTAAGAATGC TAAGGTTGCC CACATTGATA TTGACCCAGC	1020
TGAGATTGGC AAGATTATCA GTGCAGACAT TCCTGTAGTT GGAGATGCTA AGAAGGCCCT	1080
GCAAATGTTG CTAGCAGAAC CAACAGTTCA CAACAACACT GAAAAGTGA TTGAGAAAAGT	1140
CACTAAAGAC AAGATCGTG TTCGTTCTTA TGATAAGAAA GAGCGTGTGG TTCAACCGCA	1200
AGCAGTTATT GAACGAATTG GTGAATTGAC GAATGGAGAT GCCATTGTGG TAACAGACCT	1260
TGGTCAACAC CAAATGTGGA CAGCTCAGTA TTATCCCTAC CAAATGAAC GTCAGTTAGT	1320
GACTTCAGGT GGTTTGGGAA CAATGGGCTT TGGAAATCCA GCAGCAATCG GTGCTAAAAT	1380
TGCTAACCCA GATAAGGAAG TAGTCTTGT TGTGGGGAT GGTGGTTTCC AAATGACCAA	1440
CCAGGAGTTG GCTATTTTGA ATATTTACAA GGTGCCAATC AAGGTGGTTA TGCTGAACAA	1500
TCATTCACTT GGAATGGTTC GCCAGTGGCA GGAATCCTTC TATGAAGGCA GAACATCAGA	1560
GTCGGTCTTT GATACCCTTC CTGATTTCCA ATTGATGGCG CAGGCTTATG GTATTAAAAA	1620
CTATAAGTTT GACAATCCTG AGACCTTGGC TCAAGACCTT GAAGTCATCA CTGAGGATGT	1680

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TCCTATGCTA ATTGAGGTAG ATATTCTCTG TAAGGAACAG GTGTTACCAA TGGTACCGGC	1740
TGGTAAGAGT AATCATGAGA TGTGGGGGT GCAGTTCCAT GCGTAGAATG TTAACAGCAA	1800
AACTACAAAA TCGTTCAGGA GTCCTCAATC GCTTTACAGG TGTCTATCT CGTCGTCAGG	1860
TTAATATTGA AAGCATCTCT GTTGAGCAA CAGAAGATCC GAATGTATCG CGTATCACTA	1920
TTATTATTGA TGTGCTTCT CATGATGAAG TGGAGCAAAT CATCAAACAG CTCAATCGTC	1980
AGATTGATGT GATTGCGATT CGAGATATTA CAGACAAGCC TCATTGGAG CGCGAGGTGA	2040
TTTTGGTTAA GATGTCAGCG CCAGCTGAGA AGAGAGCTGA GATTTAGCG ATTATTCAAC	2100
CTTCCGTCG AACAGTAGTA GACGTAGCGC CAAGCTCGAT TACCATTGAG ATGACGGGAA	2160
ATGCAGAAAA GAGCGAAGCC CTATTGCGAG TCATTGCGCC ATACGGTATT CGCAATATTG	2220
CTCGAACGGG TGCAACTGGA TTTACCCGCG ATTAAAAATC CAACTTAAAT TTATTAAACC	2280
AGCCTAAAAA GCAATAAATA ATAGAAAAGA GAGAAAAGCT ATGACAGTTC AAATGGAATA	2340
TGAAAAAGAT GTTAAAGTAG CAGCACTTGA CGGTAAAAAA ATCGCCGTTA TCGGTTATGG	2400
TTCAACAAGG CATGCGCATG CTCAAAACCT GCGTGATTCA GGTGCTGACG TTATTATCGG	2460
TGTACGTCCA GGTAAATCTT TTGATAAAGC AAAAGAAGAT GGATTGATA CTTACACAGT	2520
AGCAGAAGCT ACTAAGTTGG CTGATGTTAT CATGATCTTG GCGCCAGACG AAATCAACA	2580
AGAATTGTGA GAAGCAGAAA TCGCTCCAAA CTTGGAAGCT GGAACGCGAG TTGGATTGCG	2640
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GTGTGCTCCT AAAGGACCAG GACACTTGGT ACGTCGTACT TACGAAGAAG GATTGGTGT	2760
TCCAGCTCTT TATGCAGTAT ACCAAGATGC AACAGGAAAT GCTAAAAACA TTGCTATGGA	2820
CTGGTGTAAG GGTGTTGGAG CGGCTCGTGT AGGTCTTCTT GAAACAACCT ACAAGAAGA	2880
AACTGAAGAA GATTGTTTG GTGAACAAGC TGTACTTTGT GGTGGTTTGA CTGCCCTTAT	2940
CGAAGCAGGT TTCGAAGTCT TGACAGAAGC AGGTTACGCT CCAGAATTGG CTTACTTTGA	3000
AGTTCTTCAC GAAATGAAAT TGATCGTTGA CTTGATCTAC GAAGGTGGAT TCAAGAAAAT	3060
GCGTCAATCT ATTTCAAACA CTGCTGAATA CGGTGACTAT GTATCAGGTC CACGTGTAAT	3120
CACTGAACAA GTTAAAGAAA ATATGAAGGC TGTCTTGGCA GACATCCAAA ATGGTAAATT	3180
TGCAAAATGAC TTTGTAAATG ACTATAAAGC TGGACGTCCA AAATTGACTG CTTACCGTGA	3240
ACAAGCAGCT AACCTTGAAA TTGAAAAAGT TGGTGCAGAA TTGCGTAAAG CAATGCCATT	3300
CGTTGGTAAA AACGACGATG ATGCATTCAA AATCTATAAC TAATTAGAAA TATATAGCGC	3360
TGGAGATGAT TTTATGAAAA AGATTATGAG AAAAATTGCA TCGTTATTAT TGGTTCTAGT	3420

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TGTATAATGT AATTACACCG TCGGTAATAG TGCTAGCAGA CCAAAATAAA GCAGATTGGT	3480
CGTATGATGA AAATGCTGTA ATTAACATTT ATGATGATGC TAATTTTGAA GATGGTAGGT	3540
TGCATATGAA CTTTGAACAA TTCTTCAAAT TGGCACAAAT AGCTAGAGAA GAAGGTCTTG	3600
AAATTCATTC TCCGTTTGAG AGAGCTGGTG CGACTAAATC TGCTCGTTAT ATAGCGAAAT	3660
GGATTTTGAG AAATAAAAAA CATTAACAAA TATAGTTGGT AAATCATTAG GACCTAAATC	3720
AGCTGTTAGA TTCGGAGAAG CTTTATCCTA TATTGAAGGT CCTCTTCGCA GAATAAATGA	3780
GACGATAGAT GCGCGTTTAT ATCAAATAGA GCAAATTATT GCATCTGGAT TGAAGAATC	3840
GGGTTTAAAT GACTGGACTG CGAAAACTTT AGCTTCAGCT ATTCGTGGGA TATTAGATGT	3900
ACTTATTTAG GGGTTGAAAT CATATGAATA TTACCAATTT GTTTTCTATC AAGACAGGAT	3960
GTGATGAAAC TGATAGGCAA CTGCAAAAC TATTTTTC AATTGGGAG	4020
AATTGACAGA TCAACTAAGA AAATTAGATT CTAATTTTGT TCCTCGTAGT CAATTTGTAG	4080
ACACGTTGGA TTTGAATGAT GTAGAATATA AAGAAATTTT AAATATTTT ATCTTCCATC	4140
GTAATGATAG TGAAGAAAGT TTGGTAGAAT GGTATATGA TTGGATTTC ACAAATCGTT	4200
ATGAACTTCC TAAAGAGTTT TCGATTTCGTA TGGCTCATAA ATACCATGAA AGTGTTACTG	4260
AAGTTTTCGG AGATGAATAA CTAATAAACA GTCATTAGTG ACTGTTTTTT ATAGAAAAAG	4320
AGGTTTATA TGTTAAGTTC AAAAGATATA ATCAAGGCTC ACAAGGTCTT GAACGGTGTG	4380
GTTGTGAATA CTCCACTGGA TTACGATCAT TATTTATCGG AGAAGTATGG TGCTAAGATT	4440
TATTTGAAAA AAGAAATGC CCAGCGTGT CGCTCCTTTA AAATTCGTGG TGCCTATTAT	4500
GCCATTTCCC AGCTCAGCAA GGAAGAACGT GAACGTGGGG TAGTCTGCGC TTCTGCGGGA	4560
AATCATGCGC AGGGAGTAGC CTATACTTGT AATGAAATGA AAATTCCTGC TACTATCTTT	4620
ATGCCCATTA CTACGCCACA ACAAAGATT GGTCAAGTTC GCTTTTTTGG TGGGGATTTT	4680
GTAAGTATTA AACTAGTTGG AGATACCTTT GATGCCTCAG CCAAAGCAGC TCAAGAATTT	4740
ACAGTCTCTG AAAATCGTAC CTTTATTGAT CCTTTTGATG ATGCTCATGT TCAAGCAGGT	4800
CAAGGAACAG TTGCTTATGA GATTTTAGAA GAAGCTCGAA AAGAATCGAT TGATTTTGAT	4860
GCTGTCTTGG TTCCTGTTGG TGGTGGCGGT CTCATTGCCG GGGTTTCTAC CTATATCAAG	4920
GAAACAAGTC CAGAGATTGA GGTATTCGGA GTAGAGGCGA ATGGAGCGCG TTCCATGAAA	4980
GCTGCCTTTG AGGCTGGAGG TCCAGTAAAA CTCAAGGAAA TTGATAAATT TGCTGATGGG	5040
ATTGCTGTGC AAAAGGTAGG TCAGTTGACC TATGAAGCAA CTCGTCAACA TATTAAAACT	5100
TTGGTAGGTG TCGATGAGGG ATTGATTTCT GAAACCTTGA TTGACCTTTA CTCTAAGCAA	5160
GGGATAGTCG CAGAACCTGC TGGAGCGGCT AGTATCGCCT CTTTAGAGGT TTAGCTGAA	5220

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TATATTAAGG GGAAAACCAT TTGTTGTATC ATTTCTGGAG GAAATAATGA TATCAACCGT	5280
ATGCCAGAAA TGGAAGAGCG TGCCTTGATT TATGATGGTA TCAAACATTA CTTTGTGGTC	5340
AATTTCCAC AACGTCCAGG AGCTTTGCGT GAGTTTGTA ATGATATCCT GGGGCCAAAT	5400
GATGATATCA CACGTTTGA GTATATCAAA CGAGCTAGCA AGGGAACAGG CCCAGTATTA	5460
ATTGGGATCG CTTTAGCAGA TAAGCATGAT TATGCAGGTT TGATTCGTAG AATGGAAGGT	5520
TTTGATCCAG CTTATATTAA CTAAATGGT AATGAAACGC TTTATAATAT GCTTGTCTGA	5580
GGACTAATAA AAAAATATCA TACCTTCATT TTGATTTCTT ATCTATTGAC AAGCATAGTC	5640
ACACTGTCTT TAATACTCTT CGAAAATCTC TTCAAACCAC GTTAGCTCTA TCTGCAACCT	5700
CAAAACAGTG TTTTGAGCAA CTGCGGCTA GCTTCCTAGT TTGCTCTTG ATTTTCATTG	5760
AGTATAAGGT ATGATTTGAT TTCTTTTGT TGACAAATAT ACTATATTAA AAAGATATAT	5820
AAGTAATTAA CTGAGCTTAT CTGTCTTGT ATCTCTATTA AGGATGGTTT AGATAATCGG	5880
GTGTCTGCTT CTAGGCTAGC ACCTCAATAT CCAAAGGAGT GATGAATTG AAGGACATAA	5940
GGAATACCTA TCTCTCAGAT GATTATTGA GGAAGAAAGA TAGGAGTTT TGAGCTAGTG	6000
AAGGCTTGA TTTCTAAAG TTAGAATAT CATCTCAGT TCTTAAATCG AAGAAATAAG	6060
CTATCTTACG GAAATAGAGA AGCATTTTT AAGAACTGA ATAATTTGCG ACCTTAAGAG	6120
GGTAATAATA CAGTATTTT ATTAGCAAT ATTTATGGT TAGAGGCTAG CAAAACCTAT	6180
ATATTATCGG ATTTAAAAAG GAAGTAAGAA A	6211

(2) INFORMATION FOR SEQ ID NO: 9:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 7939 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 9:

CCGGACTCCC CACGATTCTT CAAAATAACT GAGTATATTT CTATCTTGAT TTTCAGATAT	60
AAATTCTTCC TTCTGTGGCC TCTTCTTACG CTTGAGAAGA GCTTCTCCGA CATGGCTTCT	120
TCCTTACTGA GCAAAACCTT GAGCATAGAT AAGTTTGA CTGCAAGCGT CTCTTGATA	180
TTTGGCTCCC TTCCCACTAT TGTGGATAGC GAGGCGTCTT CTCATATCAG TCGTATAGCC	240
TATATAGTAG GATCCATCAC GACACTCCAG AACGTACATA TAAGCCTTAT GATCCATAAT	300
AAATCTCTTC GATTTCCGGC GTATAAGAGC CATCATCATT GTGGACAATC AAAGGAGGTA	360

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AGACCTTAAA GCCACTTGTT GAGCCATCCT TGATCGCCTC AATCAAAAGC ATATTGGCTT	420
CCTTTTCTCT TTTTGGATAA ACAAACCTGCA GGCGCTTAGG GGCTAGATTA TGTCGTTTTA	480
ACGTATCCAA AATATCCAGA AGTCGATCAG GACGATGAAC CATGGCCAAA CGCCCATTAG	540
ACTTGAGAAT ACTCTGGGCA CTACGACAGA TTTCTTCCAA ATTAGTCGTG ATTTCTGTGC	600
GAGCCAAGAG ATAATGTTCA CTCTCGTTCA GATTAGAATA AGGATTCAAC TTGAAATAGG	660
GTGGATTACA CAAAATCATA TCCACCTTAC TCCCCTGAAT GTGAGCAGGC ATATTTTTC	720
AATCATCGCA GATGACCTGC ATTTGCTCCT CTAATCCATT CAAACGGACA GAGCGTTCAG	780
CCATATCCGC CAAACGCTCC TGAATCTCAA CAGACAATAT CTGTGCTTGA GTACGAGTGC	840
TAGCAAAAAG CCCCACTGCT CCATTCCCAG CACAGAAATC CACAATCAAC CCCTTCTTAG	900
GAAAACGTGG AAATCGTGAT AAGAGAACAC TATCCACCGA ATAGCTAAAA ACCTCTCTAT	960
TTTGAATGAT TTTGATATCT GTCGAAAAGA GCTGGTTAAT GCGCTCTCCT GATTTTAATA	1020
ATTGTTCTTC TTCCATGGTC CTATTATAGC AAATTCATAT TAACATTACA AAAAATATAA	1080
AACTCTAAAC TACTTCTTCT TTTTAAATG GTGCAGGGCT TCTCCAGTCC AGATTGGTAG	1140
CATTCGTCGA AAGGGAGCAA AGCCGCTAGT AAAGCGGTG CTTGAAAAGC GTCTCCGTCT	1200
AGGAAACTGG TACTTTTCTT CCTCCAAGT GCGGATAGAA AGACTGGCTT TCCCTGTAAA	1260
TTTCTCTAAA TCCACTACCT GAACCTGAAC CTCTTCATCG ACTTTCAAGG TTTCATGAAT	1320
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TAATCAACA AAGGCACCGT AGGGCTGAAT CCCTGTAATA CGCCCCTTTA GCTTATCACC	1440
GATTTTCATC TTAGTCCTCG ATTTCAATAG TTTCAATTAC AACATCTTCA ACTGGCTTGT	1500
CCATAGCTCC TGTCTCAACA GCAGCAATGG CATCCAAGAC AGCGTAAGAT GCTTCATCAG	1560
CTAACTGACC AAAAACCGTG TGACGGCGGT CTAGGTGAGG TGTCACACCT TGATTGGCAT	1620
AGATTCTGTC AATCGGTTCT GGCCAACCAC CACGAGTAAT TTCTTTCTTA GAATAAGGTA	1680
GGTGTGGTT TTGCACGATA AAGAACTGGC TGCCGTTGGT ATTTGGACCA GCATTTGCCA	1740
TGGAAGAGC ACCACGGATA TTGTAAAGCT CTTCTGAGAA TTTCATCTCA AAAGATTGCG	1800
CGTAGATTGA CTCGCCACCC ATACCAGTTC CAGTTGGGTC TCCACCTTGG ATCATAAAGT	1860
CCTTGATAAT ACGGTGAAA ATGACACCAT CATAGTAGCC ATCTTTTGAA AGAGATACAA	1920
AGTTAGCCAC TGTTTTAGGA GCATGTTTCTG GAAAAGCTT GATACGTAAG TCTCCGTGAT	1980
TGGTCTTAAT AGTCGCAAGA GGACCTTCTA CTGTTTCAAT GTCTACTTGT GGAAAATGCA	2040
ATTCTTTTTC TACCATACCA AATACTTCTA AGGCAGCAA AATGCCATCT TCTTCTAATG	2100
TTTTTGTAAT ATAATCTGCT TTTTCTTGA TTTTATCATG AGAAATCCCC ATGGCAACGC	2160



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TGATTCCAGC ATAATCAAAG AGTTCCAAGT CGTTGAGACC ATCTCCAAAA ACCATGACCT	2220
TCTCTGGTTT CAAGCCCAAGG TGTTCACAA CCTTTTCCAC CCCCGTCGCT TTGGAGCCTG	2280
AAATCGGCAC AATATCAGAC GAATGTTGAT GCCAACGAAC CATGCGAAGT TTGTCTGAGA	2340
GACTGTGAGG CAAGTGCAAG TCATCTCCCT TATCTTCAAA AGTCCACATC TGATAGATAT	2400
CTTCTTTTTC ATGGAAATCG GGATCTACAT CTAAGTCGGG ATAAATTGGA TTGATAGCTT	2460
CACTCATCAT ATCGGTGCGA GTCGACAACT TGGCATCATG ACTCCCAACC AAGCCATACT	2520
CAATTCCTTC TTGCTTAGCC CAAGAGATAT ACTCCTCAAC ATCTGACTTT TCAATCTGAT	2580
GCTGATAAAT GACCTGACCT TTTTATCTT CGATATAAGC CCCATTCAAA GTTACAAAAA	2640
AGTCAGGCTT GAGATCACGA ATCTCTGGAA CAACACCAAA AATGCCACGT CCAGAGGCGA	2700
TTCTGTAA AAATCCTTTT TCACGCAACT GTTAAAAAC AGTGGGAATT GTAGTTGGAA	2760
TAAACCTGT CTTGAATTC CGCAATGTAT CATCAATATC AAAAAAGACA ATCTTGATCT	2820
TCTTTCCTT GTATCTTAAT TTCGCGTCCA TCTCACTACC TCTTCAATC TAACTCTTC	2880
CATTATATCA TAAAGTAGGC AAATCCCTTA TTTTCAAAA GTTTATCATT TTTATTTTAA	2940
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CTCTGTGTTT CAAACTCGTA AAAAGGGAGC CACTGATCCT AACTCGCTCT CTCATTTCAA	3060
AGCTGTGAA AAAAGACCCG TTGGGTCTT AATTCGCTTT CTGTTTTCA AGCTCATGAA	3120
AAAGAGACCC AACTGGGTCT TTTCTTTAAT CTTGCTTAC GAAAGGCATC AAAGCCATTA	3180
CGCGAGCGCG TTTGATAGCT GTTGTTACTT TACGTTGGTT TTTAGCTGAA GTTCCGTGTA	3240
CACGACGAGG AAGGATTTTC CCACGTCTG AAACGAAACG GCTAAGAAGC TCAGTATCTT	3300
TGTAATCAAC ATATTCAATT TTGTTGCTG CGATGTAATC AACTTTTTTA CGCGTTTGA	3360
ATCCGCCACG ACGTTGTTGA GCCATGTTTT TTCTCCTTTA TAAGTTTAGT TGTCCATTAG	3420
AATGGTAAAT CATCATCTGA AATATCCAAT GGTGTTGTTG CTCCAAATGG ATTTTCATTA	3480
CGTGAAAAGT CTGGTACTGA ATTTGTAGGT GCTGAATAGT TTGCAGTTGG TGCAGAGTAA	3540
GCTCCACCTG TGTGACCTC ACGCACACTA CGGCTTTCCA ACATTTGGAA ATTCTCAGCC	3600
ACGACCTCTG TCACGTAGAC ACGTTGCTCT TGCTGGTTAT CGTAACTACG AGTCTGGATA	3660
CGACCTGTCA CCCCATAAG TGAGCCTTTT TTAGCCAGT TAGCAAGATT TTCAGCCTGT	3720
TGGCGCCACA TAACGACATT GATAAAATCA GCCTCACGTT CACCATTTTG ACTCTTAAAT	3780
GTACGGTTTA CTGCAAGAGT AAAAGTCGCA ACTGCTACAT TTGATGGGGT ATAACGCAAC	3840
TCAGCGTCAC GTGTCATACG CCCTACAAGT ACAACATTGT TAATCATAGT TTACCTTCTT	3900

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ACGCGTCAAT TTTGACGATC ATGTGACGAA GAATGTCAGC GTTGATTTTT GAAAGACGGT	3960
CAAACCTCTTT AAGAGCTGCA TCGTCATTG CTTCAACGTT AACGATGTGG TAAAGTCCTT	4020
CACGGAAATC TTGGATTTCG TATGCAAGAC GACGTTTTTC CCAAGTTTTT GATTCAACAA	4080
CAGTTGCACC GTTGTCAGTC AAAATAGAGT CAAAACGTGC TACCAAAGCG TTTTAGCTT	4140
CTTCTTCAAT GTTTGGACGA ATGATATAAA GAATTTTCGTA TTTAGCCATT GATATGTTCC	4200
TCCTTTTGGT CTAATGACCC CAAGACTTTG CAAGGGGTAA GTGAGGTTTCG CTCACAATAA	4260
ACTATTATAC TAGAAAAAAT TTTTTCACGC AAGTAAAAAC ACTAGAATTC GAAAAACGC	4320
CACATGGGCG TTTTCCTGTT CTTATGGTTT GATACGGTGC AACATACGTG GGAATGGAAT	4380
AGCTTCACGG ATATGTTTTG TTCTGCTGC GAAGGTTACC ATACGTTGCA TACCGATACC	4440
AAATCCTCCG TGTGGAAGTG TACCGTATTT ACGAAGGTCA AGGTAGAATT CATATTCTGT	4500
ACGATCCATG CCAAGTTCAT CCATCTTAGC GACAAGGGCA TCGTAATCTT CCTCACGCAT	4560
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GTCAATGGCT TGATCGTAAG TGATACGTTT GAATGGCTCT GCAATGTAGC GTTCAAGAG	4860
TTCTGTATCA CGTTCCAAGG TTCCAAGGC TTGAGGCGCG CGGTCAAGAA CACCTGTAG	4920
AAGAGCTTTC ACATAAGCTT CTGCAAGTC AAGCGACTCA TCATGTGTCA AGTATGAGTA	4980
CTCAGCATCC ATCATCCAGA ACTCAGTCAA GTGACGGCGT GTTTTGTATT TTTCAGCAGC	5040
GAAAACCTGA CCAAAGTCAA AGACACGACC AAGAGCCATA GCCCCTGCTT CTAGGTAAAG	5100
CTGACCTGAT TGGCTCAAGT AGGCTGGCGT TCCGAAGTAG TCAGTTTCAA AGAGTTCTGT	5160
AGAATCTTCT GCCGCATTTT CTGAAAGAAT TGGGCTGTCA AACTTCATAA AACCGTTCTT	5220
GTCAAAGAAC TCATAAGTTG CATAGATAAT AGCGTTACGG ATTTGCAACA CAGCTACTTG	5280
CTTACGAGAG CGTAGCCACA AGTGACGGTT ATCCATCAAA AAGTCTGTTC CGTGTCTTTT	5340
TGGTGTGATT GGGTAGTCTT GAGATTCACC GATCACTTCG ATGTCTGTGA TGTCCAACTC	5400
ATAGCCAAAT TTAGAACGTT CGTCCTCTTT GACAATACCT GTCACATAAA CAGACGTTTC	5460
TTGGCTCAAG CGTTTGATAA CATCAAACCT CTCAAGTCCC ACTTCTTCAC CAAATTTTTC	5520
GACAAAGTTT GGTTTAAAAG CCACACCTTG AAAGAAGGCT GTTCCATCAC GCAATTGTAA	5580
GAAAGCGATT TTTCTTTTTC CTGATTTGTT GGCAACCCAA GCGCCAATCG TCACTTCCTG	5640
ACCAACATAG TCTTTTACGT CAATAATCGT TACACGTTT GTCATTATTT TTCCTTTTCT	5700

TTTTTATTCT TTATGGCAAA CCACCTCTAT ATTGTTCCCA TCCAGGTCAA TCATAAAAGC	5760
AGCATAGTAA ATCGGATGCT CACTTCGATA ACCAGGAGCC CCATTGTCTC GCCCACCTGC	5820
CTCTAAGCCA GCCTCATAAC AAGCCTGAAC TTCTTCCTTA TTTTCTGCTA AAAAAGCAAA	5880
ATGAACAGGA TCTTGTGTTC CCTGAGTCAG CCAAAAATCA CCACCAGGAT GAGGGCTGTT	5940
CGGGGATAGA AAACAAATTA GAGAACTAGT CTTAAAAGCC AATTATAGT CCAAAGGAGC	6000
GAGAAACTC CTATAAAATC CTTATGAAAT TTGTAAATCC TTTACCTTAA TCTCAAAATG	6060
ATCAATCATT CTCACTACCC ATAAATGCTT TCAAGCGTTC GACTGCTTCT TTAAGCGTGT	6120
CTAGGTCTGT CGCATAGCTG AGGCGGACAT TTTCTGGTGC TCCAAATCCA GCTCCTGTTA	6180
CCAAGGCCAC TTCGGCTTCT TCTAAGATAA CAGTTGTAAA GTCTGTCACA TCCGTGTAGC	6240
CTTTCATCTC CATGGCCTTT TTGACATTTG GGAAGAGATA GAAGGCCCTT TCGGTTTGA	6300
CCACTTCAAA TCCTGGTACC TCTGCAAGGA GGGGATAGAT GGTATTAAGA CGTTCCTCAA	6360
AGGCCTGACG CATGCTTTCT ACAGTATCTT GCTCACCTGA TAGAGCCTCA ACTGCTGCAT	6420
ATTGGGCTAC TGCTGACGGA TTCGAAGTTG TTTGACCTGC AATCTTGGAC ATGGCAGCGA	6480
TAATGTCTGC TTCTCCAACG GCATAACCAA TCCGCCAACC AGTCATGGCA TAAGTTTATG	6540
ACACACCATT GATGACCACT GTTTGCTTGC GAATCGCTTC CGATAGGCTA GAAATCGGTG	6600
TGAACTCATG ACCATTATAA ACCAAGCGGC CATAGATATC GTCTGCTAGG ATGAGAATAT	6660
CATTTTCTAC AGCCCAGTTT CCAATTGCCA AGAGTTCCTC ACGGGTGTA ATCATACTG	6720
TGGGATTAGA TGGCGAATTC AGCACCAAAA CCTTGGTCTT GTCAGTGCGA GCTGCTTCTA	6780
ACTGCTCTAC GGTACACCTTA AAGTGATTGT CTTCTTAGC AGAAACAAAG ACGGGAACGC	6840
CTTCGCCAT CTTGACCTGA TCTCCATAGC TAACCCAGTA TGGGGTTGGG ATGATGACTT	6900
CATCACCTGG ATTGACCACA GCCATAAAGA AGGTATAGAG AGAATATTTG GCTCCCGCAG	6960
CGACTGTAC TTGATTTGAC GCTACAGAAT AGCCGTAAAA GCGCTCAAAG TAGCTATTGA	7020
CCGCCGCCCT AAGCTCTGGC AGACCTGAGG TTAAGTATA AAAAGAAGCA CGCCCATCTC	7080
GAATCGATGC AATGGCGGCA TCTTGGATAT TTTTGGGAGT AGTGAAATCT GGCTCACCCA	7140
AGGTTAGAGA CAAAATATCT CTACCCTCAG CCTTCAGTGC TTTGGCACGG GCTCCAGCAG	7200
CCAAAGTCAC ACTTTCTTCC ATTTCTAAAA CACGGTTGGA TAGTTTCATA GGCCCTCCTT	7260
GTGACCAAT GCTCCTGTTT CAAAATCTAC TAGATAAAAA TCAGATCCTG ACTTAACCTC	7320
CCAGATTGGC TTATCTTGAT AACGGCCAAA GGTATCTTG TCAATCTCGC CAGCTCCCTT	7380
TTCTTAGAA ACCGTTTCTG CTTTTCCTTG TGAAACACCC TGATTTAGCT GATAAACGTA	7440

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AATCTTATGG TCATCTTTAC CAATCAGGAC AGCAAGCGCT TCTTGCTGTT TGTACGACC	7500
AAGAACGCTG TAATAAGATT CCAAGCCATT GTATAAATCA ACCTGATCAG CCTGCTCTAA	7560
TCCTGCATAC TGCTGAGCTA ATTTTCTCC TTCACTTTTA GCTGTTTGAT AGGGTTTCAT	7620
GCTAAGAGAA ACCATATACA GAAAGGAACC ACTGATAACC ACAAACAAA TCGTCATCCC	7680
TAGACCATAC TGCCACAGTA GATTATTTTT TGCTTTGTTT TGTCTTTTTT TCACTCGTCT	7740
ATTTTACCAT CTATTAGCT TTATTACAAG TGAATATAAG AATACTCTTC GAAAATCTCT	7800
TCAAACCACG TCAGCTTTAT CTGCAGACCT CAAAGCTGTG CTTTGAGCAA CCAATTCTAT	7860
TTCTCCCTTC AAACAAAACC GATTTTGAAA GTGAAACAGT TCTTACTTTT TCAGTCACAA	7920
ATGATTAGAG TTTGCCGGG	7939

## (2) INFORMATION FOR SEQ ID NO: 10:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 9897 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 10:

CCGCTCTACC GTCAAATAAT TACCATTG TTTAATACCG AAATTTTAT CTAAGAAAA	60
TTCAATTGGT CTGTTGGTAC GATCGTCGTA TACAGTACCA TTCTCAGAA TAGTATAATT	120
GTAATCAGTA TCACCTTGTT TCCTTAATTT AAGGTAATAA TTACCATCAA TTTGTTTATA	180
ACCTGAATCT TTTCTAGTTG CTTCTCTAAA ACTTACTCCA GCAGGCATCA CATCAGCAAA	240
CATGAGTACT TGTTTGTCT TTTTTCAAC AATAACAGAG TCAATATAGG TTGCACCACC	300
GCTGATTGTT AAGTCACGTC CACCAACTTC ACGAGGCCAT TCTAATGGTA CTGGCGCAA	360
ATCATCGAAT GCCAATGTTA ATTTTGGTTT AGTCCATGTC TTACCATTAT CATCACTATA	420
ACTTGTAGCA ATATTAATTT TATTCAAGAA ATCATGAGTT CCACCGTAAC GAGCGTCAAT	480
GCTTGAAAAAT ACCCGACCAT TGCTAAAAGT ATACAGAACT GGAATACGGA AATAGTTAGA	540
ACCTGTTGTA TCATTAGCCG TATAAATTAA ATGTCCAGTA ACAGCGTTTG TTGTCATCTT	600
TTTAACAGTT TCTTCATCCA ATGCACTATT AAAGAATTG ATATTTTCTA GTGTTCCGTT	660
AAAACCAAAC GCCGTTTTTC CTGCACGTTT CACTCCCCCA AGCATATAGT AATCAATACC	720
TTTAATATCC TTGATGTTTA GGAAATTATC CACTTTCTTT TCTACTACTT TTGTACCATT	780
TGCGTATAAA GAATATGTTT TTTTGACTGA ATCTGCTACT ACTGCAACAG TGTTAGTCAC	840
AGCCTCTTGT TTGTACTTAC CCCAACTGA AGCAGGCTG GATACTAGGT TATTTTATT	900

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GGAAGAAGTA TCACGCGCTT CCATCCCCAA CTCACCATTTG TCTCTAAGGA ACACATCTAC	960
ATAACTATTTT TGTTGACCGG GTTTGGAATT AGATATTCCA AACAGAGCTT GTAAGCCTTT	1020
CTCACTTGAC TGATTGTACT TAATCACTAC AGTAAAGTCA CCGCTAGTAA ATTTATCCTT	1080
TAACTCTTTA GTAACATTTT CTCCGCCCCC TGTTAAAGTA ACATTATTTT TTTCTAAGAC	1140
AGGAGTTTCT TCCGCTGTAG AAGATGGATC CTTAACAGTA GTTTCAACTG TTCGAGGTTG	1200
TACAGTAACT TCCGAAGAGT TATCCGATGT AGGTTGTACT TCCGAAATCG GAGTCGTTGG	1260
TGCAACAGGT TGCACCAACT TTGGTGTGA TACTTCAGAA GTTTCAGTCT CCTGAGCTGC	1320
AACTGAGTTA GCAACAAATG CTGATAATAC CACTACAGTA CCTAAGGTTA CATATTGTTT	1380
AATATTTTTT TTCATTTTAT TTTTCCTCGT TTAACCTTT GATAACAAGT TTTTAAACAG	1440
TTTCATCATT GCAATGAATC TTTGGTTGGT GAAGATCTTC TTCAAAAGTC ACCAACATAT	1500
TCCCTGGAAG CAATTCAACA ATTTGATAGT CTTTGCTATC GTAAAAAGCA ATATCCTTCT	1560
CTTCGCTAAA AGGTACACGT GACTGGGCAC GAACTGGGGA AGTTACTGCC ATTTTTTCAG	1620
TATTTTCAAC AACAATATGA ATATCTAAAT ATTTCTTATG AGTTTCAAAA ATATCTCCTG	1680
GAACTCCATC AGCTAGATAA GTCATACAAT TTGCAAAAAC ATTTTCCCGG TCAATATCAA	1740
TTTTTCCATC AACTAAATCT GTCAAATTTG TATTTTCTAA AAAATCACAG ACTTTTGAAA	1800
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TTTCTCTTTT CTATTAGTGA CGAACTTCCC AACTTGAATC CGCTTTAATT TCTGTAATAT	1920
CATGAATCGT TGTATATTTA GGTGCAGATA CTTTATTTCC AGTAAGAACA GATACAATAT	1980
AACCTGAAAC TACTGATACA GAGATTGAAA TCAATGAATA TGCCCAGTAG CTAACAGCTG	2040
TTGGAGGAAG GAAGTATTTA ATAAATACCA TGACGATGGT TGATACAATC AGCGCTGCAT	2100
AAGCACCTTG TTTATTGCT TTTTLAGAAA CAAATCCAAG AATAAATACA CCACCAAGTA	2160
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GAGCCATGAC AATGGAACA CCAATTGAGA ATAAACCTAC TGCTAGAGAT ACGAATTGTG	2280
CAATTTTCGT ACGACGATTG TCTGACATAT TTTTAGAAAT GACATCTTGA ATATCCAATG	2340
TCCATGAAGT TGCAACAGAG TTCAAACCTG TTGAAATAGT TGATTGAGAT GCTGCATAAA	2400
TGCTGCCAA GATCAAACCT GTGATACCTA CTGGTAACTG GTATGCAATA AAGTACATAA	2460
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CGTACAAGCC TGTACCAATC AAGTAAAAGA CTGTTGCAGT TGCAAGTGAC AAAACACCGT	2580
TTGTGAACAA CATCTTATTA AGTTTCTTAA TATTTTGTGT TGTAGTAAAA CGTTGAACCA	2640

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AGATGGAGTT TGAAAGCAAG TTAGGATCGA AAAGTTTTTC ATTTGCAGCA AGGAATTTCC	2760
CGTTTGCTAA TGTTTCTGCT ACTGCACCAA AGCCACCTTT AATATTAGCA ATCAGTACAA	2820
ATAAAGCTAA AACGACACCA CTAATCAGAA TCACACCTTG AATAAAGTCT GTCCATAATA	2880
CGGATTTTAG ACCACCAGTA TAAGAATAAA CAATTGCAAC TACACCCATC AAAATAATCA	2940
AAATATTGAT GTCAATTCCT GTCAATACTG ATAAACCAGC TGATGGGAGG TACATAATGA	3000
TAGACATACG TCCCAATTGA TAAATAATAA ACAAGAGTGC TGAAATAATA CGAAGTGCTT	3060
TAGAATTAAA ACGTTTATCC AAGTAATCAT ATGCCGTATC GATGTCTATC CGTGCAAAGA	3120
TAGTGAAGAT AAAACGAATT GTCAGTGGA TAGCTACTAC CATCCCTAAT TGAGCAAACC	3180
ATAAAATCCA GCTACCTGCA TAAGAGCTAC CAGCGAGTCC CAAGAAGGAA ATCGGACTGA	3240
GCATTGTGGC AAAAATGGAT ACCGAAGTAA CATACCAAGG AACCGAACCA TCTCCTTTAA	3300
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GTAAATAAAC AATCAAGATA ATTAAGTCAA TTATTGTAAA TCCTGTTGTG CCCATAACAT	3420
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CTGCTTGTIT TGCAACTTCC AAGTCACCTT CTGCCAATGC TTCTAAAGGT TGACGAACAG	3540
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CCTTACCTGA TATCATCTTA TAGATAACTT CATTGATAGC ATATTGAAGT TTTTAGCTG	3660
TATCTAAATC TCGTTCTTGA ATCAAACCTT CCAATTTCAA GAACAAATCT GGCATAACGC	3720
CATAAGTACC ACCAATACCA GCTTCTGCTC CCATCAAGCG ACCACCAAGA TATTGTTTAT	3780
CTGGACCATT GAATACAATG TAATCTTCTC CACCTGCAGC TACAAACATT TGAATATCTT	3840
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ACAAACTACC AGTCAACGCA ACCCCTGCCA ATTGTGGAAT ATTATAGATA ATAAATCTG	3960
TATTTGACGC AGCTTCACTC ATTGCATTCC AATATGCTGC GATTGAATAC TCTGGCAATT	4020
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CCAATTCGAT ACTATCTTTC GTGTTATTAC ATGCAATATG GTTGATAACT GTTAATTATC	4140
CTTTAGCAAC TTCCATAACA GCTTCAATAA TTTGTTTACG ATCTTCTACA CTTTGGTAAA	4200
TACATTCAAC TGAAGAACCA TTTACATAGA TACCTTTTAC ACCTTTGTCA ATGAAATATT	4260
GTACCAGAGA TTTTACACGA TCTTGGCTAA TTTCAACATT TTCATCATAG CAAGCATAAA	4320
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GAATTTTTCt TCGGCAATTA CCGGAATATT AAAATCAGCC AATTTTTTCA TTAGTTCAAA	4560
ATCAGGCTCA TCTGATTGTA CACTTGTACT TGTGTAACCT GATAATGTTG TACCAACAAA	4620
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AAATTCITCA TTATAAAGGG CTTCAACCAGG TAAAGCTTGA CAAGAAACAA TGACTCCACC	5040
TTGAACTTGG CTTATAAATT TTTCTTTAGT CCAAATTGG CTCATTTTAT TATTCCTCCT	5100
TATGGATAAT AGTTTGATTG TAATAATATT GTCTCTCTGG ACTTTCAGTA TAATTAGAGA	5160
ATAAGCAGTC TGTAATTAAA AGTATTGGAA ACTGAGGTGA TATGCGATTG CCATACGAGA	5220
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GTACAATATC AGTTTGACCT GAAATGGATG CTCCAATGAC AAGGCAATTT TCATTAAGTA	5400
GTAAGCTACT CCACAAAATC ATATCCTCGT CTGATAATAC TTCACCAATC ACTCCGAGAC	5460
GCATAAATCT CATCTTCATT TCTTGTAAG CAAGAACAGA ACTTCCTTTA CCGTAGAGAT	5520
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CCGTGTAAGT TTTTCTCAAC ATTTCTCAT AGTCGGATAA AACTTTTTCT GTTGCCTCTG	5640
TATATAATGC CAACTTTTCT TTCTCATGAA TCATCTCTTG GTATTGAAA ATGAATTGTC	5700
TAAAACCTTT AAAACCACAT TTTTTCGCAA ATCGAGTCAA TGTGCTTTG GATACATTAA	5760
GGTATTCGCA CAATGCTTTA GATGAATAAT CATTGAGAGG TTGCTGTTTT AAGAAGAATT	5820
TAGCAATGTC TTTTTCAGCA TATGCCATAT TTGGTAAGTT AGCTTCTATC ATTGGAATTA	5880
GTTCTTTTTG CAGTAACATA TGAGCTCCTT AGTTGAAGTA AACGTTTACA TTCTTTATTT	5940
TAACACTTTT TTTTTTTTTC AATATTTTTC ATAAATTAGA AACTAGTTTC CAATTCTTTT	6000
CGTTTCATAA CAGAACAACA AACATAAAAA TATAATAGTT TTTATTCTTT TTATCGTAAT	6060
TATATGTATT GTAAGAACGT TTATCACTAA TAATATGTTT ATATTAAAT ATTTTAGTAA	6120
TATTTTATTT TGTTTTTATT ATTTCTTTTC GGAATTTCTA TATAATATTT TATTTCTAAA	6180

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AAAATTGAAA AAATATTTCT AGTTTCTTTA TTTTATATAG GTAATATATT TTATTTCCTAA	6240
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AAAAAGCAGC AACTATAAA CTAAAAAGTT CCACACCAA TGTAACCCCA TACTTCCCCA	6360
TAAGTCAGAT TTATAGCGCA CCATACCTAA AAACATTCCA AGTGAAACGT ACAGACACCA	6420
AGCTAGAATG GTTCCTGGAT GATGTACTAA GGCATAATAA ACACTTGTC AAGCAACTCG	6480
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ACTCGCATTTG ATTAAGAACA ATAAAAATGA AAACCAAGGA ACTTGATGTT GAAGGCCAAT	6600
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CAGTAGACTA GCTAGTCCAA TACCAAGGCA TTTCATCCTA GTTTTCATAT TGACCTTGAC	6720
CACTTGTTTT CGTTGACCAT ACATCCATAA AAAAGAAAA AGAGACGCAC CATAGAGAAC	6780
CTGTAGTATA GTTAATCAC CGATACAAAG AAATTTCAAT AAGTATAGAG ATACCAATAG	6840
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GCCAAAATAA TGGACAAGTT CTCCCAAAAT CGTTCAGCCA TATTCTTCT CCTTTAGTTA	7140
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CTAGCCTCTT CCAATTCAG ACTTGATAA ACCCGCTTAT TTGAAACCAC AAAAGGAAGT	7260
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TCACGGTTCT TAAATCGTAA TAAATTGGGA GATAAAACT CAAACAATC TGAAGAATAG	7380
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TAAGGAATCT AACAACTTTG AGAAGTTAAT CGATTTCCTG TCTTCATCAT AAGCTTTTAC	7620
AGTTACTTGG GTTGTAAGTA TCCCCTCTTT TCCCTCGGCT CGATAGTCTT GTCAATATAA	7680
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ACTTTCAAGG AATCCATAA CGTTTTGAAG ATAGGATTCA TAAATAGTG GGTAAATTATG	7800
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AAATATTTGT TCATCCAGCT GTTGATTTT TGCATCATGT AATCTGTTT CTAATTCATC	7920
ACAATCTAGT ATTGATTCTT TATTTAATGC TTTTATCTTT TTCTCTATT TCTTTAATT	7980



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TCTTTGCGAT TCGGCAATC ACAGGAACGG TTACACTATT ACCAACTTGT TTATAGAGCT	8040
GACTATTAAT AGAGACTTTT CTAGCAGCTT CAAAAGCCTA ATCAGGAAAG CCATGCAATC	8100
GAAACACTC TTTAGGAGTG ATTCGTCGTA TTCTCAAACG GTAAAATTGT CCATCTATTA	8160
AAACACCAGC TACTTGGTAA ACTTGTTTAT CTTCTCCTTC ATAGCTAGCC ACTACTACTC	8220
CCATTTGACC ACTAGTTGTT AACGTATTAG CTATACCTTT TCCAACCTA CCACGACGAT	8280
ACTGAGAACT TGGTCTTTCT AAATTGATTG AATCCCAAT CTCTGCTTGA GCATATCCTT	8340
TTTTCGTTGC TTCCCGTACT TTTAGAAATT GGATTGGTTC TGGAAATTAGT ATTTTGGGGA	8400
TTTTATCTCC TCCTTGCAATC GTAGTCAGTG TTGGAGATAA GCCCTCACTT CCATAGACAC	8460
GACCTGTCTC CTTAAAGCTA GTCGGTAAAT CTCCAACAAC GACAATGCCA TAACGATCCT	8520
GAGTATTTAA AGTAAACATC GGCTCTTGAT TTTCTTAA GCGTCTCCCA TTTTGTCTCT	8580
TGTCTAATCT ATCTGGTGTC ATACAAGGAA TCGCAACTTT AAATCCTTCT CCTTTACCAC	8640
GAACCTAAGGT TGGCGCAAGA CCTTCTGAAT AATAGACTTT ACCGCTCATT CCACTTCTTG	8700
ATGGATTCAA ATTTCTAGT GCTTTCAAAG TCTCAGAGTT AGTTGCTTGA CCTTCTCGTC	8760
TGAAAGGAAA TAAGAGTCTG GTACCTTTCT TTCTAGAATG TCCGATAATA AACACCCTCT	8820
CTCTGTTTTT GGGAAACGCCA AAATCCTTAC TGTTAAGCAC CTGCCACTCA ACATCAAACC	8880
CCAACCTATC AAGTGTGGTA AGTATTGTGG TGAACGTCCG TCCCTTATCG TGATTGAGTA	8940
GGCCTTTAAC ATTTTCAAGA AAAAGAAAAC GTGGTTGGAT TTGTTTGGCC GCCCAGCAA	9000
TTTCAAAGAA CAAAGTTCCT CTAGTATCTT CAAATCCCA TCGTCTTCCT GCGATTGAAA	9060
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CGTCATCTGA AACATCTCGT ATGTCATGAA ATTCTATTTC TCCTTCCGTT TGAAAAATGG	9180
ACTTATAAGA TTTCTAGCA AATTATCAA TCTCAGAAA TCCCAAGCAC TCATGCCCTT	9240
GAGCTTCCAT TCCCATCCTA AAGCCTCCTA TCCCAGCAA TAAATCTAAA ACCCAATCA	9300
TTCATACCTC TCTCAACTAG ATGTAACCTA CAAAACCCCT GACCTCATGA GCCACTTTCT	9360
TCCTCCTCAT GAGGTCAGTT TTACTTTCTG CTGTTCCAGT ATCGTTTTTC CTCGCTAGAT	9420
TTCTTCAAAA GGGCAGACTC CTCCCTTGGT TCGTCACACG ATTTTTCAT CTCGACTGTT	9480
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AGGTTGACTT TTCTAATCCT AGAATAAAGT GCTGAAAACA ATTCGGAATA GGCATAGAGA	9600
CTAGACAATT TGAGGAGCTG CTTGCGTCTT GTTCGAACAC ATTTTCTTAC CACGTGAAGA	9660
AAAAGATGGC GGAAGCGTTT GATTGTTAAA GTTTGGAAGT CACCTCCAGC TAGATGTTTG	9720

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AGAAAAAGAT AGAGATTGTA GGCGATACAG CTCATCATCA TACGAACTCG TTTTGTATTA	9780
AGGTTGAACT ATCCGTTTTA TCGCCAAAAA ATCCCTCCTT CATCTCCTTG ATGAAATTCT	9840
CGGCTTGACC ACGTCCACGA TAAAGCTGAA ACTGGTCTTG GCTTGTTCGG GTACCGA	9897

## (2) INFORMATION FOR SEQ ID NO: 11:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 8148 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 11:

CCGTGGAACA AGCCAAGACC AGTTTCAGCT TTATCGTGGA CGTGGTCAAG CCGAGAATTT	60
CATCAAGGAG ATGAAGGAGG GATTTTTTGG CGATAAACG GATAGTTCAA CCTTAATCAA	120
AAACGAAGTT CGTATGATGA TGAGCTGTAT CGCCTACAAT CTCTATCTTT TTCTCAAACA	180
TCTAGCTGGA GGTGACTTCC AAACTTTAAC AATCAAACGC TTCCGCCATC TTTTCTTCA	240
CGTGGTAGGA AAATGTGTTC GAACAGGACG CAAGCAGCTC CTCAAATTGT CTAGTCTCTA	300
TGCCTATTCC GAATTGTTTT CAGCACTTTA TTCTAGGATT AGAAAAGTCA ACCTGAATCT	360
TCCTGTTTCT TATGAACCAC CTAGAAGAAA AGCGTCGTTA ATGATGCATT AAAGAACAGT	420
CGAGATGAAA AAATCGTGTG ACGAACCAAG GGAGGAGTCT GCCCTTTTGA GGAAATCTAG	480
CGAGGAAAAA CGATACTGGA ACAGCAGAAA GTAAACTGA CCTCATGAGG AGGAAGAAAG	540
TGGCTCATGA GGTCAAGGGT TTTGTAAGTT ACATCTAGTT GAGAGAGGTA TGAATGATTT	600
GGGTAAATAC AATGAGCTTG AAAGAAGTAG CAAACTCACC AAGCGCCAAT TCTTTGAGAA	660
TCAGATGCTG GATTATACCA TCATTGCGCA TGAGAGTTTT GAAATCATCC GTCATTCTGT	720
CTACCAGACA GATGATCGTG AAGTGGAAAA TGCTCTGGCT TTTGAAGTGA AAAATGATGA	780
AACAGACAAG CTGATTCTGT TATTAAAGCGA GGATATTGGT GTAGGTGAAA AATTGTGCCT	840
CGTTGACGGA ACAAATATGC GTGAAAATG TTTAGTATAT GATAAAATAA ATGAGAGAAT	900
GATTCGCTTG CAGTGCTAGA AATAGGCATT TTGAATAGTG AATATGTTAT AATAAGTATT	960
AGTAGGAGGT GTTTTAGATT GGAGAAGAAA CTGACCATAA AAGACATTGC GGAAATGGCT	1020
CAGACCTCGA AAACAACCGT GTCATTTTAC CTAACGGGA AATATGAAAA AATGTCCCAA	1080
GAGACACGTG AAAAGATTGA AAAAGTTATT CATGAAACAA ATTACAAACC GAGCATTGTT	1140
GCGCGTAGCT TAAACTCCAA ACGAACAAAA TTAATCGGTG TTTTGATTGG TGATATTACC	1200
AACAGTTTCT CAAACCAAT TGTTAAGGGA ATTGAGGATA TCGCCAGCCA GAATGGCTAC	1260

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CAGGTAATGA TAGGAAATAG TAATTACAGC CAAGAGAGTG AGGACCGGTA TATTGAAAGC	1320
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TCTCGTATCA TCGATGAGAA AAAGAAGAAA ATGGTCTTTT TTGATAGTCA GCTCTATGAA	1440
CACCGGACTA GCTGGGTAA AACCAATAAC TATGATGCCG TTTATGACAT GACCCAGTCC	1500
TGTATCGAAA AAGGTTATGA ACATTTTCTC TTGATTACAG CGGATACGAG TCGTTTGAGT	1560
ACTCGGATTG AGCGGGCAAG TGGTTTTGTG GATGCTTTAA CAGATGCTAA TATGCGTCAC	1620
GCCAGTCTAA CCATTGAAGA TAAGCATACG AATTTGGAAC AAATTAAGGA ATTTTACAA	1680
AAAGAAATCG ATCCCGATGA AAAAATCTG GTATTTATCC CTAATGTTG GGCCCTACCT	1740
CTAGTCTTTA CCGTTATCAA AGAGTTGAAT TATAACTTGC CACAAGTTGG GTTGATTGGT	1800
TTTGACAATA CGGAGTGGAC TTGCTTTTCT TCTCCAAGTG TTTGACGCT GGTTCAGCCC	1860
TCCTTTGAGG AAGGACAACA GGCTACAAAG ATTTTGATTG ACCAGATTGA AGGTCGCAAT	1920
CAAGAAGAAA GGCAACAAGT CTTGGATTGT AGTGTGAATT GGAAAGAGTC GACTTCTAA	1980
AATGAAGGAA AATGACTGC AATCTCTGTT AAGAAATAA ATAATCCAC CTAGAACAAG	2040
CTAGGTGGGA TTATTTGCCT ATGAAATGAG AAATTATGGG AGCAAGCTCC TAAATCAACT	2100
GTTTTGATC TACTTCTTTA ACTACTTGAT AAAAGTTATA GAAGTAGGCC AAACCTGAAA	2160
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GAAAGGATAT GAGGAGAAAG AAGAGGGCTG CGTTGAGGAC AGGTATCCGT TTTGATTGTA	2280
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GAGAAATAGC TCCTGAAGTA AGGGCGAAGA AAAGGAAAAT ACTGATAAAA ACATGAATGA	2400
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GCAATACGAA GTGAGTCGAC AATATGTATC ATCACTCCGA AAAAGAAAGC TCCCAGTATA	2520
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GAAAATAGAA CCGAGAATAC TTGATACACC ATTTCTTATA GTGAGAAGAG AATGAAAATA	2820
GTCTGACCT TCATCTATGA GTATCCTGAG AAGAGGAGTT ATAAAAACA TCCATAGACC	2880
AAAGAACAAA CCTGCTTCA GACCTGGGTA GTGTAGTGC TTGCTTTCTT TCTCATTGAG	2940
CATATCTGGT TCAATGACTG TGATGCCTGT TTTTTCATT TGGTAGGTGA CATAGCCAGA	3000

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AGCGATGAGG GCAATCACTA AAATCAGAGG AGGATAGATT AGAGCCACTT CTTGAGGGTA	3060
TTTATAGGCC AGAAGGAGTG GAATAAGATT TCCGAAAATC ATCAGATAAA AGAGGATGAT	3120
AAAGACTTGG TTCCAATAC TATCGGCCTC ACGCCGTTTG TATTCGTCAA GGGGACCAGA	3180
AATACCGTAT GTGCGTTTGA TCAGTTTTTC AGTGAAGGTT TCTTTTTTCA TGAGTTTGCT	3240
CCTTTTTTAA AAATCTTCCT CCCAAAAGAG ACTGTTGAGG TCAGTTTGGA GGCTGCGGGC	3300
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CTGTCTCGAG ACACCGATAT CCTTGCGGAG TTCGAGCTGG GAAATACCCA ATTCCTTGCG	3420
AAATCTTTC ACACGATTCA TCTGTTCTCC TTTCTGATTT ATGTCGTATA TATTTGACTA	3480
TATTATAGTC TTTTAAACAT AAAGTGTCAG GTATTTTGA CATATTTTTT GAAGAAATAG	3540
TAGTCTCCTT GTCTATTG TCTGACAAGT GCAAGCTGGT CGGATTGTG GTAAAATAGA	3600
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CTTGACGTAA AGCCTGATGG TATCTACGTT GATGCGACTT TGGGCGGAGC AGGACATAGC	3720
GAGTATTTAT TAAGTAAATT AAGTGAAAAA GGCCATCTCT ATGCCTTTGA CCAGGATCAG	3780
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TTTATCAAGG ACAACTTCCG TCATTTACAG GCATGTTTGC GCGAAGCTGG TGTTCAAGAA	3900
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ACAGCCTATG AAGTGGTGAA CAATTATGAC TATCATGACT TGGTTCGTAT TTTCTTCAAG	4080
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AAGCCGATTG AGACAACGAC TGAGTTAGCA GAGATTATCA AGTTGGTCAA ACCTGCCAAG	4200
GAATCAAGA AGAAGGGGCA TCCTGCTAAG CAGATTTTCC AGGCTATTG AATTGAAGTC	4260
AATGATGAAC TGGGAGCGGC AGATGAGTCC ATCCAGCAGG CTATGGATAT GTTGGCTCTG	4320
GATGGTAGAA TTTCAGTGAT TACCTTTCAT TCCTTAGAAG ACCGCTTGAC CAAGCAATTG	4380
TTCAAGGAAG CTTCAACAGT TGAAGTTCCA AAAGGCTTGC CTTTCATCCC AGATGATCTC	4440
AAGCCCAAGA TGAATTGGT GTCCCGTAAG CCAATCTTGC CAAGTGCGGA AGAGTTAGAA	4500
GCCAATAACC GCTCGCACTC AGCCAAGTTG GCGGTGGTCA GAAAAATTCA CAAGTAAGAG	4560
GGAAAAAGAT GGCAGAAAAA ATGGAAAAA CAGGTCAAAT ACTACAGATG CAACTTAAAC	4620
GGTTTTCGCG TGTGAAAAA GCTTTTACT TTTCCATTGC TGTAACCACT CTTATTGTAG	4680
CCATTAGTAT TATTTTATG CAGACCAAGC TCTTGCAAGT GCAGAATGAT TTGACAAAAA	4740
TCAATGCGCA GATAGAGGAA AAGAAGACCG AATTGGACGA TGCCAAGCAA GAGGTCAATG	4800

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AAC TATTACG TGCAGAACGT TTGAAAGAAA TTGCCAATTC ACACGATTG CAATTAAACA	4860
ATGAAAATAT TAGAATAGCG GAGTAAGATA TGAAGTGGAC AAAAAGAGTA ATCCGTTATG	4920
CGACCAAAAA TCGGAAATCG CCGGCTGAAA ACAGACGCAG AGTTGGAAAA AGTCTGAGTT	4980
TATTATCTGT CTTTGTTTTT GCCATTTTTT TAGTCAATTT TCGGTCATT ATTGGGACAG	5040
GCACTCGCTT TGGAAACAGAT TTAGCGAAGG AAGCTAAGAA GGTTCATCAA ACCACCCGTA	5100
CAGTTCCTGC CAAACGTGGG ACTATTTATG ACCGAAATGG AGTCCCGATT GCTGAGGATG	5160
CAACCTCCTA TAATGTCAT GCGGTCATTG ATGAGAATA TAAGTCAGCA ACGGGTAAGA	5220
TTCTTTACGT AGAAAAACA CAATTTAACA AGGTGCAGA GGTCTTCAT AAGTATCTGG	5280
ACATGGAAGA ATCCTATGTA AGAGAGCAAC TCTCGCAACC TAATCTCAAG CAAGTTTCCT	5340
TTGGAGCAAA GGGAAATGGG ATTACCTATG CCAATATGAT GTCTATCAA AAAGAATTGG	5400
AAGCTGCAGA GGTCAAGGGG ATTGATTTTA CAACCACTCC CAATCGTAGT TACCCAAACG	5460
GACAATTTGC TTCTAGTTTT ATCGGCTCTAG CTCAGCTCCA TGAATGAA GATGGAAGCA	5520
AGAGCTTGCT GGAACCTCT GGAATGGAGA GTTCCTTGAA CAGTATCTT GCAGGGACAG	5580
ACGGCATTAT TACCTATGAA AAGGATCGTC TGGGTAATAT TGTACCCGGA ACAGAACAAG	5640
TTTCCCAACG AACGATGGAC GGTAAGGATG TTTATACAAC CATTTCCAGC CCCCTCCAGT	5700
CCTTTATGGA AACCAGATG GATGCTTTT AAGAGAAGGT AAAAGGAAAG TACATGACAG	5760
CGACTTTGGT CAGTGCTAAA ACAGGGGAAA TTCTGGCAAC AACGCAACGA CCGACCTTG	5820
ATGCAGATAC AAAAGAAGGC ATTACAGAGG ACTTTGTTTG GCGTGATATC CTTTACCAA	5880
GTAACATGA GCCAGGTTC ACTATGAAAG TGATGATGTT GGCTGCTGCT ATTGATAATA	5940
ATACCTTTCC AGGAGGAGAA GTCTTTAATA GTAGTGAGTT AAAAATTGCA GATGCCACGA	6000
TTTCGAGATTG GGACGTTAAT GAAGGATTGA CTGGTGGCAG AACGATGACT TTTTCTCAAG	6060
GTTTTCACCA CTCAAGTAAC GTTGGGATGA CCTTCCTTGA GCAAAGATG GGAGATGCTA	6120
CCTGGCTTGA TTATCTTAAT CGTTTTAAAT TTGGAGTTCC GACCCGTTTC GGTTTGACGG	6180
ATGAGTATGC TGGTCAGCTT CCTGCGGATA ATATTGTCAA CATTCGCAA AGCTCATTTG	6240
GACAAGGGAT TTCAGTGACC CAGACGCAA TGATTCGTGC CTTTACAGCT ATTGCTAATG	6300
ACGGTGTCT GCTGGAGCCT AAATTTATTA GTGCCATTTA TGATCCAAAT GATCAAACG	6360
CTCGGAAATC TCAAAAAGAA ATTGTGGGAA ATCCTGTTTC TAAAGATGCA GCTAGTCTAA	6420
CTCGGACTAA CATGGTTTTG GTAGGGACGG ATCCGGTTTA TGAACCATG TATAACCACA	6480
GCACAGGCAA GCCAACTGTA ACTGTTCTCT GGCAAAATGT AGCCCTCAAG TCTGGTACGG	6540

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CTCAGATTGC TGACGAGAAA AATGGTGGTT ATCTAGTCGG GTTAACCGAC TATATTTTCT	6600
CGGCTGTATC GATGAGTCCG GCTGAAAATC CTGATTTTAT CTTGTATGTG ACGGTCCAAC	6660
AACCTGAACA TTATTCAGGT ATTCAGTTGG GAGAATTTGC CAATCCTATC TTGGAGCGGG	6720
CTTCAGCTAT GAAAGACTCT CTCAATCTTC AAACAACAGC TAAGGCTTTA GAGCAAGTAA	6780
GTCAACAAAG TCCTTATCCT ATGCCTAGTG TCAAGGATAT TTCACCTGGT GATTTAGCAG	6840
AAGAATTGCG TCGCAATCTT GTACAACCCA TCGTTGTGGG AACAGGAACG AAGATTAAAA	6900
ACAGTTCTGC TGAAGAAGGG AAGAATCTTG CCCGAACCA GCAAGTCCTT ATCTTATCTG	6960
ATAAAGCAGA GGAGGTTCCA GATATGTATG GTTGGACAAA GGAGACTGCT GAGACCCTTG	7020
CTAAGTGGCT CAATATAGAA CTTGAATTTT AAGGTTCCGG CTCTACTGTG CAGAAGCAAG	7080
ATGTTCTGTC TAACACAGCT ATCAAGGACA TTAAAAAAT TACATTAACT TTAGGAGACT	7140
AATATGTTTA TTTCCATCAG TGCTGGAATT GTGACATTTT TACTAACTTT AGTAGAAATT	7200
CCGGCCCTTA TCCAATTTTA TAGAAAGGCG CAAATTACAG GCCAGCAGAT GCATGAGGAT	7260
GTCAACACAG ATCAGGCAAA AGCTGGGACT CCTACAATGG GAGGTTTGGT TTTCTTGATT	7320
ACTTCTGTTT TGGTTGCTTT CTTTTTCGCC CTATTTAGTA GCCAATTCAG CAATAATGTG	7380
GGAATGATTT TGTTTCATCTT GGTCTTGATG GGCTTGGTCG GATTTTTAGA TGACTTTCTC	7440
AAGGTCTTTC GTAAATCAA TGAGGGGCTT AATCCTAAGC AAAAATTAGC TCCTCAGCTT	7500
CTAGGTGGAG TTATCTTCTA TCTTTTCTAT GAGCGCGGTG GCGATATCCT GTCTGTCTTT	7560
GGTATCCAG TTCAATTTGG ATTTTCTAT ATTTTCTTCG CTCTTTCTG GCTAGTCGGT	7620
TTTTCAAACG CAGTAAACTT GACAGACGGT GTTGACGGTT TAGCTAGTAT TTCCGTTGTG	7680
ATTAGTTTGT CTGCCTATGG AGTTATTGCC TATGTGCAAG GTCAGATGGA TATCTTCTA	7740
GTGATTCTTG CCATGATTGG TGTTTGCTC GGTTCCTCA TCTTTAACCA TAAGCCTGCC	7800
AAGGTCTTTA TGGGTGATGT GGAAGTTTG GCCCTAGGTG GGATGCTGGC AGCTATCTCT	7860
ATGGCTCTCC ACCAAGAATG GACTCTCTTG ATTATCGGAA TTGTGTATGT TTTTGAAACA	7920
ACTTCTGTTA TGATGCAAGT CAGTTATTTT AACTGACAG GTGGTAAACG TATTTCCGT	7980
ATGACGCCTG TACATCACCA TTTTGAGCTT GGGGGATTGT CTGGTAAAGG AAATCCTTGG	8040
AGCGAGTGA AGGTTGACTT CTTCTTTTGG GGAGTGGGAC TTCTAGCAAG TCTCCTGACC	8100
CTAGCAATTT TATATTTGAT GTAAGAATGG CACCCTGATG TTTCAGGG	8148

(2) INFORMATION FOR SEQ ID NO: 12:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 9909 base pairs
  - (B) TYPE: nucleic acid

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(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 12:

TACTCCACCC TTAATATCCG TTCCGTGAAA TACTTTACCG CTTTAAAGTT CATAGAATTG	60
AACTTTTAAA TGCTTGTCCT CAAGCATCTT TTCCATCCAA TTTTtaggag TTGACCAGC	120
TTTAAATAAA AACCTTGCTG GGGTGATTAG TATAGATTTA TCTGCGATTT TATAAGCTTC	180
ATCAATAAAA TAGTGATATA TCGGCTCATC TCTGGCTTCT CCTGTTTCCT GATACGGAGG	240
ATTTCTATC ACGACATCAA ATTTCAATTC ACTTTCCTCG CTAGATAGGC GCTCAAAACC	300
TATCATTTCTA TTCTTTTCC AGTCTTTGAT ATGGGTTTTA GATTCTTCTA CTTCTTGGAC	360
TTCTAGCTCA TCCGCAAAACA AACTCAATTG TTGAGATTGC TTTTGTtag CTGAATAAGG	420
ACTACTTTTT TTCAATCCAT CCATCTGAAA GACATTGTAA GAGATAATAG TCGCAATTC	480
TTCTTTTGC TCTAATGTTG GTTGATTTC AGTCTTAGCT AGATAATAGT CCTCAAAAGT	540
TGCCAAAAGA TTCTCACCGC CAAAAGGAG AGAATCTCCT TGATACTCAT AACCATACGA	600
AGCATGATAA GCATCTTTTA CAAGTTTATA AAATGTGACT TCATCTGAAA CCTCAGACT	660
AATCGTTGC AGTTTCTAT CAACAAAACC AACTCGCTCA GATAATGGAA TTTCTCACC	720
AGTTACGGTA TCATATCTCG TTACCATATA AGGTGCTTCA CCACAAGTTA CCTCTAACCA	780
TCGTAAGTCC ACATACTCCT CAAGACTTAA CGAGCCTAAT TTCGATTCTA CATATCCATT	840
TTGCTTTGCG ACCAACCACG TTGGTGTAAC CACTTCTGCC CTTATTTTGG TCCGATCTTT	900
TTGTTCATAT TTGGATTTTT CAGATCTGGG CTGAATCAAG TTGGCAAAGT TTCCAGTAAC	960
CTTACTTGGA TTGATGCGAT CACTTGGAGC AAATCCCTTT CCTAACAATT CATAAGAATG	1020
CGTAAgCCAA ACAATTGATT TCTTTGTCGT TCGATCTTTT AAAAGAATTT TTAATAAGTC	1080
AGCCGATTCT TTAGCCAAAC TTTCTTCACT AATATCTATT GTCATCAGCA ACCTCTCTTA	1140
TATTGTAAGC CCTATTATAT CATATTTTAA AGAATGAAAA TTTACTTGAA AAAAGTAATT	1200
CAATAAATAT CTCTCCGATG ACCAACTTCT AGAGTAGCAA CGACTAATTC ATCATCTACA	1260
ATTTGTACGA TAACTCGATA ATTACCAATT CTATAGCGCC ATTGACCAAC GCGATTACCA	1320
ACCAAAGCCT TTCCGTGTCG TCTTGGGTCT TCCAAAACAT TGGTTTGTA ATAGTTTGTA	1380
ATTAGCTTCT GCGTATAACG GTCCAATTTT TTCAATTGCT TGATAAAACG TCTTGTGGA	1440
ACTAATTTAT ACAAATTATT CATCCTTCAA GCCTAAATCA TGCATCATTT CTTCCCAAGT	1500
AATGGGTTCa ACTCCTTTTT CCAAGTCTTC TAAATACTCT TGATAGGCTA AATCTGCCAC	1560

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ACGAGCATCG TATTCATCTT CTAGGGCTTC AAGAGTTTGG GTGCGAATAA GTTCCGAAAG	1620
GGAAACTCCT TCAAACCTAG CCATTGCTTT CATAAATGTT TTATCAGCTT CAGAACTTT	1680
TAATGTAATA GTAGTCATCT TTTGTGCTCC CTTTTTAAAT GGTAACACCA TTGTATTACT	1740
TTTTAGGTGT TCAGTCAATA TAAAAAGAAC ACCTTCTCAG CGTTCTTTCT ATATCTCTGT	1800
CAATGGTGT GCGGTATCTG GTGAGGTATC ATAAACCTTA AAGTCTACTC CGACTCCCAG	1860
ATCAGCTTGA GCCAGCTGAT TGACCATGGT CATATGAGCC AGTTCCTTGA TATTGTTTTC	1920
CTTAGATAAA TGCCCAAGGT AAATCTTCTT AGTACGATTT CCTAGCGTCC GAATCATAGC	1980
TTCAGCACCG TCCTCGTTAG AAAGGTGACC AAGGTCAGAT AGGATTGCTT GTTTGAGTCG	2040
CCAAGCGTAA GAACCTGATC GCAAAATCTC TACATCATGG TTGGCCTCGA TAAGATAACC	2100
ATCCGCATTT TCGACAATGC CCGCCATACG GTCAGTACA TAACCTGTAT CTGTCAAGAG	2160
GACAAAATC TTATCATCCT TCATAAAGCG ATAGAACTGC GGTGCGACTG CATCATGGCT	2220
TACACCAAAA CTCTCGATGT CGATATCTCC AAAGGTTTTG GTTTTACCCA TTTCAAAAAT	2280
ATGCTTTTGC GAAGAATCCA CTTTGCCAAG ATATTTACTA TTTTCCATAG CTTGCCAGGT	2340
CTTTTCATTG GCATAAAGAT CCATACCATA CTTGCGAGCC AAAACGCCTA CTCCATGGAT	2400
ATGATCTGAA TGCTCATGGG TAATCAAGAT GGCATCCAGG TCTTCTGGCT TACGGTTAAT	2460
TTTTCAGTAG AGACTGGTAA TTTTCTTGCC AGACAAGCCT GCATCTACTA AAAGCTTCTT	2520
TTTTGAGGTT TCCAGATAAA AAGAATTTCC ACTGGAACCC GACGCTAAAA TACTGTATTT	2580
AAAGCCTATT TCACTCATTG TAGTCTTCTA CTTTCCTCTC CCATACCTCT TCTTTCAGTG	2640
CATCCTTATC ATAAGGGAGT ACAATGGTAA AGGTTGAACC CTTGCCGTAT TCACTCTTGG	2700
CCCAAATAAA GCCCTTATGT TGTTTGATAA TTTCTTTAGC GATAGACAGT CCTAGACCTG	2760
TACCACCTTG TGACAGACTT CTAGCAGCAT CCACACGATA GAAACGGTCA AAGATACGTG	2820
GTAAATCCTG CTTAGGAATC CCCAAACCGT GGTCAGAAAT GGATAAAATC ATCTGGTCTT	2880
CAGTTGTCTT CATTCTGACA GTGATTTTAC CCCCATCTGG CGAATACTTA ATAGCATTAT	2940
TTAAAAATAT GTCGACAACC TGCGTCATCT TATCTGTATC AATTTCCATC CAGATAGAAT	3000
TGATGGGATA ATCTCTCACC AACTCATATT TTTTCTCCTT TTCCTGTCCT TTCATCTTGT	3060
CAAAACGATT GAGGATAAAG GTAATAAAG CAGTGAAGTT AATCAGTTCC ACATCTAGGT	3120
GACTGGTAGC ATTATCAATA CGTGAAAGAT GGAGGAGATC CGTCACCATG CGCATCATAC	3180
GGTTGGTCTC ATCAAGAGAA ACCTTGATAA AGTCTGGTGC TACAGTTTCA CACAAAGCCC	3240
CCTCATCCAA GGCTTCAAGA TAGGATTTTA CGTAGTCAG AGGAGTCCGT AACTCATGGC	3300
TAACATTGGA AACAAAGAGT CTCGTTCTGC GTTCTTCCTT CTCCTGCTCC GTCGTATCAT	3360



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GCAAAACAGC CACCAAACT GAAATAAAGC CAGACTCTCG ACGTATCAAG GCAAAGCGAA	3420
CTCGAAGGTT CAAATATTCG CCATTGATAT CTTGGGAATC TAGCAACAAT TCTGGACTTT	3480
GGGTAATCAA ATCACGCAAT TCATAGTTTT CTTCTATCTT GAGCAATTCC AAAATGCTTC	3540
TATTCAGAAC ATCTTCCTTA ACCAACCCCA GTTGCTTCTT GGCTGTATCG TTAATCATGA	3600
TAATCTGACC CCGACGGTTA GTCGCAAGAA CCCCATCTGT CATATAAAAC AGAATACTAT	3660
TTAGCCTCTT ACTCTCTTGT TCTAGATTTT CCTGAGTGAG ACGAATAACC TCCGACAAGT	3720
CATTCAAATT ATTGGTAATA TTGGTGATTT CAGACCCACC TTGCATATCA AGAACCTTGG	3780
AATAATCTCC TGCAATCAAA TCTTAACCT TTTGATTGAC TTGCTTCAAC TGAATATTAT	3840
CACGTCTATT TTCCAGTAAT AAGAGGGTCA CAACAAGGAT GAAACCTAAC AAAATCAGGA	3900
TAAAGATAAA ATCTCTGGTA AAAATGGTTT GTTTCAGTAA ATCAAGCATT ATTTCTCATG	3960
TAATACCCTA CACCACGGCG CGTCAAGATA TACTCTGGTC GGCTGGGCGT ATCTTCAATC	4020
TTCTCAGCA GACGTCGTAC AGTCACATCA ACTGTACGGA CATCACCAA ATAGTCATAA	4080
CCCCAGACAG TCTCAAGCAA GTGTTCCGCG GTGATGACTT GACCTGTATG CGATGCTAAA	4140
TGATACAAAA GCTCAAATTC ACGATGGGTT AAGTCTAGTT CTTCCGCATA TTTTTAGCC	4200
ACGTAGGCGT CTGGAACAAT TTCTAAATCC CCAATTTGGA TAGGTTGAGG TTTACTATCT	4260
GCTTCTGAC CATCTACTGG CATAGGTTGA GAACGACGCA GAAGAGCTTT AACACGCGCC	4320
TGCAACTCAC GATTGGAGAA GGGTTTTGTT ACATAGTCAT CTGCCCCAAG TTCCAAACCG	4380
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TTACGAATGG TCTTAGCAAC TTCTAAACCA TCAATTTCTG GAAGCATCAA ATCCAGAATA	4500
ATAATATCTG GTTGCTCTGC TTCAAATTC TCTAGCGCTT CACGACCATT AAAAGCAGTT	4560
ACAACTTCGT AACCTTCCTT GGTCATATTA AACTTGATAA TATCCGAGAT TGGTTTCTCA	4620
TCATCTACAA TTAGTATTTT TTTCATATGT TCACCTTTTT CTCTACTATT ATACCAAAAA	4680
AATAGTCAGA AGACACAATA GCTAGTCTTG GCTACTGTCT AAGTTGGCTT GTGCATAAAC	4740
CTGCCAGATT TTTTGTGGG GTTTGGCAAG TGGGTAATTC TTGAATTCCT CTGGTGAAAG	4800
CCAGCGAACT TCCCTATCTG AAAAATCATG GAAGTCACTC ACCTGACCTG CTACAATCTG	4860
TACATGCCAT TTTGATGAC TAAAAACATG CTGGACTGTA TCAAAACAAA CATCAAGCCA	4920
ATCAACATCT AGGTCATAGT CCTGCTGGAA ACTCTCTTCT GGACTGGGAC CAAAGTTCAC	4980
ACTTTCTTCC GCAACCTGAT GAAAGAGGTC AAAGTCTCT TCTTGCGAAA AGTTATCAAC	5040
TTCTATAAAG GGGAAATGCC AAAAACCTGC CAAGAGCTTT TCGCTTTCAT TTTTTCAAG	5100

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TAAAAATTGT CCTTGAGAAT TTTTCACAAC TAAGGCTTTA AGATAAATAG GAACCGGCTT	5160
TTTCTTAGGA GATTTAATTG GATAACGGTC CATGGTTCCA TTCTGATATG CCGCACTAAA	5220
GTCCCTTGACT GGGCTTTCTT CAGGTCTGGG ATTTACAGGA GACTCAATAT CAGACCCTAA	5280
GTCCATCAAG GCTTGATTAA AATCACCCGG ACGATCCGGA TTAATCAAGA TCTCCATCAT	5340
TGCCTGAAAA ATTTTTCGAT TACTTGGAAT CCCAATATCG TGGTTGACTT CAAACAGACG	5400
CGCCAAGACC CGCATGACAT TACCATCTAC AGCTGGCTCA GGCAAGTTAA AAGCAATACT	5460
GGAAATGGCT CCTGCTGTGT AAGGTCCAAT CCCTTTCAAG CTGGAAATTC CTTCATAGGT	5520
ATTTGGAAAT TGGCCACCAA AGTCAGTCAT AATCTGCTGG GCTGCAGCCT GCATATTGCG	5580
AACTCGAGAA TAATAGCCCA AGCCCTCCCA AGCTTTCAGT AAATCTCCT CAGGCGCAGT	5640
TGCCAGACTT TCGACAGTTG GAAACGAGTC CAAAAATCTT TCGTAGTAAG GGATAACTGT	5700
ATCCACCCTG GTCTGCTGAA GCATGATTTT AGATACCCAG ATGTGATAAG GATTTTACT	5760
TCTCCTCCAA GGCAAACTCT TTTTGTTTTC ATCATACCAA GCGAGAAGTT TCTCACGGAA	5820
AGAAATGACT TTCTCCTCCG GCCACATGAC GATACCGTAT TCTTTCAAAT CTAACATATC	5880
TCTAGTATAA CACAGAAGGT TTCACCTGTC TTTGTATCTG ATTTATAATA TTTTCAATAG	5940
ATAGTATATA ACTTTTCTAT CTACTTATAC TCAATGAAAA TCAAAGAGCA AACTAGGAAG	6000
CTAGCCGCGAG GTTGCTCAAA ACACTGTTTT GAGGTGTGG ATAGAACTGA CAGAGTCAGT	6060
ATCATATACT ACGGCAAGGT GAAGCTGACG TAGTTTGAAG AGATTTTCGA AGAGTATAAA	6120
TCTTATTGAT GAACTGCTTG CAGTCTGAGA AAAAATGAGC TTGGATATTA TTTCCAAACT	6180
CACTTAAAGT CAATTTCAAT CCACTAGAAC AAGCCTAGTA CAGTTCCATC GCTTTCAACA	6240
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TTTCTGGTG CTCCAAGCGC ATTTGGATTG TCTGAGAAAC TGTATTGAGT TTTAGCCATA	6420
CAGATTGGCA ATTTGTCCCA ACCGTTTTGA ACGATTGAG CAATTTGTGT TTGAGCTTTC	6480
TTCTCAAAGT TCACTTTGCT ACCACGATAG ATTTCACTGA CAATTTTTC AATCTTTTCT	6540
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AATTTCAACTG GTACATCGAT TGAGGCACAG AGTTCTTTTA AGGCTGCAAT TTCAGCTTCT	6720
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TCAACGTGGC GTTTCAAGTT AGCAAAACCT GCACGAACTG CCTCTACATT TTCTTCAGTC	6840
AGAGCGTCTT TAGCCACACC ACCATTCATC TTAAGGGCAC GAAGGGTTGC GACAATAACA	6900

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AGGTCCGCAC CAAAACCAGC TTCAGTAACA GTGTAATCAG CCAAGTGAAG GGCTGTTGTC	7020
GTGCCCCAAA CAGAGTTACA GCCATGAGCG ATATTGGCAA ATGGACCACC GTGTACAAAG	7080
GCAGGTGTAC CGTAAATTGT CTGAACCAAG TTTGGCTTAA TAGCATCCTT CAAAATCAAA	7140
GCCAAGGCAC CCTCAACCTG CAAATCACCT ACAGAAACAG GCGTACGGTC ATAGCGATAA	7200
CCAATAACGA TATTGCGCAA ACGACGTTTC AAGTCCTCGA TGTCCGTTGC CAAGCAAAGA	7260
ATTGCCATGA TTTCTGAAGC AACTGTAATA TCAAAACCAT CCTCACGTGG AATACCGTTT	7320
AGAGGACCAC CAAGACCAAC AGTCACATGG CGGAGCGTAC GGTGCTTCAA GTCCACAACG	7380
CGTTTCCAGA GGATACGACG TTGATCAATT CCCAGCTCAT TCCCTTGGTG CAAGTGGTTG	7440
TCAATCAAGG CAGAAAGGGC ATTGTTGGCA GTTGTAATAG CATGCATATC TCCAGTAAAG	7500
TGGAGGTTGA TGTCTTCCAT TGGCAGAACT TGTGCATACC CACCACCAGC AGCACCACCC	7560
TTGATCCCCA TGA CTGGACC AAGAGACGGT TCGCGGATAG CAATCATGGT TTTCTTGCCA	7620
ATCTTGTTCA AGGCATCCGC AAGACCAATG GTAAGCGTCG ACTTTCCTTC ACCTGCAGGT	7680
GTGCGGTTGA TGGCAGTAAC CAAGATCAAT TTACCGACTG GATTGCTCTC AACTGCACGA	7740
ATTTTATCAA AGCTGAGTTT AGCCTTGATC TTTCCGTACA ACTCCAAATC GTCATAAGAA	7800
ATACCAAGTT TCTCTACAAC ATCAACAATT GGCTTCAACT CAATACTCTG TGCAGTTTCA	7860
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ACAAGATTTT TAACATCCTA AAACTCTCTA AACGTTGTA AATATCTCTG TTTTAAAGAC	7980
TTTTAGAGTC CTTTCTTAAA TTTTATATGG CTTTATAGTT TGAAACTATA ATAAATCTTC	8040
GTTTTACCA AAAATTTATC ACTTTCATTT TACTTACCGC TTATTTTGT GTACAATAGT	8100
GCTATGAAAA TTTTAGTTAC ATCGGGCGGT ACCAGTGAAG CTATCGATAG CGTCCGCTCT	8160
ATCACTAACC ATTCTACAGG TCACTTGGGG AAAATTATCA CAGAGACTTT GCTTCTGCA	8220
GGGTATGAAG TTTGTTTAAT TACGACAAA CGAGCTCTGA AGCCAGAGCC TCATCCTAAC	8280
CTAAGTATTC GAGAAATTAC CAATACCAAG GACCTTCTAA TAGAAATGCA AGAACGTGTT	8340
CAGGATTATC AGGTCTTGAT CCACTCAATG GCTGTTTCTG ACTACACTCC TGTATATATG	8400
ACAGGCGTTG AGGAAGTTCA GGCTAGCTCC AATCTAAAAG AATTTTAAAG CAAGCAAAT	8460
CATCAGGCCA AGATTTCTTC AACTGATGAG GTTCAGGTTT TGTTCCTTAA AAAGACACCC	8520
AAAATCATAT CCCTAGTCAA GGAATGGAAT CCTACTATTC ATCTGATTGG TTTCAAACCTG	8580
CTGGTTGATG TTACCGAAGA TCATCTGGTT GACATTGCAC GAAAAAGTCT TATCAAGAAT	8640

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CAAGCAGATT TAATCATCGC GAATGACCTG ACTCAAATTT CAGCAGATCA GCACCGAGCT	8700
ATATTTGTTG AGAAAAATCA GCTTCAAACA GTCCAGACTA AAGAAGAAAT TGCAGAACTC	8760
CTCCTTGAAA AAATTCAAGC CTATCATTCT TAGAAAGGAA AACTATGGCA AACATTCTCT	8820
TGGCTGTAAC GGGTTCAATC GCCTCTTATA AGTCGGCAGA TTTAGTCAGT TCTCTAAAAA	8880
AACAAGGCCA TCAAGTCACT GTCTTAATGA CTCAGGCTGC TACAGAGTTT ATCCAACCTT	8940
TGACACTACA GGTACTCTCA CAGAAATCCTG TCCACTTGGA TGTCATGAAG GAACCTTATC	9000
CTGATCAGGT CAATCATATC GAACTTGGAA AAAAAGCAGA TTTATTTATC GTGGTACCTG	9060
CAACTGCTAA CACTATTGCA AAAGTAGCTC ACGGATTGTC GGACAACATG GTAACCAGTA	9120
CAGCTCTAGC CCTACCAAGT CATATTCCCA AACTAATAGC TCCTGCTATG AATACAAAAA	9180
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GATTGCTCCT AAGGAATCCC TACTAGCTTG TGGAGACCAC GGACGAGGAG CTTTAGCTGA	9300
CCTCACAATT ATTTTAGAAA GAATAAAGGA AACTATCGAT GAAAAACGC TCTAATATTG	9360
CACCCATTGC TATCTTTTTT GCTACCATGC TCGTGATACA CTTTCTGAGC TCACTTATCT	9420
TTAACCTTTT TCCATTTCCA ATCAAACCGA CCATTGTTCA TATTCCTGTC ATTATTGCCA	9480
GCATTATTTA TGGTCCACGA GTTGGGGTTA CACTTGGATT TTTGATGGGA TTACTTAGCT	9540
TGACGGTTAA CACGATTACG ATTCTACCGA CAAGCTACCT CTTCTCTCCC TCGTACCAA	9600
ACGGAAACAT CTACTCAGCT ATCATTGCCA TCGTCCCACG TATTTTGATT GGTTTAACTC	9660
CTTACTTAGT CTATAAAGT ATGAAAAACA AGACTGGTCT GATTTTAGCT GGAGCCCTTG	9720
GTTCCCTGAC AAATACTATC TTTGTCCTTG GAGGAATCTT CTTCTTATTT GGAAATGTTT	9780
ATAATGGAAA TATCCAACCT CTTCTGGCAA CCGTTATCTC AACAAATTCA ATTGCTGAAT	9840
TGGTCATTTC TGCAATTCTA ACCCTAGCCA TTGTTCCACG ACTACAAACC TTGAAAAAAT	9900
AAAAACAGG	9909

## (2) INFORMATION FOR SEQ ID NO: 13:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1126 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 13:

TAATTTTCAT ATAATAGTAA AATAGAAATGT GTGATTCAAT AATCACCTCA AATAGAAAGG	60
AAATTCTATG TCAAATCTAT CTGTTAATGC AATTCGTTTT CTAGGTATTG ACGCCATTAA	120

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TAAAGCCAAC TCAGGTCATC CAGGTGTGGT TATGGGAGCG GCTCCGATGG CTTACAGCCT	180
CTTTACAAAA CAACTTCATA TCAATCCAGC TCAACCAAAC TGGATTAACC GCGACCGCTT	240
TATTCTTTCA GCAGGTCATG GTTCAATGCT CCTTTATGCT CTTCTTCACC TTTCTGGTTT	300
TGAAGATGTC AGCATGGATG AGATTAAGAG TTTCGGTCAA TGGGGTTCAA AAACACCAGG	360
TCACCCAGAA TTTGGTCATA CGGCAGGGAT TGATGCTACG ACAGGTCCTC TAGGGCAAGG	420
GATTTCAACT GCTACTGGTT TTGCCCAAGC AGAACGTTTC TTGGCAGCCA AATATAACCG	480
TGAAGGTAC AATATCTTTG ACCACTATAC TTACGTTATC TGTGGAGACG GAGACTTGAT	540
GGAAGGTGTC TCAAGCGAGG CAGCTTCATA CGCAGGCTTG CAAAACTTG ATAAGTTGGT	600
TGTTCTTTAT GATTCAAATG ATATCAACTT GGATGGTGAG ACAAAGGATT CCTTTACAGA	660
AAGTGTTCGT GACCGTTACA ATGCCTACGG TTGGCATACT GCCTTGGTTG AAAATGGAAC	720
AGACTTGGAA GCCATCCATG CTGCTATCGA AACAGCAAAA GCTTCAGGCA AGCCATCTTT	780
GATTGAAGTG AAGACGGTTA TTGGATACGG TTCTCCAAAC AAACAAGGAA CTAATGCTGT	840
ACACGGCGCC CCTCTTGAG CAGATGAAAC TGCATCAACT CGTCAAGCCC TCGGTTGGGA	900
CTACGAACCA TTTGAAATTC CAGAACAAGT ATATGCTGAT TTCAAAGAAC ATGTTGCAGA	960
CCGTGGCGCA TCAGCTTATC AAGCTTGGAC TAAATTAGTT GCAGATTATA AAGAAGCTCA	1020
TCCAGAAGTG GCTGCAGAAG TAGAAGCCAT CATCGACGGA CGTGATCCAG TCGAAGTGAC	1080
TCCAGCAGAC TTCCAGCTT TAGAAAATGG TTTTtCTCAA GCAACT	1126

(2) INFORMATION FOR SEQ ID NO: 14:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 2520 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 14:

CCGGCAACAA AAAAGAAAA ATCAACAGTT AAAAAAATC TAGTCATCGT GGAGTCGCCT	60
GCTAAGCCAA GACGATTGAA AAATATCTAG GCAGAAACTA CAAGGTTTGA GCCAGTGTCG	120
GGCATATCCG TGATTTGAAG AAATCCAGTA TGTCCTCGA TATTGAAAAT AATTATGAAC	180
CGCAATATAT TAATATCCGA GGAAAAGGCC CTCTTATCAA TGAATTGAAA AAAGAAGCTA	240
AAAAAGCTAA TAAAGTTTT CTCCGAGTG ACCCGGACCG TGAAGGAGAA GCGATTCTT	300
GGCATTGGGC CCATATTCTC AACTTGGATG AAAATGATGC CAACCGTGTG GTCTTCAATG	360

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AAATCACCAA GGATGCAGTC AAAAATGCTT TTAAAGAACC TCGTAAGATC GATATGGACT	420
TGGTCGATGC CCAACAAGCT CGTCGGATCT TGGATCGCTT GGTAGGGTAT TCGATTTCGC	480
CTATTTTGTG GAAGAAGGTC AAGAAGGGCT TGTGAGCAGG TCGCGTTCAG TCCATTGCCC	540
TTAAACTCAT CATTGACCGT GAAAATGAAA TCAATGCCTT CCAGCCAGAA GAATACTGGA	600
CAGTTGATGC TGTCTTTAAA AAGGGAACCA AACAATTTC TCGTTCCTTC TATGGAGTAG	660
ATGGTAAAAA GATGAACTG ACCAGCAATA ACGAAGTCAA GGAAGTCTTG TCTCGTCTGA	720
CGAGTAAAGA CTTTTCAGTA GATCAGGTGG ATAAGAAAGA GCGCAAGCGC AATGCTCCTT	780
TACCCTATAC CACTTCATCT ATGCAGATGG ATGCTGCCAA TAAAATCAAT TTCCGTACTC	840
GAAAAACCAT GATGGTTGCC CAACAGCTCT ATGAAGGAAT TAATATCGGT TCTGGTGTTC	900
AAGGTTTGAT TACCTATATG CGTACCGATT CGACTCGTAT CAGTCTGTGA GCGCAAAATG	960
AGGCGGCAAG CTTTATTACG GATCGTTTTG GTAGCAAGTA TTCTAAGCAC GGTAGCAAGG	1020
TCAAAAACGC ATCAGGTGCT CAGGATGCCC ATGAGGCTAT TCGTCCGTCA AGTGTCTTTA	1080
ATACACCAGA AAGCATCGCT AAGTATCTGG ACAAGGATCA GCTTAAGCTA TATACCCTTA	1140
TCTGGAATCG TTTTGTGGCT AGCCAGATGA CAGCGGCCGT TTTTGATACC ATGGCTGTTA	1200
AATTGTCTCA AAAAGGGGTT CAATTTGCTG CCAATGGTAG TCAGGTTAAG TTTGATGGTT	1260
ATCTTGCCAT TTATAATGAT TCTGACAAGA ATAAGATGTT ACCGGACATG GTTGTGGAG	1320
ATGTGGTCAA ACAGGTCAAT AGCAAACCAG AGCAACATTT CACCCAACCG CCTGCCCGTT	1380
ATTCTGAAGC AACACTGATT AAAACCTTAG AGGAAAATGG GGTGGGACGT CCATCAACCT	1440
ACGCGCCAAC CATTGAAACC ATTCAGAAAC GTTATTATGT TCGCCTGGCA GCCAAACGTT	1500
TTGAACCGAC AGAGTTGGGA GAAATTGTCA ATAAGCTCAT CGTTGAATAT TTCCAGATA	1560
TCGTAAACGT GACCTTCACA GCTGAAATGG AAGGTAAACT GGATGATGTC GAAGTTGGAA	1620
AAGAGCAGTG GCGACGGGTC ATTGATGCCT TTTACAAACC ATTCTCTAAA GAAGTTGCCA	1680
AGGCTGAAGA AGAAATGGAA AAAATCCAGA TTAAGGATGA ACCAGCTGGA TTTGACTGTG	1740
AAGTGTGTGG CAGTCCAATG GTCATTAAAC TTGGTCGTTT TGGTAAATTC TACGCTTGTA	1800
GCAATTTCCC AGATTGCCGT CATACCCAAG CAATCGTGAA AGAGATTGGT GTTGAGTGTC	1860
CAAGCTGTCA TCAGGGACAA ATTATTGAGC GAAAAACCA GCGTAATCGC CTATTCTATG	1920
GTGCAATCG CTATCCAGAA TGTGAATTTA CCTCTTGGGA CAAGCCTGTT GGTGCTGACT	1980
GTCCAAAATG TGGCAACTTC CTCATGGAGA AAAAAGTCCG TGGTGGTGGC AAGCAGTTG	2040
TTTGTAGCAA AGGCGACTAC GAGGAAGAAA AGATGGCTCT TTGTCAACTG TAGTGGGTTG	2100
AAGTCAGCTA AGCTCGAGAA AGGACAAATT TTGTCCTTTC TTTTGTGATA TTCAGAGCGA	2160

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TAAAAATCCG TTTTTGAAG TTTTCAAAGT TCCGAAAACC AAAGGCATTG CGCTTGATAA	2220
GTTTGATGAG ATTATGGTC GCTTCCAATT TGGCGTTAGA ATAGTGTAGT TGAAGGGCGT	2280
TGACGATTTT CTCTTTGTCC TTTAGAAAGG TTTTAAAGAC AGTCTGAAAA AGAGGATGAA	2340
CCTGCTTTAG ATTGTCTCA ATGAGTCCGA AAAATTTCTC CGGTTCTTA TTCTGAAAGT	2400
GAAACAGCAA GAGTTGATAG AGCTGATAGT GATGTTTCAA GTCTTGTGAA TAGCTCAAAA	2460
GCTTGTTTAA AATCTCTTA TTGGTTAAAT GCATACGAAA AGTAGGGCGA TAAAAATGTT	2520

(2) INFORMATION FOR SEQ ID NO: 15:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 10993 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 15:

TTTTCTCGAT AATAACTTCC ACCTTATTAT TTGGGATACC CTCCTCTTCT TCACCACCAC	60
GTTCATAGTA GTCATCGGA TAGAGAAAAG CTACGATATC AGCGTCTGC TCAATAGACC	120
CAGATTACAG AATATCAGAC AAGACCGGTC TCTTGTCCTG ACGTTGTTCT ACACCACGAG	180
AAAGCTGACT CAGAGCGATT ACTGGAACCT TCAATTCCTT GGCTAGTATT TTCAACTGAC	240
GAGAAATTC AGAACTTCT TGTGACGAT TTTCTCGACC AGTCCCGTG ATAAGTTGCA	300
AATAGTCTAT CAAAATCAAA CCAAGATTTT CAGTTTCTTG AGCCAATTTA CGAGAACGAG	360
AACGAATCTC TGAATCCGA ATACCTGGCG TATCATCGAT ATAGATACTG GCGTTAGCTA	420
GATTACCCTG AGCAATAGTA TATTTTGGC ACTCCTCATC TGTC AATTGC CCGTACGGA	480
TAGAATGTGA CTCCACTAAG CCTTCTGCAG CTAACATACG ATCTACCAAG CTTTCCGCAC	540
CCATTTTCGAG TGAAAAATA GCAACCGTTT TGTCCAACTT AGTCCCAATG TTCTGAGCGA	600
TATTC AAGGC AAATGCTGTC TTACCAACTG CTGGACGAGC TGCTAAGATA ATCAACTCCT	660
CCTCATGAAG TCCTGTTGTC ATATGATCCA AATCAGGATA ACCTGTCGCA ATACCTGTAA	720
TATCGGTCGT TTGTTGCGAG CGAGCTTCCA GATTTCCAAA GTTGAGATTC AACACATCTC	780
GAATGTTCTT AAACCGCTT CGATTGTCAT TTCACTGAC ATCAATCAAC CCTTTTCTG	840
CCTGAGCAAT AATTTTCATCA GCTGGTTGTG ACGCTTCGTA AGCTTGGTTG ACAGACTCTG	900
TCAACTTGGC AATTAAACGA CGTAGCATTG CTTTTTCTGC AACAACTTTA GCATAATACT	960
CCGCATTAGC AGAAGTTGGC ACAGAATTAA CAATCTCAAC CAAGTAAGAC AAGCCACCAA	1020

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TATTCTGTAA ATCACCTTGA TTATCAAGGA TAGTACGAAC CGTTGTTGCA TCTATGGCAT	1080
CACCACGATC GGATAAATCG ACCATGGCTT GGAAAATCAA ACATGGGCA TACTTAAAAA	1140
AGTCCCAGAGA CTCAATGTAT TCTCGCAGAA AAACAAGTTT ACTCTCATCA ATAAAGATAG	1200
CCCCTAAAAAC GGATTGCTCA GCTAAGATAT CTTGAGGTTG TACTCGTAAC TCTTCTACTT	1260
CTGCCATCAG ACTTCCCTTC CTTTACAAT CTTGTCAAGA AGGTGTAAC TTATCCTTCT	1320
TTACACAGAA GATTGATTAC ACTTGTGATA TCTTGATAGA TTTTCACTGG CACATCAATC	1380
AAACCAACCG CTCGAATCGG AGCTTGTACT TGAATATGAC GTTATCAAT CTTAATTCCA	1440
AATTGCTTTT GCAATTCTTC TGCAATCTTC TTATTGGTAA TAGAACCAA GGTACGACCA	1500
TCTGGACCAA CTTTTCACAA AAATTCFACA ACAGTTTCTT CTGCTCAAG TTGTGCTTTA	1560
ATTGCTTTTC CTTCTGCAAT CATCTCAGCG TGAGCTTTT CTTCCGATTT TTGTTTACCA	1620
CGAAGTTCAC CTACAGCTTG AGCAGTCGCT TCTTTGGCTA GATTCTTTT GATAAGAAAG	1680
TTTTGCGCAT ACCCTGTTGG TACTTCTTA ATTCGCTT TTTACCTTT TCCTTTAACA	1740
TCTGCTAAAA AGATTACTTT CATCTCTCTT TCTCCTTTT CTTCACTTCA TTAAATACAA	1800
TTTCTGTCAG TTTTTCACCT GCTTCTGACA AGGTTACATC TTAAATTTGA GCTGCTGCCA	1860
AATTAAAGTG GCCTCCACCG CTAACCTCT CCATAATCCG TTGTACATTC AGTTTACTAC	1920
GACTTCGAGC TGAGATAGAG ATAAATCCTT GTGTATCTT CGCAAGAACA AAACCTGCTT	1980
CAATACCTGA CATGGCTAAC ATGGCATCTG CTGCCTTACT AATAACAACT GTATCATAGC	2040
ATTCATGTC CTTAGCTCT GCTATTAGTA CATCTGAACC TAATTTACGC CCCTGTAAAA	2100
TAAGTTCATT GACCTCACGA TATCTTCAA AATCTGTCGC AGCGATTTCC TGGATAGCAA	2160
TACTATCACT TCCGCGCGTT CTGAGATAGC TAGCAACATC AAATGTCCGA CTAGTTACTC	2220
GCGAGGTGAA ATTTTGTAGTA TCCAACATCA TACCAGCCAT CAAGACACTT GCTTGATAC	2280
GACTCAAACG ATTTTCTTA GAATCTGGA ACTGAATCAA TTCCGTTACC AACTCACTGG	2340
CACTACTTGC ACCACTTTTC ATATAAGTAA TAACCGCATT ATCTGGAATA TCCTGATCCC	2400
TTCTATGGTG GTCAATAACA ATGGTTTGGG TAAATAAATC ATAAATTTCT TTTGATAATG	2460
TTAAGGCTGT CTTTGAATGG TCTACAAGAA TCAACAAAGA ACGATTGGTC ACCATCCCCA	2520
TTGCATCCTT AACAGACAAC AACTTCGTAA CTCCTTCTTT TTCTATGAAT GAAACAGCTC	2580
GTTCAATATC TGGAGACATT TGTCTTCAT CATAAAGAGC ATAGCTATTT TCAATCACAT	2640
TGCTGGCGAA CAACTGCATA CCTACAGCAG AGCCCAAAGC ATCCATGTCT AAATTTTGT	2700
GACCGACTAC AAAAACCTGA TCTACACTCC GAATCTTATC TGAAATAGCT GTCATCATAG	2760
CGCGGTACG AGTCCGTGTA CGCTTGATTG AAGCAGCAGA CCCACCACCA AAATAAAGTG	2820



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GATTTTTCGT TTCGTCGTTT TCCTTAACAA CCACCTGGTC GCCACCACGT ACTTCAGCCA	2880
AGTTCAAATT GAGCAAAGCA ACTTTCCTTA TCTCATCATG ATTTCCATCG CCATAAGAAA	2940
ATCCCATACT TAAGGTCAAG GGCAACTGTC TCTGTTTCGA CTCTTCTCTG AAAGCATCAA	3000
TAACAGAAAA TTTATCATTC ATCAAGCCCT CAAGCACCGT GTAGTCAGTA AATAGATAAA	3060
ATCGATCCAT ACTTACCCGA CGAGAAAAA TCATGTGTTT TTCTGAAAA TCTGATATAA	3120
AATTAGCTAC AAAACTATTG ATTTGACTAA TATCTGACTC AGAAGTTTCA TCCTCCAAAT	3180
CATCATAATT ATCCACAGAG ACAATCCCAA TCACTGGTCT ACTTGTACC AATTCATCTG	3240
TTATGGCTTG TTCCCTGGAT ACATCTACAA AATACAAAAC ACCGGAAGAA GCATCCATAT	3300
GAACAGCATA ACGCTTCTCA CCAAGCTTGG CATAAGTAGA CGGATTTCTT ACTGAAGCCT	3360
TGATAATCGT TTGAACAGCT TCTAAATCAA AATCACCATC TTCCTTGGTC AAAATCAATT	3420
CAGCATAGGG ATTAACCAC TCAACCTCTC CAGAAGATAA ATTCAATTTC ATAACACCTA	3480
CAGGCATCTG TTCCAATAGA GCTGTCAAAC TTTCTTCCGC TTGGTGGTTT ACATACTGTA	3540
TCTGTTCTAC ATCACTCCTT GTATAATGCA CTCTCAGTTT CTTAAATAAA AAAACATAGC	3600
CTCTACAAA AAGAAACAAA ATTAACACCG TCAACAGATT ATTATTAACA AAAATAATGA	3660
AAGTGATAA GACTCCAAAC GCAATCAATC CTACTAGAAT AGGAAAAATT GGACTTACAT	3720
AAAAATTTT CATTCAAAC CTCTGGCAC CCATTATACC ATAATACCCC TCAAAAAGCG	3780
ACTTTTTTAA AGTGTAATCA GTAATTCTAT CAATTATAAG AAAAAGGTAG TTTACAATTC	3840
AGTAAACCTA CCTTTACACA TATTGAAATT AAGATTCTTT AACCTCTAAC AAACCAATTT	3900
CGCCATCCTC ACGACGATAA ATCAGATTGG TTGTCTGATC TTCAACATCC ACATAGATAA	3960
AGAAATCATG CCCCATAAA TCCATTTGTA GAATTGCTTC TTCCAAATCC ATTGGTTTTA	4020
AATCAATTTG TTTTGAACGA ACACTTTAG ACTGGACAAT ATTTGAATCT TCCACCAAAG	4080
CATCTGTAAA TAATTGACCA GTTGCTACCT TATTTTTATT TTACGCTCG ATTTTGTGTT	4140
TATTTTTACG AATCTGACGT TCAATTTTAT CAGTTACAAG GTCAATTGAA CCATACATAT	4200
CTTGAGATAC ATCTTCTGCG CGGAGAGTAA TAGATCCAAG CGGAATCGTT ACTTCCACTT	4260
TAGCCGTTTT TTCACGATAA ACTTTTAAGT TAATTCGGGC ATCCAACCTT TGTCTGGTT	4320
GGAAGTACTT TTCGATCTTT TCGAGTTTAG AACTACATA ATCAGGAATT GCTTCTGTTA	4380
CTTCTAGGTT TTCACCACGG ATACTATATT TAATCATATG AGTACCTTCT TTCTAAACAT	4440
TTTTGTTTTT ATGATTTTAT TATAACGCTT TCATTCTATT TTTGCAAATT TTTCTCTCAT	4500
CTTACAAGGG AAAATGTTTT TACATCCTTA GCACCAGCTT CTTCCAACAG TTTCTTAACA	4560

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CGATTTATAG TTGCTCCTGT AGTATAGATA TCATCTATAA GTAGGATTTT TTTAGGAATA	4620
GTGACTCCAC TTTTAATAAA GAAAGGAAGT TCTGTCCCCA AGCGCTCTGA ACGATTTTTA	4680
GAAGAACTGG CTCTCTCTTC TCTTTTCTCT AATAAATCCA GATACTCAAA GCCTGCTGCC	4740
TCTACCAAGC CCTCAACCTG ATTAATCCT CTATTAGCAT ATCTATCAGG ACTTAGGGGA	4800
ATTACAACAA ATTGATACTC TTTGTACTTT TTCAACTCCT CACTTAAAAA TGAAGCGAAA	4860
ACTTTTCTTA ACAGGAAGTC TCCATCAAAC TTATACCGAC TGAAAAATC CTTCATAGCT	4920
TGATTGTAAG TAAAAATCGC TCTATGACTG ACTTCAACTC CCTCTTTACA CCAAAGTTGA	4980
CAATCTTGAC ACTTTGTTGA CAACTCTGTT TTCATACAAT TTGGACAGTT CTCTTCCCCA	5040
ATTCTTTTCAA AAGTAGAATC ACAGTCTGAA CAAAGACAAG AGTCATCATT CCTCAGAAGT	5100
AAGAGACTAC TAAAGTTAA AACAGTCTTC ATAGTCTGCC CACATAACAA GCACTTCATA	5160
GACCAGCCTC CTTATTCATC ATCTGAATTT CCTTAATCGC CTTCTTGATT GAAGCATTTA	5220
ACCCATCATG GAAGAAAAGC AAATCTCCTG TCGGTCTATC CATGCTTCGT CCAACTCGTC	5280
CACCAATCTG AATCAAACTA GACTTGGTAA ACAACGATG ATTGGCCTCT ACTACGAAAA	5340
CATCCACACA AGGGAAGGTA ACTCCGCGCT CCAAGATTGT CGTACTGATA AGTATTGTCA	5400
GTTCCTCCATC TCGAAAAGCT TGTACTTGCT CTAATCGATC CTCTGTTACA GAAGATACAA	5460
AGCCAATTTT CTCATTTGGA AATGCTCCT GTAAGATTTC TGCTAACTGC TCCCCTTTCT	5520
TAATTTCTGA AGCAAAAATG AGTAACGGAT AAGCTGTCTT TCTCTGCTTC TCAATATAGG	5580
ACTTTAACTT TGGTGACAAA CGATTCTGT CTAAGTAGCG ATTAAAAATCC GATAACCAAA	5640
TTGGTTTTGG AATAATCAAC GGATTTCCAT GAAACCGTCT CGGTAAATTC AGTCTTTTTA	5700
GTTCCTCTAA ACGGACCTTT TTATCTAACT CATTGGTCGA AGTCGCTGTT AAAAAGATTC	5760
TCAATCCATT CTCCTTTACA CTATTCTTGA CAGCGTGGTA AAGCATGGGA TTATCAACAT	5820
AAGGAAAAGC ATCTACTTCA TCCACTATCA GCAAATCAAA AGCTTGATAA AACTTCAATA	5880
ACTGATGGGT TGTGCAACA ACTAGTGGTG TTCGAAAATA AGGTTCCGAT TCTCCATGTA	5940
GCAAAGCTAT CCCGCAAGAA AAATCCTGTT GCAGGCGCTT GTACAGCTCC AAACAAACAT	6000
CTATGCGAGG ACTAGCCAAA CACACTGCAC CACCCGATT GATCACTTTA GCCACTACTT	6060
GATAAATCAT TTCTGTCTTT CCAGCTCCTG TTACCGCATG AACTAAGGTT GGCTTTTGCT	6120
TGTCTACTAC TTGAAGCAAT CCTCTGACA CCTTCTCTG AAAAGGAGTT AATTGGCCGC	6180
GCCATTTGAG AACATCTTGC TTTGGAAAAT CCTCCTGCGG AAAATAGTAT AAAGTTTGAT	6240
CACCTTCTGAC TCGCTTCATC AGCAAGCACT CTCGACAATA GTAAGCACCG ATGGGCAAAT	6300
ACCATTCTTC TAGAATAGTA CTATTACAGC GTTGACAGAA AAGTTTCCCC TTCTCCTTTC	6360

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TCATFGCTGG AAGTTTCTCC GCCAACTGAC GTTCTTCTTC TGTTAATTCA TTCTCAGTAA	6420
ATAAACGACC GAGATAATCT AAATTTACTT TCATACTTCT TTATTCGTAA AAAC TAGCAC	6480
TTTAGATGAT TTTT TAGTAC AATTAAATCA TGGAATTTAG GACAATTAAA GAGGACGGTC	6540
AAGTCCAAGA AGAAATCAAA AAATCTCGCT TTATCTGCCA TGCCAAGCGT GTTTATAGCG	6600
AAGAAGAGGC TCGTGACTTC ATTACTGCCA TCAAAAAAGA AACTACAAA GCGACACATA	6660
ACTGCTCTGC CTTCAATTATT GGAGAACGTA GTGAAATTAA ACGTACAAGT GATGATGGTG	6720
AGCCTAGTGG TACTGCTGGT GTTCCCATGC TTGGGGTACT AGAAAATCAC AATCTCACCA	6780
ATGTCTGTGT GGTCTGTACA CGCTACTTTG GTGGTATTAA ACTAGGCGCT GGAGGACTAA	6840
TTCTGTCTTA CGCCGGCAGT GTCGCCCTTAG CTGTCAAAGA AATTGGTATT ATTGAAATAA	6900
AAGAACAGGC TGGCATTGCT ATTCAAATGT CTTATGCTCA GTACCAAGAG TACAGTAACT	6960
TCCTTAAAGA ACATGGTCTC ATGGAGCTGG ATACAAACTT TACAGATCAA GTCGATACGA	7020
TGATTTATGT TGATAAAGAA GAAAAAGAAA CTATTAAAGC TGCACTTGTG GAGTTTTTTA	7080
ATGGAAAAGT CACTTTAACT GACCAAGGTT TACGAGAGGT TGAAGTTCCT GTAACTTAG	7140
TGTAACAAT GAATAATACA GCGTTTCGTT GACATTCTCA CAACTACTTT AGCGAGCAAA	7200
ATAAAAAGAG GCGTACCAA ATATACTAGA AAATGAAGCA ATTCAAACGA AACCTGATAT	7260
CGTTTTCCTT CACACCTATT TACTAGAATT AGCTGAACGC AATCACTTGA AAATTAATGA	7320
CTTTGATCTA TGATATATAG AAATGGTATG GATAGCGTTA TACTAAAGAT ATCTTATACA	7380
AAGAGGTATT CATATGTCTA TTTATAACAA CATTACTGAA TTAATCGGTC AAACACCGAT	7440
TGTTAAACTT AACAACATCG TGCCAGAAGG TGCTGCAGAC GTCTATATAA AGCTTGAAGC	7500
ATTTAATCCT GGTTCATCTG TAAAAGACCG TATTGCCCTT AGCATGATTG AAAAAGCTGA	7560
ACAAGATGGT ATTCTGAAAC CTGGTTCTAC TATTGTTGAA GCAACAAGTG GAAACACCGG	7620
TATTGGACTT TCATGGGTAG GTGCTGCTAA AGGGTATAAA GTCGTCATCG TTATGCCTGA	7680
AACTATGAGT GTAGAACGAC GTAAAATTAT CCAAGCTTAT GGTGCTGAAC TCGTCCTAAC	7740
TCCTGGTAGC GAGGGAATGA AAGGTGCTAT TGCTAAGGCT CAAGAAATCG CTGCTGAACG	7800
TGATGGTTTC CTTCTCTTC AATTGACAA TCCAGCTAAT CCAGAAGTAC ACGAAAGAAC	7860
AACAGGAGCT GAGATACTAG CTGCTTTCCG TAAAGATGGA TTAGATGCCT TTGTTGCTGG	7920
AGTAGGTACT GGTGAACGA TTTCTGGTGT TTCTCATGCA CTCAAATCAG AAAATTCTAA	7980
CATTCAAGTT TTTGCAGTAG AAGCAGATGA ATCTGCTATT CTATCTGGTG AAAAACCTGG	8040
TCCTCACAAA ATTCAAGGTA TCTCAGCTGG ATTTATTCTT GATACACTTG ATACTAAAGC	8100

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CTATGATGGT ATCGTTCGTG TAACATCAGA TGACGCTCTT GCACTCGGAC GTGAAATTGG	8160
TGGAAAAGAA GGCTTCCTTG TAGGGATTTC CTCAGCTGCA GCTATCTACG GAGCCATCGA	8220
GGTTGCCAAA AAATTAGGTA CAGGTAAAAA AGTCCTTGCC CTAGCACCAG ATAACGGTGA	8280
ACGTATCTC TCTACAGCAC TTTATGAATT GTAACCGTCC AATAACGAAG TCTATTGAAA	8340
AATCTCCAGA CTAGAGAACT CACGGATAGT TCCTAATCTG GAGATTTCTT ATTTGCACTT	8400
TTCTTGACATA ACTTTAGTCC ATGGTAAATA GGCCTCTAAA ACCTCTTTGT TTACGAGAGT	8460
TTCCACGTTT GGAAGACATT CTAGAAGATA GGATAGATAT TTCTCACTAT TTATAATGGA	8520
TTGAAATAAG ATATGAACAA ATCGATTAGA ACATGATGGT AAAGCGTAAT CCCTTGTTTC	8580
TCAGCTTTCC CAGACAAAAA AGTCCAATAG TAAGTCAGCT GACTATCACT CTCTAGCACC	8640
CTATAAGAAG TTTCATCCGC ATGAAGTAAG GGCTGAGTCA ATAGTCTCTC TCGCAAGAGG	8700
TTATAAAGGG GCTCCAAATA GTATTGACTC GTCTTGATAT GCCAATTAGA GATTTCTTA	8760
CGTGTGATTG GTAAACCCAT CCTAGCCCAA TCTTCTTCTT GCGGATAATT GGGTACCTTC	8820
AGATTAAACT TCTGATGGAT GGTGTGAGCG ATAATAGAAG CTGAGCCAAA GTTATGCGCT	8880
AAAGGGGCTT TAGGAATAGG AGCTTTCACA AGCTTATCCA GATGATTATC TTTTACTCGT	8940
TATGGACAAAT GCTATATGGC ATAAATCAAG TACCTTAAAG ATTCCGACTA ATATTGGCTT	9000
TGCATTTATT CCTCCATACA CACCAGAGAT GAACCCCAT TGAACAAGTGT GGAAAGAGAT	9060
TCGTAAACGT GGATTTAAGA ATAAAGCCTT TCGAAGTTG GAAGATGCA TACAAGGACT	9120
GGAGAAGGAG GTGATAAAGT CCATCGTTAA TCGGAGACGG ACTAGAATGC TTTTGTAAAA	9180
CAGATGAGTA TAAAAAGAAA GTCTCATTT CAATAGAAAT CACGACTTTC TGATGAATTT	9240
ATAGTAAAT GAAATAAGAA CAGGATAGTC AAATCGATTT CTAACAATGT TTTAGAAGCA	9300
GAGGTGTAAT ATTCTAGTTT AAATCCACTA TATTTGGGGA GTGATAGAAA AGCCCTTCAT	9360
CAGCCAATCT ACTTGTTTCA GTGCGAGAGC TTTGACATCC TTTTCTGTAC TGGACCAAGT	9420
CAGTTTTCGG TTCTCAAAGC GTTTATATAA TATCCAAAAT CCTTGACCAT CCCAGTAAAG	9480
AACTTTAAAG CGGTCTTTAC GTCCACCACA AAAGAGAAAG ACTTGATCGG AGAAAGGATC	9540
CAATTCAAAG TGGGTTTAA CTACATAGGC TAATGAGTCT ATTCCCTGCC TCATATCTGT	9600
CTTGCCACAA ACAAGGTGAA CTTGACCTAA ATCACTTAGT TGAATTATCA TAGTACAATA	9660
CCTTCTCTCC GATAATTATT TTTTATCTGG TATACTGGAA GTTGGGGAAT TAGGATAGAT	9720
ACCTTGTTAT GACGCGCTTA CTATGAATTT GAAGTATAGT CTCCTAAATG CACTTAGCCC	9780
TTATTATAGG GCTTTTGTG TTAATTATTC TAATCGAGTG AGACTGGGGA AAAACAATT	9840
TCAGGAAAAA TCTAAGCCCT ATACAAAAA GGAAGCAATT TGCTTCTTT CTATTATTAG	9900

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TTATTCAAGG CTGCTGCCAT TGTAGCTGCA ACTTCAGCTT CGAAGTCGTT TGCAGCTTTC	9960
TCGATACCTT CACCAACTTC AAAGCGAGCA AACTCAACTA CCGAAGCGTT AACTGATTCA	10020
AGGTATGCTT CAACTGTCTT GCTGTCTATCC ATGATGTAAA CTTGTGCAAG AAGTGTGTAA	10080
GCTTGGTCAA CTTTAGTGTT ATCAAGCATG AAGCGATCCA TTTTACCTGG AATAATTTTG	10140
TCCCAGATTT TTTCTGGTTT GCCTTCTGCA GCCAATTGAG CTTTGATGTC AGCTTCAGCT	10200
TGAGCAATAA CATCATCAGT TAATTGAGCT TTTGATCCAT ACTTCAAGTG TGGAAGAGGT	10260
GGTTTATTAA CCATGTCAGC GCTTTCGTTG TCTTGGTCTA TAACGTGATT CAATTGTGCC	10320
AACTCATCTT TAACGAATTG CTCATCCAAT TCTTTGTAAG AAAGAACTGT TGGTTTCATC	10380
GCTGCGATGT GCATTGACAA TTGTTTAGCA AGTGCTTCGT CTCCACCTTC AACAACTGAA	10440
ATAACACCGA TACGTCCACC GTTATGTGG TATGCTCAA AGTGTGTGC GTCTGTTTTT	10500
TCAATCAATG CAAAGCGACG GAATGAGATT TTCTCTCGA TAGTTGCTGT TGCAGATACG	10560
TATGCAGCTT CAAGAGTTTC ACCTGAAGGC ATTATCAAAG CAAGAGCTTC TTCGTTGTTA	10620
GCAGGTTTTC CTTGAGCAAT GACTTTAGCT GTAGTATTTA CCAATTCAAC GAATTGAGCG	10680
TTTTTTGCAA CGAAGTCAGT TTCAGCGTTT ACTTCAATAA CTGCTGCAAC ATTACCGTTA	10740
ACATAAACAC CAGTCAAACC TTCTGCAGCA ACACGGTCAG CTTTCTTAGC TGCCTTAGCC	10800
ATACCTTTTT CACGAAGCAA TTCAATCGCT TTTTCGATGT CACCGTCTGT TTCTACAAGC	10860
GCTTTTTTAG CGTCCATAAC ACCGGCACCA GATTTTTTAC GCAACTCTTT TACAAGTTTA	10920
GCTGTAATTT CTGCCATTTT AATTCTCCTA TATTTTTTGA AAATAGGAGA GCGCGGCTAA	10980
GCCCCGCCCTC CGG	10993

## (2) INFORMATION FOR SEQ ID NO: 16:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 8411 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 16:

CGACGGGGAG GTTTGGCACC TCGATGTCGG CTGTCGCAT CCTGGGGCTG TAGTCGGTCC	60
CAAGGGTTGG GCTGTTGCC CATTAAGCG GCACGCGAGC TGGGTTGAGA ACGTCGTGAG	120
ACAGTTCGGT CCCTATCCGT CGCGGGCGTA GGAAATTGA GAGGATCTGC TCCTAGTACG	180
AGAGGACCAG AGTGGACTTA CCGCTGGTGT ACCAGTTGTC TTGCCAAAGG CATCGCTGGG	240

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TAGCTATGTA GGGAAAGGAT AAACGCTGAA AGCATCTAAG TGTGAAACCC ACCTCAAGAT	300
GAGATTTCCC ATGATTATAT ATCAGTAAGA GCCCTGAGAG ATGATCAGGT AGATAGGTTA	360
GAAGTGGAAG TGTGGCGACA CATGTAGCGG ACTAATACTA ATAGCTCGAG GACTTATCCA	420
AAGTAACTGA GAATATGAAA GCGAACGGTT TTCTTAAATT GAATAGATAT TCAATTTTGA	480
GTAGGTATTA CTCAGAGTTA AGTGACGATA GCCTAGGAGA TACACCTGTA CCCATGCCGA	540
ACACAGAAGT TAAGCCCTAG AACGCCGGA GTAGTTGGGG GTTGCCCCCT GTGAGATAGG	600
GAAGTCGCTT AGCTTTAATC CGCCATAGCT CAGTTGGTAG TAGCGCATGA CTGTTAATCA	660
TGATGTCGTA GGTTCGAGTC CTAAGGCGG AGTAATGAT AAAAGGGaAC ACAGCTGTGT	720
TCCTCTTTTT GTATCAATTT GTATCACCAA GCATTTTCAT AAGGAAGTCT GTTATTTCTT	780
GAGAAGTTTC TTTTTTCCA TGTGCAATCC AAGTTTGCCA GACACCAAAA AGTGATGAG	840
TTAGATAGAT GCTACTATAT TCTAATTCAG TGGTATTTAG ATTCAAGTGC ATAAATCGCT	900
TTTGTAATC TGTACTAAGC ATGATATGAA GTTTATTTTCG TAAGAAATTT TGGATTTCTT	960
TAGTCCCATT TTCAGAAAGA AGGGCAGCCA GAAGTGGTTC TGAAGTCTAGA TATTCAAAAA	1020
CTTCTAAAT AGCGTCTCTT TTGTGATGAG CATGTTTTTG AAAAATATAT TCAAATGTAT	1080
GGAATAGCTT GCTTTGATAG TGCTCAATCA TATCATACTT ATCCTTATAG TGAGTATAGA	1140
AGCTGGAACG ACTAATTCGG GCTTTTTCTA CTAATTTGAC AGTAGAAAT TTATCAAATG	1200
GCTGTCCAT CAGTAATTGT ACCATAGCAT TTTCAATAGT TCGCTTTGTT TTTAAGCGTT	1260
TGTTACTTTC TTGCATATTT CCTCCTTGTA AACAAATTAG ACTATATGTC TAAAAATAGA	1320
TTTTTTATCT TGTAATTTAG ATTTTTTAAT GTATAATCTA TTATATCAAA ATTTTAGACA	1380
ATATGTTTAA AAAAGGAGAA ACTAAGTTTA AAGAAATGGA AGCAATTTAA AAAAAACCA	1440
CCTTTATTAT TGTGATGATC GGGATTTCTC TTATTCAGTA TCTGTACAAT ATCATATTTT	1500
TGTATCAAT GTGGGATCCA TATGGGCAAT TGTCTGACTT ACCTGTGGCA GTTGTAATA	1560
ATGATAAAGA GGCTTCCTAT AATGGTAATA CTATGGCAAT AGGAAAAGAC ATGGTGTCCA	1620
ATTTAAAGA AAATAAAACC TTGGATTTTC ATTTTGTAGA TGAAGAGGAA GGAAAGAAGG	1680
GATTGGAAGA TGGCGATTAC TATATGGTAG TGACTTTACC AAGTGATTTA TCTGAAAAAA	1740
CAACTACATT ATCCAATATT CAATCGACAG CAGCTTATCA ATCATTGACA AGTGAGCAAC	1800
AAACTGAGAT AAGTGATTCT GTATCTCAAA ATTCAACTGA TAGTATTCAA TCGGCTCAGT	1860
CAATTGTAGC TTTAGTACAA GATTACAGG GAAGTTTAGA AAAGTTACAA AATCAATCTT	1920
CTAATCTTTC GACTTTAAAA AATCAATCTA ATCAAGTATC ACCTATTACT TCTACTTCTT	1980
TGATAGGATT GTCAAGTGA TTAACAGAGA TACAAGGAGA TGTACTAGC AAATTAGTTC	2040

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CTGCCAGTCA GTCGATTGCA TCAGGTGTAA ACGCATATAC TACAGGTGTT GATAAAAGTTT	2100
CTCAGGGCGC AAGTCAACTA AGTGAAAAAA ATGCCACCTT GACAGGTAGT TTGGATAAAC	2160
TAGTTTCAGG CTCAAACACC TTGACACAAA AATCTTCTAG ATTGACAGCA GGAGTTGGTT	2220
AATTACAATC AGGATCTGGG CAATTAGCAG ACAAATCCAG TCAGTTACTT TCAGGTGCTT	2280
CTCCATTAGA GAATAGAGCT AATAAATTGG CAGATGGATC TGGGAAACTA GCAGAAGGTG	2340
GAACAAAGTT AACTTCTGGA TTGGAAGATT TACAGACAGG ACTTGCTTCT TTAGGACAAG	2400
GACTAGGTAA TGCTAGTGAT CAACTCAAAT CAGTATCAAC AGAATCTAAA AATGCAGAGA	2460
TTTTGTCAAA TCCACTCAAT CTTTCAAAAA CAGACAATGA TCAAGTTCCT GTAAATGGAA	2520
TCGCAATAGC TCCTTATATG ATATCAGTTG CTCTTTTTTT GCAGCAATAT CAACAAATAT	2580
GATATTTGCG AAATTGCCTT CAGGACGTCA TCCAGAGAGC CGTTGGGCTT GGTGAAATC	2640
TTGAGCTGAA ATAAATGGTA TTATAGCTGT TTTGGCAGGA ATTTTGGTAT ATGGAGGAGT	2700
TCAGCTTATT GGTTTAACTG CTAATCATGA GATGAGAATA TTTATTCTCA TCATCCTAAC	2760
AAGTTTAGTA TTCATGTCTA TGGTGACCAC TTTAGCAACG TGAATAGCC GTATAGGAGC	2820
TTTTTCTCA CTATTTTGC TTTTACTACA GTTAGCATCA AGTGCAGGTA CTTATCCACT	2880
TGCTTTGACA AATGATTTCT TTAGATCTAT TAATCCCTGG TTACCAATGA GCTATTCAGT	2940
TTCGGGATTA CGACAAACAA TCTCTATCAA CAAGTCATT TCCTAGCTGT CATACTAGTT	3000
CTATTTACTA GTTTAGGTAT GCTAGCCTAT CAACATAAGA AAATGGAAGA AGATTAAAAA	3060
AATCGACCGA TTAACCTGGT GATTTTTTAT GCCTTAGATG ACTTTCGTCT GTGATTATAG	3120
ATTCCAAATA GTAAGAGAGA AGTAAAGGAA CAGATTGCTC CAGTAATAAA ACCATTGGGA	3180
ATGAAGGAAA GTGTAATAGT TCCTTTCCCC TTGGGAATGT CAACTTTCAT AAATCCAGTT	3240
TGAGCTTGTT TAATTCTAT TTTCTTACCA TCTTGGTAGG CAGACCAACC TTTGTCATAA	3300
GGAATGGTGA AGAAAATAGA TGTATCTTGT TGGACATCAT ATGTAGCAAA AACCTTGTTT	3360
TTAGAAGTTG ATACTGTGAC AGGTGTTCT TTAATTTTTT GAATTGCCTC GGTGAAAGTT	3420
TTGGTATCTA AACGATAGAA GGTAGGAGAT TCAAATGATA CTTGTGAATT TCCAGGGAAA	3480
CTAACATTGA TATTGAAAGT TTTTCTCTCT TTAGTATATC CTAGATTAAA GAAGGAGAAG	3540
ACATTATCAG TTGTAAAAGT CTTTTTTTCA CCATTTACAA GGATGTCAAC CTTCTTTTGT	3600
TTATCCTTAG AAAAGTGAAG GTTTATGAAA GAGAGATAAA CTTGGCTGTT TTCTGGAAC	3660
TCAATTTGAT ACTGGATTGC TGCATCTTCA TTTGAAGAAC TTGTGACACT AATCAAAATCA	3720
TTAGTATTTT CTATTTTTTC TGTTTTTTCA TAAGGTATTG GAGAAAAATA ATCAAAATG	3780

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ACGTTAGCAA GTTGATTAA AAATGAGGCC TGATTATCCA AGGTATGTTT ATTGAACCTG	3840
ACATCATGT AAACAGATTG ACTCGCAACT GCAATCGGAA GAGAGTATTG ATTTTCATAT	3900
AGGGTAAGAT TATCTTTTGG ATAGATATCT TTAAAGCCAT ACTTATCAAT AGGACTGTCT	3960
GAGATATTGT ACTGGATACC AAATAAACTA TCAGCCAAAA TACTATTATT TGCATATCGG	4020
AGATTGAGAT TAGTCCCAGA GGATTTAAAA CCAAGTTTAT CTAAAGTAGA GCTTGATGAA	4080
CGATTCGAA CAGATGAAAA TTGAGAGATT CCATTGTAGT TGAATTCAT ACTGTCATTT	4140
CCTGTCTGAG TTTGTAGTTT TTCAGTACGA GTAAATGAT TTCCAATATA TGTGAGAAA	4200
GATTCCATAG CTGGGATATC TCGACTATAA GCACTTCGAG AAGCAATCC CCATTCTTA	4260
GCAATCCGT CCATTGAGA TGAAGCATTT AAACATCTT CAACCAAGT AAATAAGAG	4320
ATTAGAATGG CAAATAGATT CACAGATATA AACTTTTGA TAACTGCAAG GAGTAAAGA	4380
GAATAGACAA CCAAAAATTC AAGAGTAAGC AGAATATTCA AATCTGTAA AAAAGAATA	4440
TGCGATTTTA GATAGATGGT AGCTAAAAAT CCTGCTACTA CAAGAAAAAG CGAACTAAA	4500
AAATTCGAA CTTTAAGTTC TTTCAGACGC TTTAAGACTT CTGCTGCTGT GTAAATTAAC	4560
AAGGTAGAGA AAATCCAAGC ATAGCGATGT AAAACATGT TTGGAGTATG CATGCCTTGC	4620
CAAAATAAGT CAAGAGCTTC TATGTAAAAG CTTGCAATTA GAAATGCAA GAATATTACA	4680
TATATGAGTT TCACGTGAAA CTTAATAGAT TTCAGCGTAA AAAATAAAAT GGTCAAATA	4740
AAGGGAAATA GTCCAACAA AATCATTGGG ATGGCCCAT ACTTTGTTGT GTCAAAGGAA	4800
CCAATGAAT GCTTAGCAA GAGATCAAGA TACCAGCTAC TTTCAGTTTG AAACCTTGTA	4860
ACTTCAGTCA ATTTTCCCC ATGTGTCTGT AAATCAAATA GAGTGGGAAG AGTCATAATC	4920
AACTAGCCA TACCAGCTAA AAAGGAGATA ACTATGAAAT CAAGAACAGA TGATTTTCGA	4980
GTCTTAAAGT CCCACGAAAT TTGACAGAGA TACCAGAAA TAAGAAACAA TACTGTCATA	5040
TATCCAAAT AATAATTTTG AATAAATAAG ATTGACAGAC TTGTAAAGTA CAATAGGAGT	5100
TTCTTTTCAG TTATCAGTAG ATGTAAACCA GTTATAATTA AAGGAATCAA GATAAAACA	5160
TCTAGCCAGG TTTTATCTC TAATTGACTG ACAGTGAAC TCATCAGAGC ATAGGAAGTA	5220
GATAAGGCTA GTTTTAAAA CTGAGGGATA GATTGAAACA ATTTATTCAA ACTAAAAAG	5280
GTGACAGAC CAATCAATCC AAATTTTAAG AGAOTGTCA GATAGATAGC ATCTGGCATA	5340
TTCGTTAGAT CAAAAAGTA AACCAGAGGC GCGAGAAAAC TACCAAGTA ATAACATAGT	5400
AGGGCATAGA AGTTTAGCCC TAGACCACTT GTAAAGGTGT AAAACAGATT ACTATTCCA	5460
TGTAGGATAT TTCGTAAGGC TACATCAAAA ATAACGTATT GATGAAAGCC ATCTCCTAAT	5520
AGAGGAGAGT TGTCGCTATT CCAGTAGATA CTTTGAGATA GATATACTCC AGACATAATC	5580



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ACTACAGGAA	TGATGAAAGA	AATAAAATAG	GTTCGATATG	TTTTTAAAAA	TGATTTCATG	5640
TTACCTCGTA	GAATGATAGA	AAACTCAGTT	GGTTAACCCA	ACTGAGTTTT	GAAGTTTAT	5700
TTAGTCTTTC	CAAAGTTCTT	TAACTTTTGC	TTGTACTTCT	GCAITTTCTA	GGAATTCATC	5760
GTAGGTTTCA	TCGATACGGT	CAATGACGCC	ATTTTITAGAT	AAGACAATGA	TATGGTTAGC	5820
CAAAGTTTGA	ATAAATTCGT	GGTCATGGCT	GGCAAAGATG	ATTGATTCTT	TAAAGTTTTT	5880
CAATCCATCA	TTCAAGCTTG	AGATAGATTC	CAAGTCCAAG	TGATTTGTGTG	GATCATCAAG	5940
TACAAGGACA	TTTGATTTTA	AGAGCATGAG	TTTGAAAGC	ATGACACGAA	CTTTTCTCC	6000
CCCTGACAAG	ACATTTACAG	GTTTGTTAAC	TTCTCTCCA	GAGAAGAGCA	TACGGCCGAG	6060
GAAGCCACGT	AGGAAAGTAT	TGTCATCTTC	TTCTTTACTT	GCGAATTGAC	GCAACCAGTC	6120
AAGAATTGAT	TCTCCTCCTG	CAAAATCAGC	TGAGTTATCT	TTTGGTAGGT	AAGATTGACT	6180
AGTTGTAAT	CCCCACTTGA	CAGTTCCTTC	ATAGTCAATA	TCTCCCATGA	TTGCACGAAT	6240
TAATGCAGTC	GTTTGAATAT	CATTTTGTCC	AATAAGTGCT	GTCTTATCAT	CTGGACGCAA	6300
GATGAAACTA	ATATTATCCA	AGATAGTTTC	ACCATCAATC	TTTACAGTTA	AATTTTCTAC	6360
TGTCAGAGA	TCATTACCAA	TCTCACGTTT	CGTTTAAAG	TTGATAAATG	GATATTTACG	6420
ACTAGATGGC	ACAATCTCTT	CTAGCTCAAT	CTTATCAAGC	ATTCTCTTAC	GTGATGTTGC	6480
CTGCCTTGAC	TTAGAAGCAT	TGGCAGAGAA	ACGAGCAACA	AATTCTTGCA	ATTGTTTAAAT	6540
TTTTTCTTCT	GCTTTAGCAT	TACGGTCTGC	TAGCAATTTA	GCAGCAAGCT	CAGAAGATTC	6600
CTTCCAGAAG	TCGTAGTTTC	CGACATAGAG	TTTGATTTTT	CCAAAGTCAA	GGTCGGCCAT	6660
GTGAGTACAA	ACTTTGTTTA	AGAAGTGACG	GTGCTGGGAT	ACTACGATAA	CTGTGTTATC	6720
AAAGTCAATC	AAGAAGTCTT	CTAACCAAGT	AATCGATTGG	ATATCCAAAC	CGTTAGTAGG	6780
CTCGTCCAAG	AGAAGAACAT	CTGGTTTACC	AAAAAGTGCT	TTGGCGAGGA	GAACCTTTAC	6840
TTTTTCACCG	TTGGCCAATT	CGCTCATGTT	TTGGTAGTGT	AATTCCTCTG	GAATGTTTAG	6900
GTTTTGAAGT	AGTTGAGAGG	CTTCACTCTC	TGCTTCCCAA	CCTCCAAGTT	CGGCAAACTC	6960
TCCTTCGAGT	TCGGCAGCAC	GAACCCCGTC	CTCGTCTGAG	AAATCTTCCT	TCATGTAGAT	7020
AGCATCTTTC	TCTTTCATGA	TGCTATAAAG	TTTTTCATTT	CCCATGATAA	CGACATCAAT	7080
GGCACGTTC	TCTTCGTAGT	CAAAGTGATT	TTGACGAAGA	ACAGAGAGAC	GPTCATCTGG	7140
ACCAAGAGAG	ATGTGACCAG	TAGTAGGTTT	GATATCTCCA	GCTAAAAATTT	TTAAAAAGGT	7200
TGATTTTCCG	GCACCATTAG	CACCGATTAA	TCCGTAAGTA	TTTCCTTCTG	TAAATTTGAT	7260
ATTGACATCA	TCAAAAAGTT	TGCGATCACT	AAAACGTAGT	GAAACATCAG	ATACTGTAAG	7320

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CAATGTTTTT CTCCTATATG TGTAATATAT TTATTCTACT AGAAAATACA GAAATATTCA	7380
AATTTTTATT TGCAATTTT GTGTAAATTA TATTTACAGT ATCCTTTACA CAAATCTGTA	7440
AAAAGCAAGG CTGATTTATT TTGATAAATT ACGGTTATTT CATTAAAAAA ATGCTATAAT	7500
TGAAAGGACT ATATCGAAGG AGAACAAAAT GACTAAACCC ATTATTTTAA CAGGAGACCG	7560
TCCAACAGGA AAATTGCATA TTGGACATTA TGTGGAAGT CTCAAAAATC GAGTATTATT	7620
ACAGGAAGAG GATAAGTATG ATATGTTTGT GTTCTTGGCT GACCAACAAG CCTTGACAGA	7680
TCATGCCAAA GATCCTCAA CCATTGTAGG GTCTATCGGA AATGTGGCTT TGGATTATCT	7740
TGCAGTTGGA TTGGATCCAA ATAAGTCAAC TATTTTTATT CAAAGCCAGA TTCCAGAGTT	7800
GGCTGAGTTG TCTATGTATT ATATGAATCT AGTTTCGTTA GCACGTTTGG AGCGAAATCC	7860
AACAGTCAAG ACAGAGATTT CTCAGAAAGG ATTTGGAGAA AGCATTCCGA CAGGATTCTT	7920
GGTCTATCCA ATCGCTCAAG CAGCTGATAT CACAGCTTTC AAGGCTAATT ATGTTCTGT	7980
TGGGACAGAT CAGAAACCAA TGATTGAGCA AACTCGTGAA ATTGTTCGTT CTTTAAACAA	8040
TGCATATAAC TGTGATGTCT TGGTAGAGCC GGAAGGTATT TATCCAGAAA ATGAGAGAGC	8100
AGGGCGTTTG CCTGGTTTAG ATGGAATGC TAAAATGTCT AAATCACTAA ATAATGGTAT	8160
TTATTTAGCT GATGATGCGG ATACTTTGCG TAAAAAGTA ATGAGTATGT ATACAGATCC	8220
AGATCATATC CGCGTTGAGG ATCCAGGTAA GATTGAGGA AATATGGTTT TCCATTATCT	8280
AGATGTTTTT GTCGTCAG AAGATGCTCA AGAAATGCT GATATGAAAG AACGTTATCA	8340
ACGAGGTGGT CTTGGTGATG TGAAGACCAA GCGTTATCTA CTTGAAATAT TAGAACGTGA	8400
ACTGGGTCCG G	8411

(2) INFORMATION FOR SEQ ID NO: 17:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 9064 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 17:

TGCCGTACTC AAGTACAGCC TGCGCTAAGT TTCTAGTTT GCTCTTGAT TTTCATTGAG	60
TATTAGTAAC CAAAATCCGA CCACATAGCC AGCCCCATG AATATAGCCA TTAAAGCTAG	120
CATGGAATTT AGGAAATTAA AAACCACCGC AGATACAAAG GTTAGCACAA AAACATTAAA	180
AGCAATGGTG TCAGAAGCCA AGACTAGAAT ATAGGGTGTG AACCGATCTA AAGTTTGGGA	240
ATCTAGGAAA AATAAGTGT TATACATGAT GACCTCCTCT ATGGCTGAAA AGCAAGCCTT	300

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TTGTTTTTTT ACCCCAAGAC CCTATGTAGA AAAGTGAGCA AAAACGGGAA GGTCGCTACA	360
ATATTATTGA TCACATGCAC CGCATAGGAT GGATAAATGC TCTTGGTATA GCGGGTCAAA	420
CCAGCAAAGA TGATTCCAAC TGTTCGCAAG ACGAAGATAT CTAACAGACT AGGCAGGCTT	480
GAAAAATGAG GGAGAGCAAA TAAAAATAGAA GGAAGAAGCA AATCAAGACC AAATCGCGAA	540
TGCTTAAAGA AAGCATGTTG CAGTAATCCT CTATAAATCA ATTCTTCCAT CAGTGAACC	600
AGAAAGAACA GGGCTATATA AATACCTAGC TCTGCAAAGT TAGTCCCACT ATAACCAATC	660
AATACAGCCC AACCTTCCGC AGTTGACTGA ACATGTTTAG CTGTCTGAAC GTTAAAAGAG	720
ATCTGGAACA CTAGCACTAA TACTGTCAAA ATCGAATACC AAAGCCATT TTTTCTTGGA	780
ATGCCGAAGA GATAACCATG GCCTGTCTTA ACAAGAACCA CAATCATGAC TCCAATAAAA	840
AGTAAACTCA AGATATTTTG AATCCAGAAT AAATGCGCTA TCTGAGAAGA AAATGCCAA	900
TAGTTTTGGA CGATAAGCGT CAGCTGAGAA AGACTAAATA CGAAAAATAA GTAAGAGAAG	960
ACTGCACCTA TTTTGAATAG AAGTTGATAC TTTTTCATAG AAATCCTCCC TACTATGACC	1020
TCACCTTGTC AGGCTCTACT GCTGTAAGAT TAAGAAGACA GTTTGTTTTT TTTAAGGCTA	1080
ACCTGACTAC TAGATAATAG ATACATTAAG GCATTAAAGA CAATGAAAAT ATGTCCATAG	1140
AATAAAATCA ACCTCGCATC CAAACCAAGA TAAAGTTTGA TTATCAAAAA GATGAGCAAA	1200
AGAAATTGAA ACCATAAGGT TTTTCCAAAA ATAAATTTAA AGCGATTTCG AATATCTACT	1260
TCCTTGATTT TTACGCCAC CCCTTTATTA GCAAGAAGGA AAACCTCTGC TTCAAACAAA	1320
CCACTGTAAA GAACAAGCCA CCCAATAGAT ACGATAGAGA TTTGTAAAAA TGTCCCTAAA	1380
AGAATATCCA ACACACTACT CAAGAAAATA ACAAAAAATA ATCTGTATTT CATATTAAAT	1440
ACCTCCATTC ATTTATTTCA CTAACAATTT AATAGAGCCT TCTACTCAA TATCCTGTCA	1500
GAAAGGATA GAAAGCTACT TTTTATAATA CTTCAAGCCC CACATGAGCA GAAGCGTGAT	1560
AAACAAGCAG AGAATACACC TATATAAGCG ATTAGTTGTT GATAGAATTC TGTTTCTGAA	1620
ATACCTCTAT ACAAACAAAT GACAAACATA AAATCTGCCA AGCCGATAAA CATAAGTTGA	1680
TTGGTTCTAG GACTAACCAA ATCATCATTT ACTTATATTT AAGAGTATCT CTTTATTTT	1740
AATGTATGTT AGCACTGAAA AGCAAGACAG GCCAATAATA TTTAAATGA ACAGTAACGG	1800
GGTTAAGTCT CTAAAAAAT TATCTACTGA CACTACAAGA AATACTATAC ATATTATAGT	1860
CGAAACTATC TTTTCTTAT CCATAATTAT TTACTCCTTT CCTAACAAAT CCAGCTTATC	1920
AATCAAGAGC GATTTTAAAC ATAATGTAGC AGCACCCGTT GCAACTTTGA CAAGTTTAGT	1980
ATATCATTGT TTTTAAAAAT TTTTCATCCA AATCTTGAAT TGTCAATCGAA ACATCTTGAA	2040

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TTGTTAAAAA ATTTAAAAAG TAAGCATTAA AAACATACTT TCCTCTTTAT ATTGTATTGA	2100
TACCAACTTG TTTGTAGACT TTTTCATCTG CTATCACATA TCATTTTGAC AGGCGAAACA	2160
ATATTAAAGA AACTCCCCTG TAAATTAAGC TAGCAAATAC AGGGGAGAAA TTTATTTT	2220
AGAGAGTACT ATCCGTATCC TTTTGGGAAG ATTTTGAAAA TATTTTCTTA ATTAAGTCAT	2280
CCATATAAGG ACCAAATATA CCAACTACTA AACCAATAAT AAAACTTTTA AAATCCATAA	2340
TTACCAACCA CATATTGCTG CATAGGCTAC ACCTCCAAGT ATAGCTCCAC CTGCAGCACC	2400
AGTTACACCT ATTCCTATAG CAAATGGTCC CAATAGAAAT GTCAAACCGT TGTGACACAC	2460
CCATCAATTG CGCCATATGC AACCCCTGCT GCACAACATA TTTTCTTCC CCAATCAATA	2520
TCTCCACCTT CAACGCAAGC AAGCATTTCA TTATCCATAA CTGCAAATTG TGACATCATT	2580
TTTGTATCCA TATAGTGTAT CACTTTTCAG TTACGGAACA AGTTTAATAT AAAAATTATC	2640
AAAAAACAT AGGCAATAAA GAGAAAAAT AATTTATCAT AGATTAGAAA TAATATGACA	2700
AAACAATTCA ATGATGTAA TTCAATAGTC TTTGTTTTTT TATCGGAGAT ACTTATGGAT	2760
AGATAAATAA GATAGGTTTG AAAAGCGAAG AGAATAATAA AGAATATAGC CTTCATAAAA	2820
TTTAGCTTTC ATTTTATGA TGTAGCGGTA TAGGCTAAAT ATCCACAAAC CACTGCTCCT	2880
CCAATTCCTC CTATTGCAGC GCCCCATGGT CCTAGAAAGT TCCCATATTT CACTCCACCC	2940
GCTGCACAAC CTAAAGCAGC AACTACAGCT GCTCCTCCGG AATTACCTCC ATAAACCTCA	3000
CTCAGCATTG TTTCATTTAT ATTACAATAA GTATTCATAC AAGTCTCCTT TTATTAATAA	3060
CCACCCGTTG CCCCTGTTAC TCCTGCCCAA AGATCCACAC CAAATTAGC TCCTATGTAT	3120
CCACATGCTC CCATAAATGG TGCTCCAACA CCACTCGCAG CACAAATAGC TGTCCCTAGC	3180
CCCCAGCCAC CAAAAGCAGC ACCACCACCT TCTAAGACAT TAGTTTGCCA ATTATTCTTG	3240
CCTCCTTCAA TACTAGATAA CATAGTTATA TCCATTTCAT GAAATTGTTT CATAATTTTT	3300
GTATCCATGA CAAATACTCT TTTTATTTTT TAATTTTTGT CTTGTTGTAA CTTTGACAAG	3360
TTTAGTATAT CATCGTTTTT TAAAATTTTT CATCCAGATT TTGAATAGTC ATCGAAACGT	3420
CTTGAATTGC AAAAATTACA TTAGACTTCC TGCAAACTA GAATCCTAGT TCATGATTGA	3480
TAATACCAGC ACTCAAATTC ATTCGTAATC CGAAGCGTTT ACGATGACTT CGATAGGTTG	3540
TTGAAAACAT TTAAACGTT TTTACTTTGG CAAAGATGTT CTCAACCTTG CTTCTCTCCT	3600
TAGATAGCGC ATGGTTACAG GCTTTATCTT CAACTGTTAG CGGTTTGAGT TTGCTGGATT	3660
TACGTGAAGT TTGTGCTTGA GGATATATCT TCATGAGCCC TTGATAACCA CTGTCAGCCA	3720
AGATTTTACC AGCTTGTCGG ATATTCTGC GACTCATTTT GAACAACTTC ATATCATGAC	3780
AATAGTTCAC AGTGATATCC AAAGAAACAA TTCTCCCTTG ACTTGTGACA ATCGCTTGAG	3840

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TCTTCATAGC GTGAAATTTC TTTTACCAG AATCATTCGC TAATCTTTT TTTAGGGCGA	3900
TTGATTTTTA CTTCCGTCGC ATCAATCATT ACCGTGTCCT CAGAACTGAG AGGAGTTCTT	3960
GAAATCGTAA CACCACTTTG AACAAAGATT ACTTCAACCC ATTGGCTCCG ACGGAGTAAG	4020
TTGCTTTCGT GAACACCAAA ATCAGCCGCA ATTTCTTCAT AAGTGCAGTA TTCTCGCACA	4080
TATTGAAGAG TGGCCATAAG AAGGTCTTCT AGGCTTAATT TAGGTTTTCG TCCACCTTTT	4140
GCGTGTTTAA GTTGATAAGC TGTTTTTAAT ACAGCTAGCA TCTCTTCAA AGTCGTGCGC	4200
TGAACACCAA CAAGACGCTT AAATCGTGCA TCAGTTAGTT GTTACTTGC TTCATAATTC	4260
ATAGAACTAT AGTAAATGA AATAAGAACA GGATAAATCG ATCAGGACAG TCAAATCGAT	4320
TTCTAACAAT GTTTTAGAAG TAGAGGCGTA CTATTCTAGT TTCAATCTAC TATACTATAC	4380
CATATTTTGT TTCGCAGGA ATCTATTATA AAAGGGTAAG TATTGCAAAA AACTTTACCC	4440
TTTTCTTTTA TACTTCATTA AGCTCTACTT TTTATAATAC TTCAAGCCCC ACATGAGCAG	4500
AAGCATGATG ATTAAGCAGA GAACAGCGCC AATATAAGCG ATTATTTGTT GGTAGGATTC	4560
TCCTGCTGTG ATACCTCTAT ACAACAAAT AATAGACATA AAACCTGTCA AGCCGATGAA	4620
CATAAGTTGA TTGGTCTAG GACTAACCAA ATCATCATCT TCAAACCTCTC TTATCCTCAT	4680
TTCCCTAGTG AGATAACAG TAACCAAAT AGAAGCCAAG TTAATACTA CTAAAAGAAA	4740
TTGGAAGACT ACGGAAAAAT TTAAAACTG ACGAGATAGA AATAGATAAG TAGAAACAAG	4800
CAAGGGCAAC TGACCTAAGA ACAATCTCGC AAGGAAGATG TTCCGTTTTT TAGCAAGAAA	4860
AGTTTTCATT TCTTTTCTCC TTTCTTTTTA TTGATAGCAA AATAGATCAT AACTGCAATC	4920
ACATAGGCTA TGGTATAAAA TAGCTGATAC CAAGCACTCT CCCTAAGCGG ATATAGAAAAG	4980
ATGGACATGA TTAGATACAG AACGAAAATA ATCAATATT TTTTCTTCAT AAGATTTCTT	5040
CCTAAATGTG CGATTTATCT TAGTTGAGCA AGAACATTTA CACTGCTAGT ATAGCACTTA	5100
TTTTGACCTT GGATCACTCA AATCATAAAT GGTCATCAA ACCTCTTGAA TTGTAAAAAT	5160
TAAAAAAGCA AGCATGAAAA ACATACTTTC CTCTTTATAT TGTATTGATA CCAACTTGTT	5220
TGTAGACTTT TCATCCTGCT ATCACATATC ATTTTGACAG GCGAAACAAT ATTAAAGAAA	5280
CTCCCCTGTA AATTAAGCTA GCAAATACAG GGGAGAAAT TATTTTTTAG AGAGTACTAT	5340
CCGTATCCTT TTTGGAAGAT TTTGAAAATA TTTTCTAAT TAAGTCATCC ATATAAGGAC	5400
CAAATATACC AACTACTAAA CCAATAATAA AACTTTTAAA ATCCATAATT ACCACCAACA	5460
TGTTGCTGCA TAGGCTACAC CTCCAAGTAT AGCTCCACCC GCAGCACCAG TTGCTGCACC	5520
TTGCCATGTT CCTGTTTTAA TGCCTAGTTG AAGACCTCTT GCTGCTCCTC CTCCAACACC	5580

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TGCTTTGGCA AAATCTCCCC AATTGCATCC GCCACCTTCA ACGCAAGCAA GCATTTTCAGT	5640
ATCCATAACA GAAAATTGTG ACATCATTTT TGTATCCATG ACAAATACTC CTTTTTTAAA	5700
AAACTAAAAA AAATCAGAAT AGAATCCTCA TAATTTTACT ATAAGTCTTA CCAACTTAGT	5760
CCCAATTTAT CACCAACCAT ACCTCCTAAG CATGTTAATC CACCCCAAT TGCACCAATG	5820
TGTGCTCCAA CAAATGCACC AGCAAGTCCA GCTACTCCTA AAGTGGCCAA ACCTGCTCCA	5880
GTTCCACCAG TTATAATTCC CGTAGTGAAT CCTGTAATCA GTGCATTTTG ACAATCAGTG	5940
GAGCTATACC CCCCTTCAAC TTTCGCAAGC ATTTTCAGTAT CCATAACCTC TAACTGTGAC	6000
AACATTTTGT TATTCATGAT GAATACCTCC TTTTATTTT CAATTTGTTA CCAAAGTCTT	6060
AAATTCAATA AACAAATAGA TTTTATATAG TATCTTTTGT ATTTTCTTAA AAAAGTATAT	6120
ACGCTACTA TCTTCTTAAA GGTAGCAGTA CCTATTTTGT AGTCTAAGAT TTCAATAATC	6180
TTGAGTATCT AAAATATCTT AATTTCTGTA TTCTCCTTGC AATAAAAAGT TTTACTATAC	6240
TATTTATTAA CTTCGAGAAA GCAAAAATA TTAGTAAATA ATAGTTTATA GTTAAGTTT	6300
TTATTCCTAC CAATCCATCA ACTAAGTAAA GCATCAACGA TTACATAAAC GATTGATAAT	6360
ATAATTAAAA TTTTGCTAAC TATCTTATTC TCATCATTCT TAGATAAATT TGATATTTTG	6420
TAACTAAGTA AATAAGACAG TAAATTAATA GCGATAATAA TACTATATTT AAGAAATCATA	6480
ATCTTACAAA GAGGACATAA TTCCTGAACC TACACAAATA AGTGTGTGCT CTCCCCAGT	6540
TATCGGACCA GTCGCAGCAG CTAATAGTAC TGCTCCAATA CAACCACCGA TTGCAGATCC	6600
TAAATGCGCT CTTCCTCCAC TAACTATTTT GAGTTCTTCA TTATCCATAA CAGAAAATTG	6660
TTCCATCATT TTTGTATTCA TGACAAATAC TCCTTTTTTC TTTTATTATT TTTGTCTTGT	6720
TGTAACCTTG ATAAGTTTAG TATATCATCG TTTTITAAAA TTTTTCATCC AGATCTTGAA	6780
TTGTCATCGA AACGTCTTGA ATTAGCTTTT TTATTTCAGG CCACCTCTAA ATGTTTAAAA	6840
AAAATAATTT CTAATCACTT TTTTACCATT CAGGAAGTTT TAATGACTAT TCAAGATTTC	6900
ATAAAATATG AACTTAGTTT TATGACATAA TAGACCTATC CACTATATGA AAGGAATTGC	6960
CAATGACTTC TTATAAACGT ACATTTGTTC CTCAAATAGA TGCGAGAGAC TGTGGTGTCTG	7020
CTGCCCTAGC CTCGATTGCT AAATTCATG GTTCAGATTT TTCTCTAGCT CACTTGAGAG	7080
AACTTGCAAA GACCAATAAA GAAGGGACGA CTGCTCTTGG CATTGTAATA GCCGCTGATG	7140
AAATGGGCTT TGAAACAAGA CCTGTTCAAG CAGATAAAAC GCTCTTTGAC ATGAGTGATG	7200
TCCCCTATCC ATTTATCGTT CACGTTAACA AAGAAGGAAA ACTCCAACAT TACTATGTTG	7260
TCTATCAAAC AAAGAAAGAC TATCTGATTA TTGGTGATCC TGACCCTTCT GTAAAAATCA	7320
CTAAATGTC AAAAGAACGC TTTTCTATG AATGGACTGG AGTAGCTATT TTTCTAGCTA	7380

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CCAAACCCAG CTATCAACCC CATAAAGATA AAAAGAATGG TCTACTAAGC AAGCTTCCTT	7440
CCTCTGATTT TCAAACAAAA ATCTCTCATT GCTTACATTG TTCTCTCAAG CTTATTGGTC	7500
ACTATTATCA ATATAGGTGG TTCTTACTAT CTCCAAGGAA TCTTGGATGA ATACATTCCA	7560
AATCAGATGA AATCAACTTT AGGAATCATC TCAGTTGGTC TGGTTATCAC CTATATCCTC	7620
CAACAAGTCA TGAGCTTCTC CAGAGATTAT CTCCTAACCG TTCTGAGTCA GAGATTAAGT	7680
ATTGATGTGA TTTTATCCTA TATTCGCCAT ATTTTGAAC TTCCCATGTC TTTCTTTGCG	7740
ACACGTCGTA CAGGAGAAAT CATTTACGA TTCACAGATG CTAACCTAT TATAGATGCC	7800
TTGGCTTCTA CCATTCTTTC TCTTTTCTG GATGTTCTA TTCTGATTCT TGTAGGAGGC	7860
GTCTTACTGG CAAAAACCC TAATCTCTTC CTTCCTTCTC TTATTTCCAT TCCTATATAC	7920
ATGTTATCA TCTTTCTTTT TATGAAACCT TCGAAAAA TGAACCATGA TGTCATGCAA	7980
AGTAATTCTA TGGTTAGCTC TGCCATTATC GAAGATATCA ACGGGATTGA AACTATAAAG	8040
TCGCTCACGA GTGAAGAAAA TCGCTATCAA AATATAGACA GCGAATTTGT AGATTATTTG	8100
GAAAAATCCT TTAAGCTCAG TAAATATCT ATTTTACAA CGAGTTTAA GCAGGGAACA	8160
AAATTAGTTC TGAATATCCT TATCCTATGG TTTGGCGCTC AATTAGTCAT GTCAAGTAAA	8220
ATTTCTATCG GTCAGCTGAT TACCTTTAAC AACTTTTTT CTTACTTTAC AACTCCTATG	8280
GAAAATATTA TCAACCTCCA AACCAAACTC CAATCTGCGA AGGTCGCTAA TAACCGTTTG	8340
AACGAAGTCT ATCTAGTCGA ATCTGAATTT CAAGTTCAAG AAAACCTGT TCATTACAT	8400
TTTTTGATGG GCGATATTGA ATTTGATGAC CTTCTTTATA AGTATGGTTT TGGATGAGAT	8460
ACCTTAACAG ATATTAATCT CACGATTAAA CAAGGAGATA AGGTTAGCCT AGTTGGAGTT	8520
AGTGGTTCTG GTAAACAAC TTTAGCCAAA ATGATTGTCA ATTTCTTTGA ACCCTACAAA	8580
GGGCATATTT CCATCAATCA TCAGGATATT AAAACATTG ATAAAAAGT CTTGCCCGT	8640
CATATTAATT ACCTACCCCA ACAAGCCTAT ATCTTTAATG GCTCTATTTT GGAAACTTA	8700
ACCTTGGGCG GTAATCATAT GATTAGTCAA GAAGATATTC TAAAAGCTTG TGAAGTAGCT	8760
GAAATCCGTC AAGACATTGA AAGAATGCCT ATGGGCTATC AACTCAGCT CTCTGATGGA	8820
GCTGCTCTAT CAGGAGGACA GAAGCAACGA ATCGCTCTCG CTCGTGCTCT TTAACTAAA	8880
TCTCCTGTTT TAATACTAGA TGAAGCTACT AGCGGTCTTG ATGTCTTGAC TGAGAAAAAG	8940
GTATAGATA ATCTTATGTC TCTAAGTAT AAAACCATTC TCTTTGTAGC CCATCGTCTC	9000
AGTATAGCCG AACGAACCAA CCGTGTCATT GTTCTTGACC AGGGGAAAAT CATTGAAGTT	9060
GGTA	9064

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## (2) INFORMATION FOR SEQ ID NO: 18:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 7780 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 18:

CTCCATTTTT TTGATTTCAT AAATAAACAA CCTCTCTGTT AATTTTGTAT AATTATAACG	60
ATATCCAAGT TACTTGTCAA GTGTTTTTTA AATTTTATC TCAAAATAT TTTTCGTTT	120
AAAAAAGGA GCCATCAGT GATTCAAGC TCCCTTTTAT ACAGAATTAA ACTATTTTAT	180
AGTTCGACAA TCTTACCTGT TTCAAAGTAG ACAACCCATT CACAGATATT TTTAGCATAG	240
TCACCGATAC GCTCCAAGTA GGAAATAACT TGGAAATAAT CACGACCCGT AACAATGGCT	300
TCTGGATTTT TCTTAATCTC TTCAGTCGCA AGGTCACGGA TAGTTTCAAA ATAGTGGTTA	360
ATTTGCTCAT CCATGGAGGC CACCCGGTAT GCGTCGTCAA CAGAACCATT AAGATAAAGA	420
TCAAGTGCTG CTTCCACAAC GCTTTTAACT TCACGTCCCA TTTTTTAAAT TTCTTCTCT	480
ACAGCTGGAA TGCGCTCTTC CCCCTTCATA CGGATGGTTG CCTGGGCAAT GGCTACAGCG	540
TGATCCCCCA TACGCTCCAC ATCTGATACA GCCTTAAGGA CAGTCAAGAC TGTACGCAAA	600
TCTTGAGAGA CTGGTTGTTG GAGTGGGATC ATTTCAAATG ATTTCTTTTC CAGTTTCACT	660
TCGTATTTCAT TTAATTCTGC ATCATCTTCG ATGACCTCTT TTGCCAGGTC ACGGTCATGC	720
GTGACAAAAG CACGTACCGT ACGATTGATT TGTGAGAGCA CTTCTTGTC CATAGCGTAG	780
AACTGGTTAT GTAATTTCTC TAAATCTTCT TCAAATTGAG ATCGTAACAT CTTTCATCTC	840
CTTATCCAAA TTTTCCTGTA ATATAGTCTT CCGTTTCCTT GTGTTGGGGA TCAAGGAACA	900
TCTGCTTGGT ATCATTAAAT TCAATCAAAT CTCCATCTAG GAAAAATCCT GTCTTATCAG	960
AGATACGTGA AGCTTGCTGC ATGGAACGGG TTACCAGAAG CATGGTGATC TTGTCTTTTA	1020
GACCATACAA GGTTCTCTCA ATTTTACCAG CTGAAATCGG ATCCAAAGCC GAAGTTGGCT	1080
CATCCAAGAG GATGATTTTA GGACTAGTTG CCAAGACACG GGCCACGCAG ACACGCTGCT	1140
GTTGACCACC TGACAATCCA ATAGCTGAAT CATATAGACG ATCCTTGACC TCATCCCAGA	1200
TAGAGGCACC TTGCAAGGCT TTTTCTACGG CTTTATCCAG AACCTGCTTA TCCTTAATTC	1260
CATTGATACG AAGCCCGTAG ACAACATTCT CATAGATAGT CATAGGGAAA GGATTAGGTT	1320
GTTGGAAAAC CATTCGGATT TCCTTACGTA ATTCAACCGT ATCTGTACGC GGACTGTAGA	1380
TGTTGTGACC ATGTGTACACC ACGGATCCAG TTGTGGTCAC CTCTGGATTG AGATCTCCCA	1440



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TGCGGTTGAG AGACTTGAGG AGGGTTGACT TCCCTGATCC AGATGGACCA ATCAAGGCTG	1500
TAATTTCTTT AGGTTGGAAA GATAGGAAA CACTATTCAA AGCCTTCTTT TTATTATAAT	1560
AAACGGACAG GTCTGATACC TGTAATAATCG CATCTGTCAT ACGGTTTCCT TTCTAACCAA	1620
AGTGACCAGA TACATAGTCA TTGGTGGACT GTAGCTTGGC ATTTTGGAAA ATAGTTGCAG	1680
TCTTGTGATA CTCAATCAA TCACCCAAGT AAAAGAAGCC TGTATAGTCA CTTGCACGAG	1740
CAGCCTGCTG CATATTATGC GTTACAATGA TGATGGTAAA GTTTTCTTTG AGCTCAAACA	1800
TGGTCTCTTC TAGTTGCATG GTCGCAATCG GATCCAAGGC TGAGGCTGGC TCATCCATTA	1860
AGAGGATATC TGGCTTAACA GAGATGGCAC GAGCGATACA GAGACGTTGT TGCTGACCAC	1920
CTGATAAGGT CAAGGCTGAC TTGTGGAGAT CGTCTTTAAC CTGATCCCAG ACGGCAGCCT	1980
GACGAAGGA GGTTCCTACG ATTTTCATCTA GGACTTGCTT ATCCTTAAC CCAGCACGTT	2040
CATGCGCAAA GGTAAATATTA CGGTAAATG ACTTAGCAAA TGGATTGGGA CGTTGAAAAA	2100
CCATTCCAAT GTGTTTACGC ATTTTCATAAA CGTTGATTTC TGGACGGTTG ACATCAATTC	2160
CACGATAGAG AATCTGCCCA GTTACTTTAG CAATATCAAT AGTATCATTC ATGCGATTGA	2220
GACTGCGTAA GTAGGTAGAT TTCCCCGATC CCGACGGGCC AATCAAAGCT GTAATTTTAT	2280
TTCTTTCAAA TTGCATATCA ATCCCCTTAA TGGATTCAAT TTTACCATAG TAAACATGGA	2340
CATCCTTAGT AGAAAGGGCT ACTTTTCTTT CAGGAAAGGT AAGGATATGC TTCTCATCCC	2400
AGTTATATGT TGACATGGCT TCTCCTTTAG GCAGCGGTTA ATTTCTTGTG TAGATAGCTT	2460
CCGAACCTAC GAGCTCCAAA GTTAAAAATC AGGATAAAGA TCAGGAGCAC AGCGGCAGAA	2520
CCTGCTGATA CAATGGTTCC ATCTGGAATA GTGCCTTCAC TATTGACTTT CCAGATATGG	2580
ACAGCCAAGG TTTCTGCTTG ACGGAAGATA GAGATGGGGC TAGTCACACT GAGGATATTC	2640
CAGTTAGACC AGTCAAGAGC TGGCGCCGAT TGCCCTGCTG TATAGATCAG AGCTGCAGCT	2700
TCGCCAAAGA TACGACCAGA TGCCAAGACG ACACCCGTTA CAATACCTGG AAGCGCTTCC	2760
GGAATAACAA CATGAACCAC TGTCTCCCAG CGAGAAATCC CAAGAGCCAG ACCAGCCTCA	2820
CGTTGGGTAT GGTGAACGTG TTTCAAACTA TCCTCTACAT TACGCGTCAT CTGAGGCAAG	2880
TTAAAGACTG TCAAGGCCAA GGCACCTGAA ATGATTGAAA ATCCATACTC AAAGTGGACT	2940
ACAAAGATCA AGTAACCAA GAGACCCACC ACCACTGATG GTAAAGAGGA CAAAATTTCA	3000
ATACAAGTCC GCACAAAGTT GGTAAACAGGA CCTTTTCTAG CATATTCAGC CAAGTAAATC	3060
CCAGCTCCCA TAGAAAGAGG TACAGAAATA ATCAAGGTAA TGACCAATAG GAAAAGGAA	3120
TTGTAAAGCT GAATGCCAAT CCCACCACCT GCTTGAAAAG CAGAAGACCT TCCAGTCAAG	3180

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AAAGACCAAG AGATATGGGG CAAGCCCCGA ACCAAGATAT AGAGAATCAA GGAAGCCAAG	3240
ATTGTCACAA TGATGCTAGC AATCGTATAG AGGACAGCTG TTGCAAGTTT ATCTAATTTC	3300
TTAGCGCGCA TAATTTTTCT TTCTCTTTC TTTCGTAATC AATTTAATCA CACTGTTAAA	3360
AACTAAGCTC ATCAAGAGCA GTACCAAGGC CAGTGACCAG AGAACATTAT TATTTACAGT	3420
TCCCATGACA GTGTTCCCAA TTCCCATAGT TAATATAGAA GTTAAAGTTG CAGCTGGTGT	3480
GGTCAAGGAA GTTGGGATAA CAGCTGAGTT TCCGACAACC ATCTGGATAG CTAGAGCCTC	3540
ACCAAAGGCA CGCGCCATCC CAAAGACCAC TGCAGTGAAA ATACCAGAAC GGGCCGCCTT	3600
CAAGATCACA CGCCAGATAG TCTGCCAGCG AGTGGCTCCC ATAGCGAAAC TGGCTTCACG	3660
ATAATAACGA GGAACCGCAC GCAAGCTATC CGTTGTCATA AAGGTTACGG TCGGCAAAAT	3720
CATGACAAAG AGGACGGAAA TCCCTGACAA AATCCCAAAA CCAGTCCCAC CAAAGACACT	3780
GCGAACAAAG GGAACGACGA CTTGCAAGCC AATAAATCCG TACACTACTG AAGGAATCCC	3840
AACCAGGAGT TCAATAGCTG GTTGCAAAAT CTTGCCCCCT TTTGGTGATA CTTGCGTCAT	3900
AAAAACTGCT GCACCAATAG CAAAGGGTGT TGCGATAAGG GCTGAGAGAA TGGTAACGAT	3960
AAAGGAACCC AAAATCATAG GAAGGGCACC AAATTCTTTA CTAGAAGGAT TCCAAGTTCC	4020
TCCCAAAAGA AAGTCAAAGA TATTCACACC ATTGACAAAG AAGGTCGACA AGCCTTTTTG	4080
CGCTACGAAA ACCAAAATCA TGGCCACAAG GATGACTATC AAAGAAAGAC AGGCAAAGGT	4140
CAACCTTTT CCTAATTTCT CCAGACGAGA ATTCTTTGAT GGAAGCAACA TTTTCTTAGC	4200
TAATTCTTCT TGATTCATTA TTGTCTCCCT TCCAACACTG TCACAGTTCC GGCAGCATCT	4260
TTTTCAACCT TCATTTCCCT AATCGGAATA TACTTCAATC CTTTGACAAT CCCTTCTTGG	4320
GTCTCATCCG AGAGAACAAA ATTGAGAAAT TCTGCAGCCA ACTCATTGGG CTGCCCAAT	4380
GTATACATAT GCTCATAAGA CCACAAGGGC CAATTATTGC TACTTATATT TTCTGGACTT	4440
AAGTCATAGC CATTCAACTT CATGCTTTTG ACCGAATCAT CTATATAGGT AAGAGATAAA	4500
TAAGAGATAG CTCCTGGACT TTTTGATACG ATTGATTTTA CCGCTCCATT TGAATCCTGC	4560
TCCTGACTTT GCATGGCAGA CTGACCTTCC ATAATGACAG TATCAAAGGT AGCAGGAGAG	4620
CCAGAGCCGG CTGCCCGATT GATAACAGAG ATGGGTAAGT CCTTACCACC AACCTCTTTC	4680
CAATTGGTTA CCTCACCTAT GAAGATTGA CGAAGTTGCT CTGTCGTTAG GTTATCAACA	4740
TCAACCTCCT TATTGACAAT CAGAGCCAAG CCAGCTACCG CGACCTTGTG GTCAACAAGA	4800
GCAGAAGCAT CAATTCGTC TTTTTCCTCA GCAAATACAT CTGAGTTTCC TATATCAACT	4860
GCCCCAGACT GAACCTGGGA CAAGCCTGTA CCAGAACCTC CCCCTTGGAC ATTGACCGTT	4920
TTTCCAACAT GGATCGTGCC AAATTCATCT GCCGCTACTT CAACCAAGGG TTGCAAGGCA	4980

GTTGAGCCAA CAGCCGTAT GGATTCTCCA CGATCAATCC AGCTAGCACA GCCTACTAAA	5040
CAAGCCGTCA GCCAAAAAGC GATAAGAGAC AGAGCAAGCT TTTTCTTTT TTTCACTGTT	5100
TTTCTCCTCG AAAATAATTA TGAATACTGT GAATTTTTTA AGTAGTTCTT TATGAGTTGA	5160
CGCATGAATT CTTACCAAAT TTCTGCGCAA TTGATTATTT ATATAATATA GGCTATATTA	5220
CTCTTTCTTA ACCTCCTTTT TTCATATGTG GATAAAATCT CTTGTCTATC CCTTCCCCCA	5280
TTGTCACCCA TTATAGTCAT TTCGTGTCTC TTTTCCCCT TTTTAATGCA AGGGAAATTA	5340
CTCTCCTTAG ATGATAATCC AAAAGCTAGA AAGGTATCTC AAACCTCTCT ACTCTCCCAG	5400
ACTAGTTTAC AACTAAAAGG AAAAGATTCT ATTTTATGAG AAATCTAGTT TACAAGCGGT	5460
AAGAACGCTA ATAATAAAC TTCTTGTAAT CTTTGAAAAT CTCTTCAAAC CAGTGTTTTG	5520
AGCTATCTAT GGCTAGCTTC CTAGTTTGCT CTTTGATTTT CATTGAGTAG TAAACTACA	5580
TGTAATGGCA ATCAAGATAT CAAGAATCAT CCTACTAAAA AAATCCATAC TTTCACTATA	5640
ACATAGAATA AGATATTTGA CTAGCATTTT CATTTGAATC TGAGGCCTTT TGGAAAATAA	5700
TTTTTCAAAA CATTTCCAGT AACCTTTGCA AAGCCCAAGC CATTGCCCTT AACCAAACT	5760
TGGTACCAAC CATTTGGCAG ACTTTCTGCC AGCTGAACGG TTTCTCCAGC CGCATACTTG	5820
ACAAACGCTT CTGGCCAAT TTCAACCGAC TGTTGACCT GACTCGGTTT CAAGGCTAAA	5880
CCAAGAGCGA AACTGGGCTC AAAGCGTTC TTCTTAAAG TACCCAGATG CAGTCCATTG	5940
CGAGCAATCT TGAGCTTCCA TAAATCTGGC AAAAGTTCTG GCAAGAGATA AAGCTGGTCT	6000
CCAAAAATCT GCAAGATACC CGGTAGATTG ACCTTCAAAT GGTTTTGGGC AAATTCCTGC	6060
CACAAGGCAA CTTGTTACAG GCTGAGGTTA CTCTTACTTG CCTTAAATTT AGGAGCTGGA	6120
TTGTTACCTT TAAACTGTAG ATGGGCAACA AACTGACCTT CTCCCTTAAA CTGATGAGGA	6180
TACATCCGAG CCGTTTCTGG CAGGTCAATA CCAGCTACCA TTCCATTGAT ATGCTCTACT	6240
GGCAACAAGT CAAAATCATA CTCTTCCAGC AACCAATTGA CAATCTCTTC GTTTTCTCTG	6300
GGTGCCAGG TACAGGTCGA ATAAACCAGA TGACCACCTT CAGCTAACAT GGTCACTGCA	6360
TCCTCCAGAA TTTCTCTTTG CAAGCTAGCA CATTGACTCG GATAATCTAA GCTCCAATAG	6420
TCCATAGCAT CAGGTTGCTT ACGAAACATT CTTTACCAG AGCAAGGGGC ATCAAGAACG	6480
ATTAAGTCAA AATAGCCTTT AAAGACCTTG ACCAAGCGGT CGGCAGATTC ATTGGTCACC	6540
ACGACATTTG TCGCTCCAAA ACGCTCCATG TTTTCAACCA AAATCTTAGC CCGTTTGCTT	6600
GAAATTTTAT TGGAANCAAG TAGCCCCCTC CTGCTAGAT AGGCTGCCAG TTGAGTTGAT	6660
TTGCCCCCGG GTGCAGCAGC CAAGTCCAAG ACCTTCATAC CAGGACTGGG TTGGGCTACT	6720

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TGAGCCACCA TTTGAGCAGC AGGTTCTTGC GAATAAACTA AACCTGTAGC ATGCTCAGGC	6780
GATTTCCTTG AAACCTTCCC ATAGTGGCCC CAAGGGGTTT GAGTAATGGC ATCAGAAAAG	6840
GAAAGTTGCT CTTCTTTTAA GGGATTGACC CGAAAGGCCG AAACCGCTTC CTCCTCAAAA	6900
GAGGCAAGAA AATCTCTTGC CTCATCTCCT AGTATCTCTT TATATTTTTC AACAAATCCT	6960
TCTGGAAATT GCATTTAAGT TCTTTTCCTT TCGTAAATAT AGGACTGAAT TTCCTCCTGC	7020
ATCTCAAGAG GCACCATCAT GACCGGCTGT CTGGTTTGAA AATCAGGAGC TTCACCAAAA	7080
AGGGTCACAA CCCGATAGCC CAGACTTTCC CCTAAAATAC TAGCTGCGGC ATAATCCCAT	7140
GGTTCAGAT AAGTGAGATA GGTCACAAA CGCCCTGACA AAATCTTGGC AAAACTAATG	7200
GCCGCACTTC CATAGACACG AACACCAAGA ACCGCTCGGC TCAAATCAGC CAGCCCCCAT	7260
TCATTGGTTT CCAGCATACC ACTATTCCTT GCAATGAGAA AATCTCCAAG TGGTTTAGTT	7320
TTAAAAGGAG CTAGGGACCT ATCATTTAGA CAAACTGGAA ATTCCCCACC ACCGTGGTAA	7380
CAATCCCCTT TGACCACATC ATAAATCAGA CCAAATGTC CCTGACCATT TTCAAATAA	7440
GCCATCATAA CAGCAAAATC TTCCTGCTGG GCTACAAAAT TATTGGTACC ATCAATGGGA	7500
TCAATGACCC AAACCTTGCC CTCTGAACC GAGGCTCGCA GACAACCTTC TTCAGCACAA	7560
ATCTTATCCT CAGGATAACG GGACAAAATC TCACCAACCA AGAGTTCCTG AACTTCTTTG	7620
TCCAGTCTGG TCACCAATC TGTGGAGAG GACTTGTTT CAACACGCAA GTCTTCCTGC	7680
ATATGGTCAA GAATGTACTG ACCTGCTTTC TTAACAAGCT CTTAGCAA TTCAAATTA	7740
CTTCCAAGA GAAATCTTTC CTTCCTTTT TTCTTTGGGG	7780

(2) INFORMATION FOR SEQ ID NO: 19:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 4820 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 19:

GTAATGATAT AGGAACACCA GGTGACCTGA TGGGACGTCG TAAGCCTATG AACTACTAGC	60
TGCTAAAGGC TTAAAGATG GTATGGTACC ATATATCTCA AACCAATACG AAGAAGAAGC	120
CAACAAAAAG GGCAAGACAA TCAATCTCTA CGGTAAAACA AGAGGTTTGG TTACAGATGA	180
CTTGGTTTGG GAAAAGGTAT TTAATAACCA ATATCATACT TGGAGTGAGT TTAAGAAAGC	240
TATGTATCAA GAACGACAAG ATCAGTTTGA TAGATTGAAC AAAGTTACTT TTAATGATAC	300
AACACAGCCT TGGCAAACAT TTGCCAAGAA AACTACAAGC AGTGTAGATG AATTACAGAA	360

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ATTAATGGAC GTTGCTGTTC GTAAGGATGC AGAACACAAT TACTACCATT GGAATAACTA	420
CAATCCAGAC ATAGATAGTG AAGTCCACAA GCTCAAGAGA GCAATCTTTA AAGCCTATCT	480
TGACCAACA AATGATTTTA GAAGTTCAAT TTTTGAGAAT AAAAAATAGT GTCTACTATT	540
AGGAAATAAA GTTTAAAAAG GTGATGAAGA ACAAAACCAAG ATTCAAGCAG GAATTCCTAC	600
TGATAATGAA GTAAGTTATG ATCTTATTTA TCAGCAGGAA ACTCTTCCTG CAACAGGTTT	660
ATCAACTTCT GAGCTTACAG CTTTAGGCCT ATTAGCTGTT GGTAGTTTAG TTCTTTGGT	720
TCATAATATG ACGGGAACAG TTTTGTGCTC CCTCTGAAAA GTCATCATTT GATGGCTTTT	780
TTCTATATAG GGTAAAAGAT AGGGTAAAAG GCTATCATCG GACAAAATAA AGAAGGCATG	840
ATATAATATA AAGTAGATTT CTATGTCATA AAACAAGAAC TGTTTGGACA TCATTCATTT	900
GAAACTCTC TATGTTCAAA CAATAGTAAA ATAAATAGG GGATCTAAAT CCTTGCTATG	960
AAAGGAAAAA ACTCAATGGC TACTATTCAA TGGTTTCCTG GTCACATGTC TAAAGCTCGT	1020
CGACAGGTGC AGGAGAATTT AAAATTTGTT GATTTTGTA CGATTTTAGT AGATGCACGC	1080
TTGCCTCTAT CTAGTCAAAA TCCTATGTTG ACCAAGATTG TTGGTGATAA ACCAAACTC	1140
TTGATTTTAA ACAAGGCCGA CTTGGCTGAT CCAGCAATGA CCAAGGAATG GCGTCAGTAT	1200
TTTGAATCAC AAGGAATCCA GACGCTAGCT ATCAACTCCA AAGAGCAAGT GACTGTAAAA	1260
GTGTAACAG ATGCGGCCAA GAAGCTCATG GCTGATAAGA TTGCTCGCCA GAAAGAACGT	1320
GGGATTGAGA TTGAAACCTT GCGTACTATG ATTATCGGGA TTCCAAACGC TGGTAAATCA	1380
ACTCTGATGA ACCGTTTGGC TGGTAAAAAG ATTGCTGTTG TTGGAAACAA GCCAGGGGTC	1440
ACAAAAGGTC AACAATGGCT TAAAACCAAT AAAGACCTGG AAATCTTGA TACACCGGGG	1500
ATTCTCTGGC CTAAGTTTGA GGATGAAACT GTTGCACTTA AGTTGGCATT GACTGGAGCT	1560
ATCAAAGACC AGTTGCTTCC TATGGATGAG GTTACCATTT TTGGTATCAA TTATTTCAAA	1620
GAACATTATC CAGAAAAGCT GGCTGAACGC TTCAAACAAA TGAAAATTGA AGAAGAAGCG	1680
CCTGTGATTA TTATGGATAT GACCCGCGCC CTCGGTTTCC GTGATGACTA TGACCGTTTT	1740
TACAGTCTCT TCGTGAAGGA AGTCCGTGAT GGCAAACTCG GTAACATATAC CTTAGATACA	1800
TTGGAAGACC TCGATGGCAA CGATTAAAGA AATCAAAGAA TTCCTTGTGA CAGTCAAGGA	1860
GTAGAAAGC CCTATTTTTT TAGAGCTTGA AAAGGATAAT CGCTCAGGAG TTCAAAGGA	1920
AATCAGCAAG CGTAAAAGAG CCATTCAAGC TGAATTAGAT GAAAATTTGC GCTTGAATC	1980
CATGCTTTCT TATGAAAAAG AACTTTATAA GCAAGGATTG ACCTTAATTG CAGGTATTGA	2040
TGAGGTTGGT CGTGTCTCTC TTGCTGGTCC TGTAGTCGCT GCGGCCCTTA TTTATCTAA	2100

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AAATTGTAAG ATTAAAGGTC TCAACGACAG CAAGAAAATT CCTAAAAAGA AACATCTGGA	2160
GATTTTCCAA GCCGTTC AAG ACCAAGCCTT GTCGATTGGA ATTGGTATCA TAGATAATCA	2220
GGTCATCGAC CAAGTCAACA TCTATGAAGC AACCAAATA GCCATGCAAG AAGCAATCTC	2280
CCAGCTCAGC CCTCAACCAG AGCACCTTTT GATTGATGCC ATGAAACTGG ACTTGCCCAT	2340
ATCACAACC TCCATTATCA AAGGAGATGC CAACTCCCTC TCTATCGCAG CAGCATCTAT	2400
AGTAGCCAAG GTAACACGTG ATGAATTGCT GAAAGAATAC GATCAGCAGT TCCCTGGCTA	2460
TGATTTGCT ACTAATGCAG GATATGGCAC AGCTAAACAT CTGGAAGGCC TCACAAAAT	2520
AGGAGTTACC CCAATTCAAC GAACAGCTT TGAACCCGTT AAATCACTGG TTTTAGGTAA	2580
AAAAGAAAGT TAATTGAAAG GAAATAACAT GGAGGAACAG TCGGAAATAG TCCGTTCTAA	2640
GAAAGAATTC GCCTTTGCAT CCAGCACTAT ACTATCCCAA GTTGGTCGAG GAATCATGT	2700
CGGCCTCATC GTTGAATTA TCGTCGGATC CTTTCGTTTC TTAATTGAAA AGGGCTTCCA	2760
CCTGATACAA GGAGTTTATC AAGATCAAGG GTACTTAGTG CGCAATCTTT TTGTACTGGT	2820
TTTGTTTAT ATACTCATCT GTTGGCTCAG TGCCAACTA ACACGGTCAG AAAAAGATAT	2880
TAAAGGCTCA GGAATTCCTC AAGTCGAAGC CGAACTGAAA GGCTCATGT CCCTCAACTG	2940
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GCTGGGTCGA GAGGGACCCA GCATTCAACT TGGAGCAGTT GGTGGTAAAG GAATTGCCAA	3060
GTGGCTCAA TCCAGTCCAG TAGAGGAACG TTCCTTGATT GCCAGTGGAG CTGCAGCAGG	3120
TTTAGCCGA GCCTTTAATG CTCCTATTGC AGCACTTCTC TTTGTTAGT AAGAAGTCTA	3180
TCACCATTTT TCGCGTTTT TCTGGGTCTC AACTCTAGCA GCCAGCATCG TAGCAAACTT	3240
TGTGTCTCTA CTCATGTTG GTTTGACACC AGTATTGGAT ATGCCAGATA ACATTCTCTC	3300
CATGACCCTA GATCAGTATT GGATATATCT CGTCATGGGA ATTTTCCTTG GATTTTCAGG	3360
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AATCCATTTG GATAGGGCTT ATTATCCCAT CTTGGCTTTT ATCCTTATCA TACCAGTCGG	3480
AATCTTCTTA CCTCAAATCA TTGGTGGCGG AAATCAGCTT GTCCTTTCTT TAACTGAACA	3540
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GCTTGGTGCC TTAGTTGGTG TTATCTGTGT CAATCTTGA CTTGTCAGTC AAGAGCAATT	3720
CCCTATATTT GTCATTCTAG GAATGAGTGG CTATTTTGA GCCATATCAA AAGCTCCCTT	3780
AACCGCTATG ATCCTCGTAA CTGAGATGGT AGGAGATATT CGCAACCTTA TGCCACTTGG	3840
TCTTGTCAC TTTGTTCTT ATATTATCAT GGATTTGCTC AAAGGTACGC CAGTCTATGA	3900

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CAACGTCCTC ATCACAATC AAGTCCATAA TGGCAAGAGC CAAACAGTTA ACGGCTCAAC	4080
CAGAATGTAT CTGGGTGATA TGATTCACCT GGTATTCCA AAAAGTGAAA TTGGAAAAGT	4140
CAAAGATTG TTGTTGTAGT ATGAGTATTT ACATAATTTA TGTATGTAA ATGATCAGTT	4200
TGATTTATTT AGAAAACCGA TTCTCAGGAA TGAGATCGGT TATTTTAC TGATGAGGAA	4260
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AAAGTATAAA GCTAGAAAGG AGTTACTGT ATCAAATCTG TACAGTAAGA TTAATCAT	4380
GAAAAAGAAA ACAATAGCAA TTATATAGAG AAATGAAATA GAAATAGGAT AAAACAATCA	4440
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TATTAACAGA AGTTTAGTGG GTGAGATTTT TATTATTTT CTTATTCTGT TTGTTTGTA	4620
GGTCTAAGTC TTTTATCAC TTGAAAAC TCCTATAACA TCTTCCGAA AACTATAAT	4680
TTTCTTGAAA AATATACAAG TCTATGCTAT ACTACTAGTA TACTTACTTA TGGAGAAAAT	4740
ACATGAAACG TGAGATTTTA CTGGAACGAA TCGACAACT AAAACAATC ATGCCCTGGT	4800
AAGTTCTGGA ATACTACCA	4820

## (2) INFORMATION FOR SEQ ID NO: 20:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 21338 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 20:

CTACGACATC ATGATTAACA GTCATGCGCT ACTACCAACT GAGCTATGGC GGATAAAATA	60
GTCCGTACGG GATTCGAACC CGTGTACCG CCGTGAAAAG GCGGTGCTTT AACCCCTTGA	120
CCAACGGACC TTCTATCTGT AGCAGATATA ACCATTATAT CAATTTCTTG CTAATTGTCA	180
ATCACTTTTG AGATTTTTC TCTAAAATAT CTTTAATTT TCTAATTTT AATCTTGAAA	240
TAGGACAACG ATGGTCTTCA TAGAAAACAA TTTCTAAGTT TTTTCGATCA ATTTCTCTGA	300
TATTACCTAT ATTTACCAA AATGACTTGT GAGGAGAATA AAATCGCTGA GTATGTTTGT	360
CCTTTTCCTG AATATCTGTC ATGGTACCAT AAAACTCTTT TGCAAAATTC TTACCAATAA	420

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TGCGCAATTT ATGAGATACC CCTGTTGTTT CAATATACAA AATATCATGG TAAGGAATTT	480
TTAAATCATT TCCCTTGTA TGTAGTCGA AATAATCTAC AACATCTTCA TTTTCAAGTA	540
ACATACTCTT CGTGTAGAAG ATATTTTGCT CAATTCTCTT CTAAACATC TCATCATTGA	600
TATCCTTATC AACAAAATCT AGGGCTGATA CCTGGTATTT ATAGGTTAGA GTCGAAACT	660
CTGATCGACT AGTGATAAAG ACGATAATAG CGTAAGGATT GTAATGACGA ATGAGCTGAG	720
CCACTTCAAA TCCCTTTTTC TCAATTCCAT GAATATCGAT ATCTAGGAAA TAAAGCTGAT	780
TTACTTCATC ATTTTCAATG TATTCTTCAA ATTACGGAC TTTTCCCGTT GTCTTGATG	840
ATATTGGAAT ATTCGATTCT TTCGAAATTT CATCCAATAT TCTCTCTAGT CTCACTTGAT	900
GTTCATAAC ATCTTCTAAA ATTAAACTT TCATTCAAAT TCCCTCTTAA ATCTAATGAT	960
TTGTCTAAAT GTACTGCCTT CCATCTCTGT TTCTAAAATA ATATTGTTGT ACTTATCTAG	1020
TAGTTCTTTC ACATTATTTA ATCCGACTCC GCGATTCTT CCCTTAGTGG AGAATCCTAA	1080
GGCAATAGA TCTCCTGAAG GAGTCATCGT CATTTTACAT GAATTCTGAA TCACAATAAC	1140
TGTTTCAGTT TCCATCTTAA TAACTGCTAC TTCCATCTGC TTTTATAGC TATCAGCCGA	1200
TCCTTCGACA GCATTATTCA ATAAAACGCT CATGATACGA ACCAAATCCA ATAGTTCAAT	1260
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TTGAACCTTA TGAGAATTCA TTGCAAAGAA GGTCAAAGG AGAGAGATAA AGACAATAGA	1680
TGACAAAATA CTTCAAAAC TATTCAAATG TTTAATCGTA CTTACCATAT CTGAAACGAA	1740
AGATACAATA TGTAGCAATA GTAAAGCAAA AAATACTTTT TTCAAGAAAG GATAAAGGTA	1800
GTCTTGTCA AAATAGGCTA GTTCCAAATG GAAATAGTAA ATGATTTTTA ATGTAACAAA	1860
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TCCTGTTATA GAGGAGAAAA TTACGGACAG AAAGTTATGA GTGCTCTCAT ATAAAAGAGA	1980
TAGTAGTAAA CTTAGGAATA GTCCTCTATC CCTCTCATAC TGTTTCATCC ATCGAAAATA	2040
GGAATATAAG CCCAAAGGAA ATAAAAATCT TTCAATCCCT ATTTTATCTA AATATAGAAG	2100
ATAAAAGGAA AATTCAAGTA CTATTTCACT TAGTAATGTA TAAGCACCAA AAACGTATAA	2160
TTCTTTTCTA TTTATTCGAC CTTTACAAAT TAAACGGTAA CTGTGACTAA TAATTAAAAA	2220



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ATCTTTTGTA AGTCTTTTTC CTTCAAAGCT ACAAAGTGT CCAATTTAAC TGTGTTTTTC	2400
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TTTTTTAAGA AAAAGCCGG GAAATTTCCC AGCTTTGCTA TTATATTGAT CCCAGCAGGA	2580
TTCGAACCTG CGACCGTTCG CTTAGAAGGC GAATGCTCTA TCCAGCTGAG CTATGAGACC	2640
TAATACAATT ATTTACCAA AAATTC AATTTCAAT AAAAGTCAAT TTTCTATTTA TGGTAGGGGA	2700
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CTTATTCAGA TACGGGATTA AAAGAAAAGT ATACCTTTGA TAACTTTATT CAAGGGGATG	5940
GAAATGTTTG GGCTGTATCA GCCGCTTTAG CTGTCTCTGA AGATTGGCT CTGACCTATA	6000
ACCTCTCTTT TATCTATGGA GGACCAGGCC TTGGTAAGAC TCACTTATTA AACGCTATTG	6060
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AACAGGTGTC CACTTCGTAT TGAGTCAACA CAAAGAGTTA AAAACAGTTG CAACAGACTC	7620
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GGTCATTTGA AGTAGAACA CAATTATCGA AAGAAAATAA GACAGAACTC ACTATCTTTC	10980
CAGCTAGTGA TATGCTTTTG AGAGAAAAGG ATTATCAACG AGGACAGTCA GCTTTAGAAA	11040

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AACAAATTTC AAAAATTTA TCACCTATTT TGAATCATA CCTAGAAGAA ATTCTTTCAA	11100
GTTTTCACCA AAAACAAAGT CATGCAGACT CTCGGAAGTT TTTATCTTTG TGCTATGATA	11160
AGACATGGAC TGTCTTTGAT TATATTGAAA AAGATACTCC AATATTCTTT GATGATTATC	11220
AAAAATTGAT GAATCAGTAT GAAGTCTTTG AAAGAGACTT AGCGCAGTAC TTTACAGAAG	11280
AATTACAGAA TAGTAAAGCA TTTTCTGATA TGCAGTATTT TTCTGATATT GAACAAATCT	11340
ATAAAAAACA AAGTCCAGTG ACCTTTTCTCT CTAATCTTCA AAAGGGTTTA GGAAATCTCA	11400
AATTTGACAA AATTTATCAA TTCAATCAAT ATCCTATGCA GGAATTTTTC AATCAGTTTT	11460
CTTTTCTAAA AGAAGAAATT GAACGATATA AAAAAATGGA TTACACCATT ATTCTGCAGT	11520
CTAGCAATTC AATGGGAAGT AAAACATTGG AGGATATGTT AGAGGAATAT CAGATTAAAT	11580
TGGATTCTAG AGATAAGACA AATATCTGTA AAGAATCTGT AAACCTAATA GAGGGTAATC	11640
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AAGATTACAA TGAACCTGAA AAAGGGGACT ATGTTGTCCA TCATATCCAT GGGATTGGTC	11820
AATATCTAGG AATTGAAACC ATTGAAATCA AGGGAATTCA TCGCGATTAT GTCAGTGTCC	11880
AATACCAAAA TGGTGATCAA ATTTCTATCC CCGTGAACA GATTCATCTA CTGTCCAAAT	11940
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AGCCCAAGCA AAAGGTTAAG AACCAGGTAG AGGATATAGC TGATGATTTA ATCAAATCT	12060
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CCTTTGATGA TGCTTTCCCT TATGTTGAAA CGGATGATCA ACTTCGAGT ATTGAGGAAA	12180
TCAAGAGGGA TATGCAGGCT TCTCAGCCAA TGGATCGACT TTTAGTTGGG GATGTTGGTT	12240
TTGGAAAGAC TGAAGTTGCT ATGCGTGCAG CCTTTAAAGC AGTCAATGAT CACAAACAGG	12300
TTGTCAATCT AGTTCCGACG ACGGTTTTAG CGCAACAGCA CTATACGAAT TTAAAGGAAC	12360
GATTCAAAA TTTTGCAATT AATATTGATG TGTGAGTCG CTTTAGAAGT AAAAAAGAGC	12420
AGACTGCAAC ACTTGAAAAA TTGAAAAACG GTCAAGTCGA TATTTTGATT GGAACACATC	12480
GTGTTTTGTC AAAAGATGTT GTGTTTGCTG ATTTGGGCTT GATGATTATT GATGAGGAAC	12540
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CTTATCTCAT GTATCGTCCA GAAAAATCAA TCAGTGAAGT CTCTGAAAAG AGATTAGAAG	13140
CGATTAAAGG ATTTACAGAA TTGGGCTCTG GCTTTAAGAT TGCAATGCGA GATCTTTTGA	13200
TTCTGCGAGC AGGAAATCTT TTAGGAAAAT CCCAGTCTGG TTTCATTGAT TCTGTTGGTT	13260
TTGAATTGTA TTCGCACTTA TTAGAGGAAG CTATGCTAA ACGAAACGGT AATGCTAACG	13320
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ATACTTATAT TTCTGATCAA CGACATAAGA TTGAAATTTA CAAGAAAATT CGTCAAATTG	13440
ACAACCGTGT CAATTATGAA GAGTTACAAG AGGAGTTGAT AGACCGTTTT GGAGAATACC	13500
CAGATGTAGT AGCCTATCTG TTAGAGATTG GTTTGGTCAA ATCATACTTG GACAAGGTCT	13560
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GCATCGCTGA GAATAAGGGA TTAATGGAGC TTGTATTTGA TGTCCAAAAT AAGAAAGATT	13740
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AGGAAGAAAA TTCCATTGTA TATTTTCTT CTATAAATA GATAAAATG GTACAATAAT	13860
AAATTGAGGT AATAAGGATG AGATTAGATA AATATTTAAA AGTATCGCGA ATTATCAAGC	13920
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TGTATGAAAT TATCAGTGAA ACACGGGTAG AAGAAAATGT CTAAAAATAT TGTACAATTG	14160
AATAATTCTT TTATTCAAAA TGAATACCAA CGTCGTCGCT ACCTGATGAA AGAACGACAA	14220
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TTGCAAACTC AGTATCAAAC TTTGAGTGAT GAAAAGGATA AGGAGACAGC ATTTGCTACC	14400
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TCGAGGGAAA AAGTTTATAC GATTCCTGAC TTGCTTCAA GGTGATAAAA TGAAAAATTT	14520
ATTAGACGTA ATAGAGCAAT TTTTGAGTTT GTCAGATGAA AAGCTGGAAG AATTGGCTGA	14580

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TAAAAATCAA TTATTGCGTT TACAAGAAGA AAAGGAAAGG AAGAATGCGT AAATTCTTAA	14640
TTATTTTGTT GCTACCAAGT TTTTGGACCA TTTCAAAAGT CGTTAGCACA GAAAAAGAAG	14700
TCGTCTATAC TTCGAAAGAA ATTTATTACC TTTCACAATC TGACTTTGGT ATTTATTTTA	14760
GAGAAAAATT AAGTCTCCC ATGGTTTATG GAGAGGTTCC TGTATTGCG AATGAAGATT	14820
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TAAATAACA AGGAATTCCA GTATTTAAGC TATCAAATCA TCAATTTATA GCTGCGGACA	14940
AACGATTTTT ATATGATCAA TCAGAGGTAA CTCCAACAT AAAAAAGTA TGGTTAGAAT	15000
CTGACTTTAA ACTGTACAAT AGTCCTTATG ATTTAAAAGA AGTGAAATCA TCCTTATCAG	15060
CTTATTCGCA AGTATCAATC GACAAGACCA TGTTTGTAGA AGGAAGAGAA TTTCTACATA	15120
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AAGTTCAAGA AATGTTATCT GAAAAATATC AGAAAGATTC TTTCTCTATT TATGTTAAGC	15240
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TAGATACGAC TGTAATAATAC GTATCTGCAG TCAATGATTT TCCAGGTTCT TATAAACCAG	15420
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CAAACCAATC TGATGCCACA TTCAAATCCA AGATGTCTGC CATTATGGGA GATGATTGGG	15600
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AGAGTTCATG AAAAAGACAG GTGCGACAGC TTTAGTCACT GCCCACCATG CTGATGATCA	16260
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TAAGGAGAAG CAAGTAGTCG GAGAGATAGA AATCATTCGT CCCTTCTTGC ATTTTCAGAA	16380



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AAAAGACTTT CCATCAATTT TTCACCTTGA AGATACATCA AATCAGGAGA ATCATTATTT	16440
TCGAAATCGT ATTCGAAATT CTTACTTACC AGAATTGGAA AAAGAAAATC CTCGATTAG	16500
GGATGCAATC TTAGGCATTG GCAATGAAAT TTTAGATTAT GATTGGCAA TAGCTGAATT	16560
ATCTAACAAT ATTAATGTGG AAGATTTACA GCAGTTATTT TCTTACTCTG AGTCTACACA	16620
AAGAGTTTTA CTTCAAACTT ATCTGAATCG TTTCCAGAT TTGAATCTTA CAAAAGCTCA	16680
GTTTGCTGAA GTTCAGCAGA TTTTAAAATC TAAAAGCCAG TATCGTCATC CGATTAAAA	16740
TGGCTATGAA TTGATAAAG AGTACCAACA GTTTCAGATT TGTAAAATCA GTCCGCAGgC	16800
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TTTATTTTCT TTTGGACTTC CATTAGAAGG TGAATTAATT CAACAAATAC CTGTTTCACG	16920
TGAAACATCC ATACACATTC GTCATCGAAA AACAGGAGAT GTTTTGATTA AAAATGGGCA	16980
TAGAAAAAAA CTCAGACGTT TATTTATTGA TTTGAAAATC CCTATGGAAA AGAGAACTC	17040
TGCTCTTATT ATTGAGCAAT TTGTGAAAT TGTCTCAATT TTGGGAATTG CGACCAATAA	17100
TTTGAGTAAA AAAACGAAA ATGATATAAT GAACACTGTA CTTTATATAG AAAAATAGA	17160
TAGGTAAAA ATGTTAGAAA ACGATATTAA AAAAGTCCTC GTTTCACACG ATGAAATTAC	17220
AGAAGCAGCT AAAAACTAG GTGCTCAATT AACTAAAGAC TATGCAGGAA AAAATCCAAT	17280
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TACACATATT GAAATGGACT TCATGATGGT TTCTAGCTAC CATGGTGGAA CAGCAAGTAG	17400
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CGATGGTAAT GTAAAAGAAT TAACTTACCA ACCAAATGGT AGTGTATCG AAGTTTCTGG	17940
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TGTTACTAAG GTAGAGAAAT TTACCAGCAC TATTCTTCCT GCAGATACTA CCGTATCAGA	18060
ATTGCAAAAA CTGCTACTG ACCATAAAGC AGAAGTAACT GTTAAGCATG AAAGTTCAAG	18120

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TGGTATATGG ATTAATCTAC TCGTATCCAT TGTGCCATTT GGAATTCTAT TCTTCTTCCT	18180
ATTCTCTATG ATGGGAAATA TGGGAGGAGG CAATGGCCGT AATCCAATGA GTTTTGGACG	18240
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AGCTGAGGAA GAAAAACAAG AACTAGTTGA AGTTGTTGAG TTCTTAAAAG ATCCAAAACG	18360
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AGGTAAACT TTGCTTGCTA AGGCAGTCGC TGGAGAAGCA GGTGTTCCAT TCTTTAGTAT	18480
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TGTACCACGC GGCCGTGCAG GCGGATACAT GATTGCACCT CCTAAAGAGG ATCAAATGCT	19200
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AGAAATTATC TTTAATGTCC AAACCACAGG AGCTTCAAAC GACTTTGAAC AAGCGACACA	19320
AATGGCACGT GCAATGGTTA CAGAGTACGG TATGAGTGAA AAACCTGGCC CAGTACAATA	19380
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AAAATAACCC TGAGAGAGGC TGGAGCCTCT CTTTTTTGTG CAGTTTAGGA GCTAAAGGGA	19740
ACAGAATGGA GAAAATGGAA CAAATGTGTT TTCTAATCTG TTAGACTGTA TCTAGAAAGG	19800
GGAAATTTAT GATTAAAGAA TTGTATGAAG AACTCCAAGG GACTGTGTAT AAGTGTAGAA	19860
ATGAATATTA CCTTCATTTA TGGGAATTGT CGGATTGGGA GCAAGAAGGC ATGCTCTGCT	19920

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TACATGAATT GATTAGTAGA GAAGAAGGAC TGGTAGACGA TATTCCACGT TTAAGGAAAT	19980
ATTTCAAGAC CAAGTTTCGA AATCGAATTT TAGACTATAT CCGTAAACAG GAAAGTCAGA	20040
AGCGTAGATA CGATAAGAA CCCTATGAAG AAGTGGGTGA GATCAGTCAT CGTATAAGTG	20100
AGGGGGGTCT CTGGCTAGAT GATTATTATC TCTTTCATGA AACACTAAGA GATTATAGAA	20160
ACAAACAAAG TAAAGAGAAA CAAGAAGAAC TAGAACGCGT CTTAAGCAAT GAACGATTTT	20220
GAGGGCGTCA AAGAGTATTA AGAGACTTAC GCATTGTGTT TAAGGAGTTT ACTATCCGTA	20280
CCCCTAGTA AGTCATGCAA AAAAAATGAA AAAAATTAGA AAAAGTAGTT GACAAAAGTTT	20340
GAAAAGGCTG TATAATAGTA AGAGTTGAAA ATAACAATC AGGTCCGTTG GTCAAGGGGT	20400
TAAGACACCG CCTTTTCACG GCGGTAACAC GGGTTCGAAT CCCGTACGGA CTATGGTATG	20460
TTGCGTCAGG ACCACTTGAT GAAAAAAGT TTAATAAAC TTAATAATCT TCAAAAAAGT	20520
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ACAAAGACCT TTGAAAACG AACAAAGACG ACCAATGTGC AGGGCGCTAC AACGTAAGTT	20640
GTAGTACTGA ACAATGAAAA AAACAATAAA TCTGTCAGTG ACAGAAATGA GTAAGAACTC	20700
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GCAGCAGTAG GGAATCTTCG GCAATGGACG GAAGTCTGAC CGAGCAACGC CGCGTGAGTG	21120
AAGAAGGTTT TCGGATCGTA AAGCTCTGTT GTAAGAGAAG AACGAGTGTG AGAGTGGA	21180
GTTACACTG TGACGGTATC TTACCAGAAA GGGACGGCTA ACTACGTGCC AGCAGCCGCG	21240
GTAATACGTA GGTCCCGAGC GTTGTCCGGA TTTATTGGGC GTAAAGCGAG CGCAGGCGGT	21300
TAGATAAGTC TGAAGTTAAA GGCTGTGGCT TAACCATA	21338

(2) INFORMATION FOR SEQ ID NO: 21:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 6273 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 21:

TGTTTTTAAA GAGCCGTGTC TGGATAGACT TTCGGACGCA ACGCTCTATT AGATAATGAA	60
CTGCCTATAC ACAAGATTTC TAACCTTAGT CGACATGAGC TGAAACCTCT TATTGTGTAA	120
GTAGTTCACA AAATATTATA CACCTATTTT ATGAATAGTC AACTGTCTTT ACAGTAAAT	180
TTTAGAAAAT CATGAAAATT TTCTCTTTCT TTCCATTTTA AGTGACATTC AGTCATTCTC	240
ACATCAAAAA AGCCCAGACG AAATTGCTCG AGCATTCTTT TATCTAGTCG TTAAAGGAAG	300
TTGAGTTCAG TATGTTTAAA GTCTCTGTCC CATCATTTCT TCAACAAACC TTGTCTTGG	360
AGAAACTCCT TGGCTACTTG CTTTGCTGAC TTGCCTTCAA CACCGACTTG GTAGTTGAGC	420
TGGCTCATCT GGCTTTCTGT AATCTTACCA GCCAATGTAT TAAGAACTCT TTCCAACCTCT	480
GGGTGTTTCT TGAGAAGAGC TTCTTTCATG AGTGGAGCCC CTTGATAAGG TGGGAAGAGT	540
TGCTTGTCAT CTTCCAAGAC CTGTAAATCA TAACGCTCCA ATTCCGCATC AGTCGAATAG	600
GCATCCGTGA TTTGAATATC CCCTGACTGA ATAGCCTGAT AGCGAAGGGC TGGCTCAATG	660
GTGCTACATG TGAGATTGAG ACCATACATT GATTGCAAGC CCTTATTTC ATCTTCACGG	720
TCGTAAACT CGAGTGTAAC ACCTGCCTTC AACTGCCCTT CCCTTTTTT CAAGTCTGAA	780
ATGGTCTTCA AGCCATATTC TTGAGCAATC TTTTTCGAA CAGCTACAGC ATAGGTGTTT	840
TGATAAGACA TGGGTTTGAG ATAGGCTAGA TGATCCTGCT TAGCAATGCC ATCAGCGGCC	900
ACCTGATAAA CCTGTTCTGG TTCATGACTC ACCTTGGGTG ATGGTTGAAG CAAACTTTCA	960
GTCAACGTAC CAGTAAATTC AGGATAGATG TCAATATCGC CTTTTTTCAG AGCTTCATAA	1020
AGGAAGCTTG TCTTCCCAAA ATTCTGTTTA ACAGTCGCAG TCATGCTGGT ATTTTCTTCA	1080
ATCAGCAACT TATACATATT GGCCAAAATT TCTGGTCTG GACCTATTTT CCCAGCAATA	1140
ACCAAGTTTT CTTCTCTTT TTGAACCAA AGAGCTGGAC TATAAGACAG ACCCAGTAAT	1200
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ATAACAGGCA TGGCGAGTGG AATTTCAAAT TTCTTGAGAC GTTCCCATCT GGTCAATCCA	1500
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CCCATCAAAG GGATAAAGAG CCCCACAAG GCCAGAGACG GGATGGTCTG GAAATACCT	1680
GCAATCTGCA AGACCCAGTC GGCCAGCTTC TCATGATAGC GAAGAAAAAC AGCCAAGGGA	1740

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ATCGCAAGCA AAATAGCTAG TAACAAGGTC AAAAGCGACA ACTGCAAAATG TTGAGATAGA	1800
GCTGTCAACC AATCACTAAA ACGATCCTGA AAAGTTGCAA TTAAATTAGT CATGAACACT	1860
ACCTCCAAAC AAGTCTGCTA CAAAGTCTGT TGCAGGCGCT TTAAAAATTG TCTCGGGATT	1920
CGCTACCTGG CGAATTTCTC CATCCTGCAA GACAGCAATA CGGTCCGCCA ACTTCAAGGC	1980
TTCATCCGTA TCATGGGTTA CAAAAATCGT TGTCATCCCA AACTCTTTAT GCAATTCTTT	2040
TGTCAGAACC TGCAACTGTT TTCTCGAAAT AGCATCCAAG GCCGAAAAGG GTTCATCCAT	2100
GAGGAAAATC TTGGGCTGAC CAATCATAGC TCGGACAATA CCGACCCGTT GCTGTTCTCC	2160
ACCAGATAAT TCACTAGSTA AGCGATGCCC ATACTCGGCT ACTGGTAAAC CAACCTTAGC	2220
CAAAAGCTCT TCTGTTTCT TCGTAATTC TTCTTGCTC CACCCCTTCA TTTCAGGAAT	2280
GAGAGCAATA TTTTCCGCAA CTGTTAGATT TGGAAAAAGA GCAATAGCCT GTAAACATA	2340
ACCAGTAGAA AGACGAAGT CACGCTCATC ATAGTCTTTG ATGCGCTTCC CATCCATATA	2400
AATATTTCCA TCAGTTGGTT CAAAAGACG GTTAATCATC TTGAGCATGG TCGTCTTACC	2460
TGACCCAGAA GGCCCTACTA AAACCATAAA TTCCCCATCC TCAATCTGTA AGTTGACATC	2520
TCTCAAGACA TCCTTTCTG TGTAGCGCAG TGCTACATTT TTGTATTCAA TCATTCTTTG	2580
TCCTCAATTT AAAACTTCCC TCGATTGGTC AAGTCTTCTA CCTTAGGCAT AACTTCCTTA	2640
TTATCCCAAT GCTCCACAAT TTTCCCGTTC TCTAAACGGA AGATATCGTA CTGGGCATAA	2700
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TGGAAAACAA AGTCAAAAGT GACACTATAT TCAGCCACAT AGTTTTTATA AGCAGCACTT	2820
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GCTTTCTTAT CCAAATCCTT GATTTCAAAA TCTCCAAAAA TTTGATCTAG TTGGTCATTT	3000
TCAGGTGTTT GATAGTAGTC AATGACATCC CAATGCTCAA CAATACAACC ATTCTCATCC	3060
TCACGGAAAG TATCCGTCGT CACCCATTGA GCTTCTCCAC CATTCAGATA TTGATGAACA	3120
TGAACAAAGA CCAGATTGCC ATCCTCAATG GTGCGGACAA TCTTAATCTG ACGCTCTGGA	3180
TGACGCTCAA AGAAATCTGC AAAGAAGGCT GCAAATCCTT CTTTCCCGTC AGGAACACCT	3240
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TCTTGAATGG CATGGATGTA TAGGTTGTGA GCATTTTCA CTTGTTGTGA CATATTCTAA	3360
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TGAATTTCTT CCTCTGAAAA TCCTTTGTAA AAGATAGTAT CCAATTTCTG ACTGACACGA	3480

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TGCCCCACTT CTTTCTGGGA CTTGCCTAAC TCCGTTAAAA CTAAATACTT CTTACGCTTG	3540
TCTTTTCCAC ACGGACTAAC AATTACAAGC TTTTGTTCCT CTAGCTTTTT TATCATAGTC	3600
GTCAGCGTAT TATTCGCAAG TCCAGTCGCA AGCGCGATAT CTGTCGCAGT TCGCGAGCCA	3660
GTTTCACTAT TCCATAAAAC CGCTAAAATC TTGCCCTGTT CACCCCTATA AAGAGCCTCA	3720
GGATCTTGAC TCAGTAACTT TTGAAAAATC CGCCCATTC ACAAACGAAT ATGATGGGCT	3780
AGCAAATGAC CATCTTTCAT AACACCTCCA ATTTATTTTCG ATATCGAAAT GAATAAACA	3840
ATTGTAACAC TCATCGTTCT AACTGTCAAC TATTTTCGATT TAGAAATAAT TTTTGATAAT	3900
TATCCACACC ACCATACTCC GGCTCAACTA ACTTTTAACG AGAGTTTCTA AACTCCTTCG	3960
TCCTCCAGTC TACAAAAGCC TTCCATTTCG ACTATCCTAT ATTTTATGAG GGGACACATT	4020
TTTCCTATCA GACCATTTAT TTAAAGATA GAAGTAAATC ATAATTGCTT CCATCTGTTC	4080
TTTTATAGTA TATTGAAGTT AGACTAGAGC ACTGTATCTT CTAAACATT GATAGAAAGC	4140
GATTTGAATT TCCCAATCAA TTTGTTCGTA TTTATAGCAT TTCGAACTG GAATAGGACA	4200
CCATGACTGC TAAAGATTT CTATAAATC ATTTAATTC CTCAATCAAT TTGTTTATAT	4260
CTTATTTTCAT TCCGCTATAA TTTCACCTTA CCCTATCTTT TTCGTAGCAC CCTTCAAACA	4320
GCCTATCCCC TACCGTTTGA CGATTCTCA CTTGCTCCA CTTCCATTAC AGAAGTTTCT	4380
TCACTACTAT GGGCTCGGCT GACTTCTCAT GATTCCTTGT TACTACTATT TGAACGCTCA	4440
CGAGATAGAT CTTACAAAAA ATGCTTTGAT CCACAATGGA ATCAAAGCAT TTAAAGAGT	4500
TCCTCATACA TAAGCGCAGA AGTCGCAGTT CCTCTGTACT TGGCTTCTTC TCTTTTGACA	4560
AAGCGAGCCA AGTTGAGCAA CTCAGGTGCT GGATGTTTGG GATTTAGGAG CAATTCACGA	4620
TTGACCAGGC CTGAGAGACG AACTGCCTGC AATTGCTCAT TTGTAGTAGG CAGTTTTTTA	4680
GTAGTCTCTA GGAGAGCAGC AACTAAATCT TCACTCAAAT CATGTCGAGC ATGATTGTAA	4740
AGATCTTTTA TAAGGCTTTC TAGGTTTGGT TCTACCATCC CTACCACCTC CCTTATGGTT	4800
TAATAATGTT TAATCAAATC AACCGTTGAA CGATCCAATT TCTTCACCAA GGCTTGTAAG	4860
AAAGCTTGCG CTTCTAGGAA GTCATCCATT GCATAGAGGG TTTGGTGAGA ATGGATATAA	4920
CGAGCGCAGA CACCGATAGT TGTGATGGG ACACCACCAT TTTTCAGATG AGCTGCACCT	4980
GCATCTGTTC CGCCTTTACC ACAGTAGTAT TGGTACTTGA TACCAGCTTC TTCAGCCGTT	5040
GTCAAAGGA AATCCTTCAT CCCTGGGAGA AGCAAGTGAC CTGGATCATA GAAACGAATC	5100
AAGGTTCCAT CTCCAATCTT GCCTTGACCA CCGTAGACAT CACCTGCTGG TGAGCAATCA	5160
ACTGCGAGGA AGACTTCTGG GTCAAACCTG GTTGTAGAGG TATGAGCGCC ACGCAGACCA	5220
ACTTCTTCTT GGACGTTAGA ACCCAGATAG AGTTCATTGC CGAGTTTTTG ACCCGATAAA	5280

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GCTTCAGCTA GCTCGCTTAC CATGAGGACA CCGTAGCGGT TATCCCAAGC TTTTGAGATG	5340
ATATTTTTTTT CATTTGGCTGT CAAAATTGCA GAACTATCTG GTACAATGGT ATCACCAGGA	5400
CGGATGCCAA AACTTTCTGC CTCAGCCTTG TCCGCAAAAC CACCATCAAA AACGATATCG	5460
GCAATGGCTG GCATGGTTGG TCCCCCTTT CCACGAGTCA AATGCGGAGG AACAGAACCT	5520
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ACCATGGGGT TCCAGCCACC GATTTCTACG ACACGGAAGG TACCATCTGG CTTGATTTTCG	5640
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GCTTCTGAAT GTTTGATACC AAAAATACCA CCCAAGCCAT CTGTCACCAC TTATCCACA	5760
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AGTATCTTAG TCCTGCTCTA TCTTAGAAAA GGATAGTATT CTCTTGCATG TAGTGCAAAA	6000
TCTAGTAAAC ATTCCAAAAT TAACTCGAAT ATTTATTTC AAACAAAAA ACAATACACC	6060
ATCAAAGTTG TTTGGATTTT TCATGAAATT TACAGAAAAT AGTTGACTTC CCTTCTCTCT	6120
TTCTTTAAAT ATATAGTTGG TTGAGTTGG AATAGTACGC TGCTAGCTGCT AAAACATTTT	6180
TAGAAATTAA TTTGACTTTC CTAATAGAGT TGTTCATATC TTATTTCAT TACTATAGT	6240
ACAAAAC TAG AAAAGGAAAA AATCATGACC AGG	6273

## (2) INFORMATION FOR SEQ ID NO: 22:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 28171 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 22:

ACAACCTTTT TCAAAAATC ACCTTGGTAC GGAGATGTTT TGCTTTCTGC TATTATTTTC	60
GGTTATATTC ATATCAATTT TGCTTTAACT CCTCTTGCTT TTTTCATTTA TGCTAGTGGA	120
GGTCTTATTT TAGCTCTATT GTATCGCATG ACTAAAAATC TCTACTATCC AATACTAGTT	180
CATATTCTCA TTAATATCAC TGCCTTCTGG GATGTGTGGT TGCTCCTATT TTCAGGAAGT	240
TAGCTTACTA AAATAATGTC GGAACTTTCC GGCATTTTCT TTTTTCACAA ATAGTCAACG	300
TTTTTCTTTT CGATATTGTA GTGGTGTGTA TCCAGTTATT TTTTGAATT GATTTTGAAA	360

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ATAAGGTTGA CTTGAGAAAG GCAGATAGTG AAGATAGTTA AGAAGAATAG GATGTTCTTT	420
TTTCCTTTTT GGAAAACTTC TAAAATATGG TATAATGAAA AGATAAAGAA GTTGGGGGTA	480
GAAGATGAAC ATTCAACAAT TACGCTATGT TGTGGCTATT GCCAATAGTG GTACTTTTCG	540
TGAAGCTGCT GAAAAGATGT ATGTTAGTCA GCCGAGTCTG TCTATTTCTG TTCGTGATTT	600
GGAAAAAGAG TTGGGCTTTA AGATTTTCCG TCGGACCAGC TCAGGGACTT TCTTGACCCG	660
TCGTGGGATG GAATTTTATG AAAAATCGCA AGAATTGGTT AAAGGATTTG ATATTTTCA	720
AAATCAGTAT GCCAATCCTG AAGAAGAAAA AGATGAATTT TCTGTTGCTA GCCAGCACTA	780
TGACTTCTTG CCACCAACTA TTACGGCCTT TTCAGAGCGC TATCCTGACT ATAAGAAGTT	840
CCGTATTTTT GAATCAACTA CTGTTCAAAT ATTAGATGAA GTGGCGCAAG GGCATAGTGA	900
GATTGGGATT ATCTACCTCA ACAATCAAAA TAAAAAGGGG ATTATGCAAC GGGTTGAAAA	960
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TCATCCTTTA GCCCAGAAAG AGGAATTAGT CATGGAGGAT TTAGCGGATT TACCAACGGT	1080
TCGTTTCACT CAAGAGAAAG ACGAGTACCT TTATTATTCA GAGAACTTTG TCGATACCAG	1140
CGTAGCTCA CAGATGTTTA ATGTGACAGA CCGTGCCACC TTGAATGGTA TTTTGGAGCG	1200
GACGGACGCC TATGCGACAG GTTCTGGATT TTAGATAGT GACAGTGTTA ATGGCATTAC	1260
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GGAGCTTAGT CAAGCTGGGA CTCTCTTCGT AGAAGTCATG CAAGAATATT TTGATCAAAA	1380
GAGGAAATCA TGAAAAAAG AGCAATAGTG GCAGTCATTG TACTGCTTTT GATTGGGCTG	1440
GATCAGTTGG TCAAATCCTA TATCGTCCAG CAGATTCCAC TGGGTGAAGT GCGCTCCTGG	1500
ATCCCAATT TCGTTAGCTT GACCTACCTG CAAAATCGAG GTGCAGCCTT TTCTATCTTA	1560
CAAGATCAGC AGCTGTTATT CGCTGTCAAT ACTCTGGTTG TCGTGATAGG TGCCATTTGG	1620
TATTTACATA AACACATGGA GGACTCATTC TGGATGGTCT TGGGTTTGAC TCTAATAATC	1680
GCGGGTGGTC TTGGAAACTT TATTGACAGG GTCAGTCAGG GCTTTGTTGT GGATATGTTT	1740
CACCTTGACT TTATCAACTT TGCAATTTTC AATGTGGCAG ATAGCTATCT GACGGTTGGA	1800
GTGATTATTT TATTGATTGC AATGCTAAAA GAGGAAATAA ATGGAAATTA AAATTGAAAC	1860
TGGTGGTCTG CGTTTGATA AGGCTTTGTC AGATTTGTCA GAATTATCAC GTAGTCTCGC	1920
GAATGAACAA ATTAAATCAG GCCAGGTCTT GGTCAATGGT CAAGTCAAGA AAGCTAAATA	1980
CACAGTCCAA GAGGGTGATG TCGTCACTTA CCATGTGCCA GAACCAGAGG TATTAGAGTA	2040
TGTGGCTGAG GATCTTCCGC TAGAAATAGT CTACCAAGAT GAGGATGTGG CTGTCGTTAA	2100
CAAACCTCAG GGAATGGTTG TGCACCCGAG TGCTGGTCAT ACCAGTGGAA CCCTAGTAAA	2160



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TGTTCAACCGT ATTGATAAGG ATACGTCAGG TCTTCTCATG ATTGCTAAAA ACGATGATGC 2280  
GCATCTAGCA CTGCCCCAAG AACTCAAGGA TAAAAAGTCT CTCCGCAAAT ATTGGGCGAT 2340  
TGTTCATGGA AATCTACCTA ATGATCGTGG TGTAAATTGAA GCGCCGATTG GCCGGAGTGA 2400  
AAAAGACCGT AAGAAACAGG CTGTAAGTGC TAAAGGGAAG CCTGCAGTGA CGCGTTTTCA 2460  
CGTCTTGGA CGCTTTGGCG ATTATAGCTT AGTAGAGTTG CAACTGGAGA CAGGGCGCAC 2520  
TCATCAAATC CGTGCCACA TGGCTTATAT CGGCCATCCA GTCGCTGGTG ATGAGGTCTA 2580  
TGGTCTCGC AAGACTTTGA AAGGACATGG ACAATTTCTT CATGCCAAGA CTTTAGGTTT 2640  
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AAGTTTATCG AACTGACCAG CAAGGAGCTA TACGTTTTAA GGGGTTGGAT AGTTGAAAAA	25380
TCGAAAGTGT TCGATAGGAA GGATAAATGT TGTAGATTAG TGAAATAAAC TAAAAATTTG	25440
TTGCATAATA ATGATAAAAA TGGTATAATG AAAACGTATT CAATATTGAG GATATAAAAT	25500
CATTAAAAAT CAGCAAAAGT TGTTTTATTA GTTAGTTTAT AATCTATTGG TCTTCTTCAG	25560
TCCAGTGTAT CTGCTGTGAC AGTCACTAAA AGTTACAAGT ATGATTGGAA TACGGTTTGG	25620
GAATATAGTA CCAACTATCA CGACCATCAG TATGCTTGGA TTCCGTCATG GTCTCGTTAT	25680
GACAGCTATT CTGAGTATAA AGTTGGCCGA GGCTGGAAC TACGCTCGTTA TGAGGTCATA	25740
AACTATTACA GCGGAGGCTA TTAATTCTTA AAGAGTGAGA AAAAGGAGGG CTAGATATGT	25800
TGCAGCTTAC TCATGTGACC TTA AAAACGC GACAAGTCAT CTTGCAAGAT GTGGATTTC	25860
CCTTTAAAAA GGGTAGGGTT TATGCTCTTC TTGCTATCAA TGGCTCTGGA AAGACGACCC	25920
TGTTCCGTGC CATTAGCAAT TTAATTCCTA TAAGTAGTGG AAATATCGCA GCCCCCTCTT	25980
CTTTATTTTA TTATGAGAGT ATTGAATGGC TGGATGGAAA CTTAAGTGGG ATGGACTACC	26040
TTCTCTTAT CAAAAACATC TGGAAGTCAG GTCTGAACTT GAGGGATGAA ATCGCCTATT	26100
GGGAAATGTC TGACTATATC AGTCTTCCCA TTCGCAAGTA TTCCTTAGGC ATGAAGCAAC	26160
GCTTGGTGAT TGCCATGTAT TTCCTCAGTC AGGCCAAATG CTGGCTCATG GATGAGATTA	26220
CAAATGGCTT AGATGAGTAT TATCGACAGA AGTTTTTTGA TAGGCTAGCA CAAATCGATA	26280
GACAAGAACA GCTGGTTCTT TTAAGTTCCC ACTATAAGGA AGAGTTGGTT GATGTCTGCG	26340
ATAGAGTAGT AACCATTCAAT CAGGGGCAGA TAGAAGAGGT TTAGTTTATG AAAGATGTTA	26400
GTCTATTTTT ATTGAAAAAA GTTTTCAAAA GCCGCTTAAA CTGGATTGTC TTAGCTTTAT	26460
TTGTATCTGT ACTCGGTGTT ACCTTTTATT TAAATAGTCA GACTGCAAAC TCACACAGCT	26520
TGGAGAGCAG GTTGAAAGT CGCATTGCAG CCAACGAGAG GGCTATCAAT GAAAATGAAG	26580
AGAAACTCTC CCAATGTCT GATACCAGCT CGGAGGAATA CCAGTTTGCT AAAAAATATT	26640
TAGACGTGCA AAAAAATCTT TTGACGCGAA AGACAGAAAT TCTGACTTTA TAAAAAGAAG	26700
GGCGCTGGAA AGAAGCCTAC TATTTGCAGT GGCAAGATGA AGAGAAGAAT TATGAATTTG	26760
TATCAATGA CCCGACTGCT AGCCCTGGCT TAAAAATGGG GGTGACCCG GAACGGAAGA	26820
TTTACCAAGC CCTGTATCCC TTGAACATAA AAGCACATAC TTTGGAGTTT CCGACCCACG	26880
GGATTGATCA GATTGTCTGG ATTTTAGAGG TTATCATCCC AAGTTTGTTC GTGGTTGCTA	26940

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TTATTTTAT GCTAACACAA CTATTTGCAG AAAGATATCA AAATCATCTG GACACAGCTC	27000
ACTTATATCC TGTTCACAAA GTGACATTTG CAATATCCTC TCTTGGAGTT GGAGTGGGAT	27060
ATGTAAGTGT GCTGTTTATC GGAATCTGTG GCTTTTCTTT TCTAGTGGGA AGTCTGATAA	27120
GTGGPTTTGG ACAGTTAGAT TATCCCTACC CAATTTATAG CTTAGTGAAT CAAGAAGTAA	27180
CTATTGGGAA AATACAAGAT GTATTATTTT CTGGCTTGCT CTTAGCTTTC TTAGCCTTTA	27240
TCGTCATTGT GGAAGTTGTG TACTTGATTG CTTACTTTTT CAAGCAAAAA ATGCCTGTCC	27300
TCTTTCTTTC ACTCATTGGG ATTGTTGGCT TATTGTTTGG TATCCAAACC ATTCAGCCTC	27360
TTCAAAGGAT TGCACATCTG ATTCCCTTTA CTTACTTGCG TTCAGTGGAG ATTTTATCTG	27420
GAAGATTACC TAAGCAGATT GATAATGTCG ATCTAAATG GAGCATGGGA ATGGTCTTAC	27480
TTCTTGCCT GATTATCTTT TTGCTATTGG GAATTCATT TATTGAAAGA TGGGGAAGTT	27540
CACAGAAAA AGAATTTTTT AATAGATTCT AGCTTTCCTA TAGGTAGGGA AAATAAGTAA	27600
AACTAACAT AGAGAGGGAA TCAACTTGAT TCTCTCTTTT TGATTGCGAA ACCAAACCAA	27660
AATACAAACA CAACTTTTC AAAAAATAAC TTTTATCTT GACAAGAGCT AGAAAATTG	27720
GTATCATATA AAAGTTGAGA AAAGCAGAAG TGAGAGCTTC TCGCCTTGTG ACATTAAGTT	27780
GCCTGGCCCT ACGGATGAAA AGTTTCGAAG AAACGCTATC ATAACGTGCG GGCTTGATA	27840
TTTACAAGTC CGCTATTGTT TTTCTCTAAT AAAACAAAAG AGGTGAAAC CATAGCAAAG	27900
CAAGACTTAT TCATCAATGA TGAGATTGCT GTACGTGAAG TTCGCTTGAT TGGTCTTGAA	27960
GGAGAACAGC TAGGTATCAA GCCACTCAGT GAAGCGCAAG CTTTGGCTGA TAACGCTAAT	28020
GTGACCTAG TATTGATTCA ACCCAAGCC AAACCGCCTG TTGCAAAAAT TATGGACTAC	28080
GGTAAGTTCA AATTGAGTA CCAGAAGAAG CAAAAGAAC AACGTAAAAA ACAAAGCGTT	28140
GTTACTGTGA AAGAAGTTCG TCTAAGTCCG G	28171

(2) INFORMATION FOR SEQ ID NO: 23:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 7147 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 23:

CCGCTCAACT TTTGCAATCA AGGCTAAGTA GACAGCAGCA AATTTCATAT TGTATAATTT	60
CTGACTCATA CTTCTCTCTT TCTATGTGTA CTAGTATAAA TAAGAAAAAG AAGGCCGTCA	120

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AGCCTTCTTT TGATTTATTC TTCTGCTTCA TCTTCTGTAA ATTGACTATT GTACAAGTCA 180  
GCGTAGAAGC CACCTTGCGC CATCAGTTCC TCATAGTTGC CTTGCTCGAT GATATTTCCA 240  
TCTTTCATGA CCAAGATCAA GTCTGCATTT CGGATGGTTG ACAAGCGGTG GGCAATGACA 300  
AAGGATGTGC GTCCTTCCAT CAAACGGTCC ATGGCTTTTT GGATCAATTC CTCTGTCCGT 360  
GTGTCAACAG AAGAAGTCGC CTCATCCAAA ATCAAAAGCG GTGCATCCTT AAGAAGGGCA 420  
CGAGCAATAG TCAATAGTTG TTTTGTCTTT ACAGACAAGG TCACGGTGTC ATCCAAGATG 480  
GTATCATAGC CATCTGGCAA GGTGATAATA AAGTGGTGAA TTCCCACAGC CTTACTAGCT 540  
TCCATCATTC GTTCATCACT AATCCCTATT TGATTATAGA TGAGATTGTC TCGAATAGTT 600  
CCTTCAAAGA GCCAGGTATC CTGCAAGACC ATTGAAAAGG CATCATGCAC TTCTGAACGC 660  
GTCATAGCCT TGGTATCCAC ACCATCAATG CGAATACTTC CTTTATCAAT CTCATAGAAT 720  
TTCATCAAAA GATTGACAAT GGTGTGCTTA CCAGCCCCAG TCGGCCCAAC AATGGCAACC 780  
TTTTGACCAG CATGAGCTGT CGCAGAGAAG TCATAGTCTT GAACATTGAC ACCGTCCACC 840  
AGAATTCTC CTGCTGACAC GTCGTAGAAA CGTGGAAATCA GATTGACCAG AGTTGATTTA 900  
CCAGAACCTG TTGACCCAAT AAAGGCCACT GTTTGACCAG TTTCTGCTTT AAAGCTAACA 960  
TGTTCAATAA CTGCTCCGA ATTTGCCGCA TAGCGgAAGG TCACATCCTT AAATCGACC 1020  
TGACCTTTGA AGTTTTCATC AGTCAGCTGC ACTTGAACAG GGTTTTGGAT AGAAGAATGC 1080  
AAATCTAAAA CTTGATTAAT CCGCTTAGCA GAGACCATAG TTCGGGGAAG AACCATGAAG 1140  
AGTGTCCCA TGAGAAGGAA GCCCATGACA ACCTACATGG CATAAGACAT GAAAACAATC 1200  
ATGTCATAA AGAGAGGCAG ACGCGCTATC GGAGCAGCGT CGTTAATCAC ATAGGCCCCA 1260  
ATCCAGTAAA TCGCCACACT CAAACCACTT GAAATCCCCA TCATGATAGG ATTCAAAATA 1320  
GCCATAAGAC GGTGACAAA CAAATTCAAA CGGGTCAATT CATCATTTAC TGCTGCAAAT 1380  
TTTTTCATTTT GATAATCCTC TGCATTGTAG GCACGAACGA CACGAATACC TGTAAACTC 1440  
TCACGAGTGA TACTGTTTCTG TTTATCTGTC AGCCCCTGAA TCAAGGACTG TTTTGGAAAG 1500  
GCTAGCGTCA TCAAAACGGT CGTCATCAGG ACGTTGATAA TCACTGCCAC AAGTACGGCC 1560  
CAGAGCCAGT ATTCTGAATG ACCTAAAATC TTCCCAATAG CCCAGATAGC CATAATTGAA 1620  
CCACGCGTTA CCACTTGCAA GCCCATAGTA ATCAACATTT GAACTTGAGT AATGTCATTG 1680  
GTAGTACGCG TCAAGAGGCT AGGAATTGAA AATTTCTTAA TCTCTGTCTG CGAGTAATCC 1740  
AAAACCGGT TAAAAATATC ACTTCTCAGC CTACTAGTAT AAGAAGCCGC CACTCGGGAT 1800  
GCAAAAAATC CAACTGCAAC TACGGACAAG AAGGCAAGAA AGGACATTCC CATCATCATG 1860  
CTTGCCGACT GCCACAATC ATCTAAATTA GTTCTTGAC TACCTAGCAA ATCCGTAATT 1920



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TTCGAGATAT AGGTCGGCAC TTCCAACCTCT AGATAGACCG AAAAGCAAGT AAAGAGAATG	1980
GCTAGTAAAA TCATCCCCCA TTCTTTTCTA CTAATTCCTT TGGCTAATTT CTTTATTCTC	2040
TCCTCCTATT CCCTTGATAT TTTGCCTGTA GTTGACCGAG AACCTTCTCA AAAATCAGTA	2100
ATTCATCTTC ATCAATGTCT TCCATCAACT GCTTGTCTAT GCGTTCAAAA AAAGCCTTAA	2160
CCTGTTCAT CTGAGAACGT GCTTTGTCCG TCAGACGAAC AAAGTTAGCC CGCTTATCAA	2220
CAGGACTCGC CTCCAATTCC ACCAAACCAT TTTGCACTAT ACGCTTAACC AGATTACTAG	2280
CAACAGGCTT GGTAAATATG AGTTCCTGCT CGATATCTTT AATCAAGACC AAGTCTTGGT	2340
TTTTCTCGCG ATTATCCAAA AAACGCACAA CCTGACCTTG CGGCCACCC ATAAATTCAA	2400
TGCCGCAACG TTTGGCTTCC TTTTGCACCA TCAGGTGAAT TTGATGACCA AAACGCTTAA	2460
AGACTAACAT CGGTTTATCC ATAATCTCCC CCTTCTAAAT AAAAATAGTT CTCTGGAGAA	2520
TAATTAAATT TCTATGAGAA CTATTTTCTT GATTAAAAAA ATCCCAAGTG ATTTTCTCAC	2580
TTAGGATCAT GTTCTATAGG TTAAATTAAA ACCCATCTAC GTTCGTATAA ATCTTTTGGA	2640
CGTCTTCGTC GTCTTCAAGA ACGCTGTAAA GTTTTCAAA GGTTTCAAGG TCTTCGCCTG	2700
ACAATTCCAC TTCTGACTGA GGAATCATTT CCAATTCAGT CACTTGAAT TCTTCAATAC	2760
CAGACTCAGG GAGGGCAACG ATAGCCTTGT GAAGTCAGT TGGCGCTGTG TAAACTGTGA	2820
TTGTACCTTC TTGTGCTTCT ACGTCATCCA CATCCACATC CGCTTCGAGC AATGCTCAA	2880
AGACTGCGTC CGCATCTTCA CCTCCAAATA CAATAACACC TTTGTTGTCA AAGAGGTAAG	2940
AAACAGAACC TGAAGCGCCC ATGTTTCCGC CGTTTTTACC AAAGGCTGCA CGGACATTGG	3000
CTGCTGTACG GTTGACGTA GAAGTCAAAG TATCCACAAT TAGCATAGAG CCATTTGGCC	3060
CAAAACCTTC GTAACGTCTT TCTGTAAAGG TTTCGTCTGT GTTTCCTTTG GCTTTATCAA	3120
TCGCTTTATC GATAATGTGT TTTGGCACTT GGGCTTGTTC AGCACGGTCG ATAACGAATT	3180
TCAAAGCTGA GTTTGATTCT GGATCTGGAT CACCTTTTTT AGCTGTACA TAGATTTCTA	3240
CACCAAATTT TGCATATACT TTAGAGTTAG CTCCATCTTT AGCCGTTTTT TTGGCTACGA	3300
TATTGGCCCA TTTACGTCCC ATTAGGAATC TCCTTTTTTC ACATTTTAAT CTTTCTTATT	3360
ATAACACAAG TTTTTTGTAT TTCACTAGA GGAAATGGAT TTTATTAGCA AATCAAGCTA	3420
GGATAGCACT TTACCTGCTA AGATGGTCTT GCCTTTCTAT CTTTATCAAC AGGCACTCAT	3480
CCACATTCAA AAAACAACT AGACCATTAT CTGCAAATAG AAAGTTTCAG CCAAGTTTGA	3540
CAAAGTCAGC TCAAATTACT GTTTGAAGTT TGATAGATATA AGCGACAAAA ACAATCATAC	3600
TGCACCTTTT GTTGACAGTC TACTCCAGAC ATATCATAGT TCAAGTAAAT ACTTTGAAAT	3660

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TCAACAGTTC TTATAGGCGC TATTGTATTC TAAGAAATCA ATAGAAGAGT TTCTAAGCAA	3720
ACCTCTAATA CTCAATAAAA ATCAAAGAGC AACTAGAAA GCTAGCCTCA GGTTGCTCAA	3780
AACACTGTTT TGAGGTTGCG GATGGGGCTG ACATGGTTTG AAGAGATTTT CGAAGAGTAT	3840
AATTACGTG TTCCAAGAT GGAGAAGTTA GACTAGTACA CTGGCACTTC TAAAACATTG	3900
CTAGCAATTG ATTTGTTTCAT ATTAAATTC ATTTTTCCTA TAAATGGGT TTAGATATAA	3960
ACAGCAAAAT ATTTCCGATA CGTGTCTGTC TTGAATTTC AATCATCTAA AACAAGTAAA	4020
GGATAATCAA TCCCCTGTAT ATCAAGGAAT TGGCTACCC TTTTACTTTT TTACACATTG	4080
TGTTGATAG ATTCAATTTA ACATCACGAG CATACTCAA TGGAAATCG TAGGCAAGAG	4140
ATAAACTTTC AGATATCCGC AGAGAGATCA TCGCCTCTTT TTGTCGCAAG CATTCTCCTC	4200
TCCTAGTCAT TTTCTACCTT ATCTTCTACC TGAGGATAGA GAGTTGTTC CCAAATAGAA	4260
ATCGTCCGCT TACGCACTAG TGGCAAATCG GTTTTTCAT AAACCGTACG CCACCATTCC	4320
CAGGCAAGCC CGGTACACTC TCTAATTTG ACAGAGAGAT TACGAACAT CCCTTTTAAA	4380
GGAATACTAG TGGTAAAGT AGCCGTTAAA TCCTGCCCAT TTCTGTCCCA AGCCTTAGGA	4440
GTCAAGACTT CTTACCTTG ATGATCATAG GATAATTCAT TCCAAGTAAT ATAATATTGG	4500
GCAACATAGG CACCACTATG ATCCAGCAGT AAATCTCCGT TTCTGTAGC TGTAACCTTA	4560
GTCTCAACAT AGTCTGTACT ATTTTGAAAG GTCGCAACTA CATTGTACG TAAAAAGAA	4620
GTGTATAGG AAATCGGCAA GCCTGGATGA TCTGCTGTAA AGCGACTGCC TTCTGAATC	4680
AAGTCTCTA CCATATCCAC CTTGCCTGTT ACAACTCGGG CACCCGAAGT TGGGTGCCCC	4740
CCTAAAATAA CCGCCTTCAC TTCTGTATTG TCCAAATCT GTTCCACTC TGTCTGAGGA	4800
GCTACCTTGA CTCCTTTTAT CAAAGCTTCA AAAGCAGCCT CTACTTCATC ACTCTTACTC	4860
GTGGTTTCCA ACTTGAGATA GACTTGGCGC CCATAAGCAA CACTCGAAAT ATAGACCAA	4920
GGACGCTCTG CAGAAATCC TCTCTGTTT AAATCCTCTA CCGTTACAGT ATCTTGAAAC	4980
ACATCTCCTG GATTTTAAAC AGCATCTACG CTGACTGTAT AATAAATCTG CTTAAAATTA	5040
ACAATCTGAA TCTGCTTTC GCCTGAATGG ACAGAGTTAA AATCAATATC AAGAGAATTC	5100
CCTGTCTTTT CAAAGTCAGA ACCAAACTTG ACCTTGAGTT GTTCCATGCT GTGAGCCGTG	5160
ATTTTTCAT ACTGCATTCT AGCTGGGACA TTATTGACCT GACCATAATC TTGATGCCAC	5220
TTAGCCAACA AATCGTTTAC CGCTCCGCGA ACACTTGAAT TGCTGGGGTC TTCCACTTGG	5280
AGAAAGCTAT CGCTACTTGC CAAACCAGGC AAATCAATAC TATAAGTCAT CGGAGCACGA	5340
TCGACCGCAA GAAGAGTGGG ATTATTCTCT AACAAGGTCT CATCCACTAC GAGAAGTGCT	5400
CCAGGATAGA GCGACTGTC GTTGGTAGCT GTTACAGAAA TATCACTTGT ATTGTGCGAC	5460

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AAGCTCCGCT TCTTTCTTTC GATAACAACA AACTCATCGG GTAGCTGATT ACCCTCTTTG	5520
ATGAAACGAT TTTCATACT TTCTCCCTGA TGGGTCAAGA GTTCTTTTT ATCGTAATTTC	5580
ATAGCTAGTA TAAAGTCATT TACTGCTTTA TTGCCATCT TCTACCTCCT AATAAGTTCC	5640
TGGATTGAGT TGCATAAACT CAGACTTGTT CAGCGAAATC AGCCGTGTTT GGACTAAGTA	5700
ATCCAAAATT TCCTCGTACA ATTCTTCTGA GACATTGCGT CGCCGTCTGG CTAAATAAGA	5760
AGTCGGAATG ACCGTATTAT CCAACATAAA TACCTTATCT AAGTCAATCA AGGTTGGTCT	5820
TGTAAGAGGA TTACGAGCTA GATCCGGCTC TTCTATCATA AAGTTCTTGA CCAAACGTCT	5880
GGTCAAGAGA GCTGGTTTGA AGGTCTGATT TTTAACCAAC TCTTTGTTTT TAGTCATGCT	5940
GTGTGCAATA CAGATATACA TATGATTCTT CACAGCCAAA TCGCTACTAA TAGTCGGAAA	6000
AGGCAAAATA AGAGCTACAA CATCTCCTCT CTTAATCAAG CAAGAGCACC CCCTTTTCTC	6060
CTAATGTAAC ATAGACAGGA TTGACCAAGT CTTCTGATTG ACTCAGAATT TCCAAAGTTT	6120
GAGTTTGGCG CGCTGTCAAT TTAGTAGCAT CTTGTCTCTT CAATACAAAA TGCTTGTCGC	6180
CAATAACCTT GACAATATAA TCCTTCTCCA AAGCTGACTG GTAAATCCAC ATCAGATGTT	6240
GTCTGTCTG AGAATCAAG AGAGAAGGAT TTTCAAGCCT CCCGATAGTC TGATAAAAAT	6300
CAAAACAGG AGCTAACTCC TGCCAATCTG ATTGGCTAGT TGTCAGGCT AGAAAAAGGG	6360
CTTTCGAGC TGATACTTCT TGTTAGCCT TGAGAGTTAC TTTCCCTCC AAGTTTTTTA	6420
GAAATCGGA AACTCCAGAA AGCAAATTTT TCTCTAAGT CGAGAAATAA AAACCTTTCG	6480
TTCCAGACA TAAGTCTTTC ATGTCGCTTT CTCTAGCAA TAAGAGCTCA AACATTGAT	6540
AGTAAAGAA AAATATCTGG CACTGGGTCG CGCTCATCTT TTCCTTATCG GCTTCTTTTT	6600
TTAACCAGAG CAAGGGCGAC AGGTAGCTGG ATTGAGACAT TTCCTCTACC TCCTACTCTT	6660
TTTAACTGG AGCATCTGCA CTAGCTGCCA CTTCTTTTGA CTGGATACTT TCCCACTGGT	6720
TAATCTCCTC TGAGATAAGA CCTTCGCATG TCTTGACAAA TAGGGCAAAA GCCTTGGTCT	6780
TTCTGCATA TTTCTCCGTG TGGCATTGAT AGAGGAATTT TTCTTTCTCC AGGAGTTGCG	6840
CAGTTTTTTG GTAAGAAATC CAATTTTCTT TTGCATTATA CAAATTGATA ATCCCCTCAC	6900
ACAGCAAGCC GAGACTGGAT AAGGCAACCG AAATCAAACG GTAGCGATCA CCTGGCATAG	6960
GAATAGCACA AAAGACAGCT ATGAGGAAAC CTGCCACGAT TTCTGTTATT TTTAATACCT	7020
TATAGCGCCT ACGATGTTGA ACGCTTTTCT TTAATAAATG AGCTATCTGT ACGTCTAATC	7080
GCTCTGTGAG GTACATTTCT TCTGGCGTCA TATTCGTAAC TCCTTTCATT TACTTTGATA	7140
ATCAGGG	7147

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## (2) INFORMATION FOR SEQ ID NO: 24:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 755 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 24:

CCGCATGGGA TTGGTGTCTT TTTGGGCAAT CTCTTTGACC AAACGGAAA CATGTTTAT	60
GCGCCTGCCT TPACTGCCCT TGTCGGCGGT ACGTCTATAT GATCCTAGTC GCAAAAGTTC	120
CGCGCTTTGG AGCCATTACC ACTATCGGCC TTGTCATTGC CCTCTTTTTC TTGGGAACTA	180
AACACGGTGC TGGTTCCTTC CTTCTCGGAA TTATCTGTGG CCTCCTAGCA GATGGAGTAG	240
CTCATTTAGG AAAATACAAG GACAAAACAA AGAACTTCCT TTCTTTCATT ATTTTCGCCT	300
TTAGTACAAC AGGACCAATC TTGCTTATGT GGATTGCGCC CAAAGCCTAT ATGGCTACTC	360
TTCTGGCAAG AGGAAAATCC CAAGAATATA TCGACCGTAT CATGGTCGCT CCAAACCCTG	420
GAACGTCTCT TCTATTTATC GCAAGTATTG TCATCGGAGC CCTAGTGGGT GCCTTGATTG	480
GACAAGCCTT GAGTAAAAA TTTGCCGAGA AAATCTGATC AGTTAAAAAG AGCCACGCGG	540
CTCTTTTITA TTTATGGCTC AATTTCCTAG TCAAGAAATC TCCCAAGAAT TGGATTGCAA	600
AGATAATCAA AATGATAATA ATGGTTGCCA AGATGGTCAC ATCGTGATTG TAGCGGTAA	660
ATCCATAAGC GATGGCTACG TTACCGATAC CACCAGCTCC AACCGCACCG GCCATAGCTG	720
TTtccCAACA AGGGaAtCAA GGTcACAGTC GTCAC	755

## (2) INFORMATION FOR SEQ ID NO: 25:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 3010 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 25:

TTCAATTGGT ATCTCAATCA ACGGTCTTCA CATGGTTTCA ACTGGTTTGA CTCTTGAAAA	60
AGCGAAAGCT GCTGGTTACA ACGCAACTGA AACAGGCTTT AACGATCTTC AAAAACCAGA	120
ATTTCATGAAA CATGACAACC ATGAAGTAGC AATTAAGATT GTCTTTGACA AAGATAGCCG	180
TGAAATTCCTT GGTGCCCAAA TGGTTTCACA TGATATTGCA ATTAGCATGG GAATCCACAT	240
GTTCTCACTT GCTATCCAAG AGCATGTGAC AATTGATAAA TTGGCATTGA CAGACCTCTT	300

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CTTCTTGCCA CACTTCAACA AACCATACAA CTACATCACA ATGGCTGCCC TTACGGCTGA	360
AAATTAAAAA TGAATGAGCT ATCTGGCCTT AAGTTAAGGT CAGATAGTTT TTAGCTAATT	420
TGTCCCCATA CAATTATAGT TTTTATCT TGTGCTTCAT TCTGTTCTGA CTTAAATGA	480
AAAGGTAGCT ACCAATACAA ATGATGAGGA TAAACAAAT GACTGAAAT CGTTATGAAC	540
TAAATAAAAA CTTGGCACAG ATGCTCAAGG GTGGTGTTAT TATGGATGTG CAGAATCCTG	600
AACAGGCTCG TATCGCAGAA GCTGCTGGTG CGGCAGCTGT GATGGCCTTG GAACGAATTC	660
CGGTGATAT TCGTGCAGCT GGAGGAGTTT CCCGCATGAG CGACCCAAAG ATGATTAAGG	720
AAATCCAAGA AGCGGTTAGT ATTCCAGTAA TGGCTAAGGT CAGAATCGGG CATTTGTGTG	780
AAGCTCAGAT TTTAGAGGCT ATTGAAATTG ATTATATCGA CGAGAGTGAA GTTCTATCTC	840
CAGCTGATGA CCGTTTCCAT GTGACAAGA AAGAATTCCA AGTTCCTTTT GTCTGTGGTG	900
CTAAGGATTT GGGTGAAGCC TTGCGTCGTA TCGCTGAAGG TGCTTCCATG ATTCGTACCA	960
AAGGAGAACC AGGGACAGGG GATATCGTCC AAGCTGTTCG TCATATGCGT ATGATGAATC	1020
AGGAAATTCG CCGCATTCAA AACTTACGTG AGGACGAGCT TTATGTTGCT GCCAAGGATT	1080
TGCAAGTCCC TGTAAGATTG GTCCAATATG TTCATGAACA TGGAAATTG CCAGTTGTAA	1140
ATTTGCTGTC TGGAGGTGTT GCAACGCCAG CAGATGCTGC GTTAATGATG CAATTAGGGG	1200
CAGAGGGGGT CTTGTGCGGT TCAGGTATTT TCAAGTCAGG AGATCCTGTT AAACGAGCGA	1260
GTGCCATTGT TAAGGCTGTG ACTAACTTCC GTAATCCTCA AATCCTAGCT CAAATCTCTG	1320
AAGATTTAGG AGAAGCCATG GTTGGTATTA ATGAAATGA AATCCAAAT CTCATGGCTG	1380
AACGAGGAAA ATAGATGAAA ATCGGAATAT TGGCCTTGCA AGGGGCCCTT GCAGAACATG	1440
CAAAAGTGCT AGATCAATTA GGTGTCGAGA GTGTAGAACT CAGAAATCTA GATGATTTTC	1500
AGCAAGATCA GAGTGACTTG TCGGGTTTGA TTTTGCCTGG TGGTGAGTCT ACAACCATGG	1560
GCAAGCTCTT ACGTGACCAG AACATGCTAC TTCCCATCCG AGAAGCCATT CTATCTGGCT	1620
TACCACTGTT TGGGACCTGT GCGGGCTTAA TTTTGCTGGC TAAGGAAATC ACTTCTCAGA	1680
AAGAGAGTCA TCTAGGAACT ATGGATATGG TGGTCGAGCG TAATGCTTAT GGGCGCCAAT	1740
TAGGAAGTTT CTACACGAA GCAGAATGTA AGGGAGTTGG CAAGATTCCA ATGACCTTTA	1800
TCCGTGGTCC GATTATCAGT AGTGTGGTG AGGGGTGAGA AATTTTAGCA ACAGTGAACA	1860
ATCAAATGTT TGCAGCCAA GAAAAAATA TGTGGTAAG TTCTTTTCAT CCAGAATTGA	1920
CTGATGATGT GCGCTTGAC CAGTACTTTA TCAATATGTG TAAAGAAAA AGTTGAGATT	1980
GAATTTCTCA ACTTTTTTAC ATGTAATAAA CAATAGCGAT GTATTGAAGT GCGGACGCAG	2040

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CTAGGATAAA GAGATGCCAA ATCATGTGGA AATAAGGTTT TTTCTTGGCA TAAAATCCAG	2100
CTCCAACGTG ATAACAGAGT CCGCCAGTTA CCATGAGACT CCAGAAAACG GGTGTCGTTT	2160
GACTGATAAT GGCAGGAATG ATAGCCAGAA CCAACCAGCC CATAATCAGG TAAAGAGCAA	2220
GGCTAAATTT CTCATTGACC TTTTtagCAA AGATTTTATA GAGAATACCA AAGATGGTCG	2280
TTCCCCATTG GATGACAATA ATCAGATAGC CAAACCAGTT ATTCATCAAG GTCAAGACAA	2340
CGGGCGTGTA TGAGCCCGCA ATGGCAACGT AAATCATAGA ATGGTCAATG ATTGCGAAAA	2400
CATATTTGTG GGTGGAACCA TAGGCCATAG AGTGATAAAT GGTGGATGAT AGGAACATGA	2460
GAAAGAGACT GATGACGAAA ATGGAAACGC CGATAGAGGA TAAAAATCCG TGTGCTTCAT	2520
AACTATAGAT GGATGAAATA GGCAGCAAGA TAAGCATGAT GACTGCACCC ACAGCATGGG	2580
TCACGCTATT AGCAATCTCC TCTCCAAAAC TGAGTTGTTT GCTGAGTTTA AGACTAGTGT	2640
TCATTGGATT ACCTCCTCTT GAGTATGATC GATTAACTCT AGAGTTTGAT GATAGAGTTT	2700
AACGGTTTGG CAGCTGGTTT GGATAATAGG GTTAGCTGGG TCAATTCCTT GGTCATGTA	2760
GTCCACAAAA GCATCGTAGA GTTGGTCTGA ACTTGCTTGA GTTGTAGAG TATTAAGTGT	2820
CTGGGCTATT TCTTGAATAG AAAATACAGA CTTGAGGGTT GTGATAGCAA TCAAACGGGC	2880
AATCTGTTGG CGTTGGTATT TTTTttTGTC AGGCTTTGTC AGGTAACCAT TTTTCACATA	2940
ATTGTTGACC ATAGATGCTG TTAGGCCCTT GTCTTTATTA GGAGAGATAG GGGCGCAGAC	3000
CTGATTGACA	3010

## (2) INFORMATION FOR SEQ ID NO: 26:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 15213 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 26:

CATAAATCGG TGCAAATAAC TTAATAGTGA AGTAGCCATT TCTTCGTAT TTACCTGAGG	60
CATATTCCCT AGACGAAAGA ATATTATTAT CAATCAAATC ATTGAATGAA CGTAGTCTTT	120
CAACTTCTTC TACTGTTAGA TTCTGACAA CATTTGTTGC ATAGACCTTA TTTCCATCAG	180
GATCAGGATG GTA CTCA TTT GTA ACTTTTC TAAGAAGTTG TTGTTTTTGA TTCGTATCCA	240
ATTTAAGAAT TGAATTTCTT TCGAGATATT CCAACATATA AACAACTCA AACATGTTGT	300
GGACATATTG CTTCAAATCA TCTGCATTAT TAAATCTTGT AGTTGGATCA AGTACTTGTA	360
ATCGTCGACT TTCTGTACTA TCAGATTTTG AATGTTTCAA GATGGAGTTG ATGGTAATGG	420

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TCGCATCATC TGGATGGTCT GGTGCTTGTA ATAATCCTTT AGCAAAGAAC TCTGGTCCCA	480
AGCCACTTCT TCGACCATAT CCTCCAAGAT AAATGTCCTG ATCTGAGTCA TGTGTCATCT	540
CATGCGTATA AGTAATAGCT CCATCCTTAT CCAACATTCG ATAACCCATA TAATAAACTG	600
CATCACCTGT AGCATAAGCA CCGTGTTGAT TATGCCCAAC TTTATTTCCA ACAGGTCCAA	660
AGAAATGTTG CATTGCAGGA TTTGGATTAT CAAAATCTGC CACTTCTGTA GCTTTCCCTA	720
CGGTATTATC ATCGCCAAAT TTATAAGCAT CGTAAAGCAA AATATTTCTA TAAAGTTTTT	780
CACGTGCATT GTCGTCTAAA ATACGATACC AATAATCGTA GTGATCTCGC TGACGTTTGG	840
CTGTTTCACG CGCATTTTCT TCAACAAAAT CATTGAGAGC CTTGCCCGCT TTATGGTCAC	900
TACTGCGGTA GCGATCATAA GCTCCAAATC CTAGACTAGA CATGGTCGAG ATGACAAATA	960
CGGATCTCTC TGGCAAGGTC AGGAGAGGCA AGACCATATT GCGGTATTTT CATGTGGCAC	1020
TCGTGATACG ATCATAAACA CCGATAGAAT ACTTGGTGCC AGCTAACCTT TGCTTCGTTT	1080
TCACCTCTTC GATAGTGGAT TTTTCTTCGA CAATGTAAGC CTTAGTCTCT GATTTAAACC	1140
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AATCTGTCGT TCCATGTGA CTGGCAAGAC TGATACCATA AGTATCGACA TTATCTTAG	1260
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TCCCCTTACC AAAGAAGTCC AAATGGTACA GAACTAGGTC TTTGACATTC ACCTGACCAT	1380
AGCTAAAGTT ATACCACCGT TCCAGATAGG TCAAGCCAAG TAGCAAGGCT TCCTTGTTGC	1440
GTTTGATTTT ATCTACAAGA TAACCTTCAG TGACGGGGTT AGCACTAGCC AGTCCAGCAT	1500
CCGCTGACAA GAGTTTTCCT AAACGTCTCT CCAGTTGTTG TTTTGTTTTG GCGAACTGGT	1560
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CTTCTGAATG ATAGTCAACC TTTTGTAAGT CAGGTAAGAC TTGCTTGATG ATAGAGGTTT	1680
GGTCATACAG GAATTGGTTT GGCGTATAGA GAAGTCCAGT ATTGCCCAGA CTATATTCTG	1740
CTAATTTGGC GAAATCATTG TGGTATTTGA GATCCAGCTT CTCAGATAAA TCATCCTTGT	1800
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TGTCCTTCAT CATGACTGCT GACAAGAGTT CTTTGTGATA TAAAAGACTG TTCTCATGTA	1920
CCAGGTTTCC GTATTTGACG ATGGTTGCCT TGTTGTAGAA AGGTAGCAAT TTTTCAATGT	1980
TTTTATAAGT CAAGTTGCGC TTAGCTTGAT AATAGGCCAC CTTAGAAAAA TCACTGTCTT	2040
TTTGGCCACT TGTTGAAAGT GGCTCCACTG TTGGTAAAAT GAGAGGATTG ATTTCTGCTT	2100
TTTTGCTTGC AATTTGAGAA GCATCTAGCA TTGTTCTCTT TTCTTCAAAG GATTCCCTGC	2160

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TAACATCGCT GAGAACATTG GTCAAACCTC CAGCATGCCT AACATCACCA GAAGTTCGAT	2340
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CAGTCTGATC TGAAGTATTT GTGTTAGATG AAATGGCTAC TGTCGCTTTT GACTTAGTAA	2520
GTAAAGCCTT GTCACCTGTC AAATGACCGA CCATACCACC GATATTGTAG GCAGCAGTCG	2580
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TACCTGAATT TTCTGGTTTT GTTCAGTTC CGTTTTTTC TGGTTGATTT GATTCTTCAA	3540
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TCTCTGAATT CGTTGTTGAT TCTTCTGCAG GTTGAACCTG ATTTTCTGCT TCTTGAATTG	3900
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CGGGCAACTC AGGCTGAATT GCGGGTCAA CAATAGCTCC AGACTGTACG TCCTTATGTT	4260
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CATCTGTCAG	AAGACTGGTG	TTTTGAGAAA	TTTTTGGTAA	ATTGTCCTGA	GTTAGTCCAA	12300
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CAAGACCGAT ATCATCAAGA GTAGTTTTCG CTGGTAAATC ATTCAAGACC AGATAGCGAG	13800
CCATTTGAGC AAAGCGCGTG ACGGTAATCG AAAAGAAGC CTGCTGGGAC AAGTATTCCA	13860
GCACGGCGCG TTCTTTTCA AAAGAAAGAG AGTTGGGGGC AATGTAGAAG ACCCGCTTGC	13920
CAGCTGCAAC TAGCTCTTCT GCCTCTCTTG TTAGAATTTT TGTCAAAGAA GTCCGAATAT	13980
CAGTATAAAG TAATTTATC TCAGCCTCGT TGAATTTT CATCACCTA TATTATACCA	14040
TGATTAGCCT CGTAAATCTG TTAAATATT TAGGCCATCC TTCTTTTCT TCATCATCTG	14100
CTAAATCTTA AATACTTAGC TTTACTTGTA TTAGATAGAA TAAGTCTGGC TACTGAAAT	14160
CACATAATAA AAAAGCCTCG GTAACAAGGC TTTGAGTTT ATGATTGTT CTTAGGTACG	14220
GAATACACTT CAATGTGTTG TCCAGTATC TTAATGTCGA CTGGTAGATT GTCTGATTTA	14280
TGCCCATCAA CATCGGACTC TAATTCGATA TCAGAAGAAG TTTTAATATT ACGTGCCTTT	14340
ATATATTCAA TATTCCTGAT AGAATGATTG AACTATAGTA AATTGAACT ATAATAGTAC	14400
ACCGTGGATG CTAAATATT TCTAGAAAT AATTGATTT CCCTAATCAA GCTATTCGTA	14460
TCTTATTTC ATCTACTATA ATAAATGAA CCAAAATAG TACACAATGT GGTATAATCT	14520
TCTTATGGCA TATTCAATAG ATTTTCGTAA AAAAGTCTC TCTTATTGTG AGCGAACAGG	14580

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TAGTATAACA GAAGCATCAC ACGTTTTCCA AATCTCACGT AATACCATT ATGGCTGGTT	14640
AAAGCTAAAA GAGAAAACAG GAGAGCTAAA CCACCAAGTA AAAGGAACAA AACCAAGAAA	14700
AGTTGATAGA GATAGACTTA AAAACTATCT TACTGACAAT CCAGATGCTT ATTTGACTGA	14760
AATAGCTTCT GACTTTGGCT GTCATCCAAC TACCATCCAC TATGCGCTCA AAGCTATGGG	14820
CTACACTCGA AAAAAAGAAC CACACCTACT ATGAACAAGA CCCAGAAAAA GTAGCCTTAT	14880
TTCTTAAGAA TTTTAATAGT TTAAAGCACC TAGCACCTGT TTAGATTGAC GAAACAGGAT	14940
TCGATACTTA TTTTATCGA GAATATGGTC GCTCATTAAA AGGTCAGTTA ATAAGAGGCA	15000
AAGTATCTGG AAGAAGATAT CAGAGGATTT CTTTGGTTGC AGGTCTAACA AATGGTGAAT	15060
TAATCGCTCC AATGACTTAC GAAGAGACGA TGACGAGCGA CTTTTTGAA GCTTGGTTTC	15120
AGAAGTTTCT CTTACCAACA TTAACCACAC CATCGGTTAT TATAGTAAAA TGAAATAAGA	15180
ATAGGGGGGG GGGGGGAGGG GGGGGGAGGG AGA	15213

(2) INFORMATION FOR SEQ ID NO: 27:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 6004 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 27:

TTATTACCTG AAACATTAAA TTTAATTGGA CATCCCGTTA TCAATTTTAT AATATCATCA	60
AGATTTTAT TATCTGATTC AGGAATTTTA TCTGATATAA CAACACCATT TTCAAGATAG	120
TTCATTAAAT TATTGATTC ACTAACATTA GTGTTTGTAT CTCCATCAAG CCAAAAAATAA	180
TGGTTATCGG AATCTAAATA CGATGAGTTT AAAATATTAT TACAAATTAT TTGATTTGCT	240
CCACCAGGAA TATATCTCAC TACTAAATTC TGTTTAAGAT TCTCACTACC TGAATGAGTG	300
ATAACAAACT CTAGAATATA TTTAGCTAGT CTATCTTCAA CATAAATCAT CTTCTAGAA	360
TGATACACAT CACCTAATTC AAAAAATGCA TCCTGATAAT CAATATTTTC AATAACATCT	420
ACCTTTTCTC CGTTTTTCAC TAAAAGTTTC ACGGCTTCTC TAGGAAAATC TTTTATAAGT	480
TGTGTAGAAT GTGTAGTGAT AATAATTTGA TGTTTTTTAT TTAAACACTC TTGAAGTAAA	540
AACTCTTTAA ATTTATAGAT TGCACTCGGA TGAAGTGAGA TTTCAGGTTT ATCTATTAAT	600
ATTAATGAAT TTGATTGCGC ATTTACTATA TCATTTACTA ACAAATAAAT TCTAGCCTCA	660
CCTGTCTCTG CAAAAGCCTC GGAATATTCT TTTCCAGATT TTTTCATCCA AATAGTTTGT	720

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GAAGCTTTTA TATCATCACC TTTTGAATAC AACCTATGTG TTAAAAATTG AATGTCTGTA	780
TAAGATTCAT CCATTATTTC ACTAATAATT TCACAAACTT TATCATCAAC TTAAACATTA	840
TCTATAACCA TTTCCTTTTT ATAACGCGTA TAGCTACTTG TATTATTCTT TAAAATATCA	900
GCAACTGGCT TAGATCGTAA TCTTATAAAA TCTTGTTTAC TACGTTGAGT AGAAATTTTT	960
TTAAAAATTAT AGTGATAGAA AAATAAATCA AAAGCAGAAA CATATTCTTT ACAATCACAA	1020
AAGACAACAT TTTTTCAT GGCATCCCAT CTGCTGTCG AAGAACTTCC AATATATTTA	1080
TTTTTGCGTA ATCTTCCAT CTCATATGT TTTTGAGGAG CATATGGTTC CCAATAATCT	1140
AATCCTTTTT TTGTTCCAGA ACGGCCTTTA AGAACTTCTA CATTTCTAGA AGCTTTAATG	1200
TTATAATATG AATAGATTAA ACATTGTTTC CCATCCACTT CATCTATTTG ATCAACATTT	1260
GTAATAAACC AATATTCAGA CACACTTTTA TTGGCTGGAG AACCATATAA AGCTTGTAAG	1320
ATTGAAGTTT TATTTACTCC ATATCTATTA CAGACACCTC AGGATTATTT AACTTATAAG	1380
TTTTTAACAGC TACGGAATCA ATTTCAACAG CAACTTGAAC ATCTATGCCT GATTTTTTAA	1440
GGCCACTTGT AGTGCCACCT GCACCGTTAA ATAAATCAAT AGCAACAATT TTCCCATAG	1500
TATTTCTCTA AAGTTTCTCC TTTTATTAT AACATTATCA AATGTAAAAC CCAACCCGAT	1560
AGGGTTAGGT TTTTAACATC ATTTACCAA CTCTTCATC TCATCAATAC GTGCGACGGT	1620
CGCGTCATAT TTAGCTTGGT AGTCAGCTTG TTTGTCGCAT TCTTTTGGG CGACTTCTGG	1680
TTTGGCGTTG GCTACGAAGC GTTCGTTAGA GAGTTTCTTA CCAACCATGT CCAGTTCTTT	1740
TTGCCATTTA GCAAGTTCCT TGTCGAGACG GGCCAGTTCT TCTTCAACAT TGAGGAGATC	1800
GGCCAGTGGC AGGTAGATTT CTGCTCCTGT GATGACACTT GACATAGCCA GTTCAGGTGC	1860
AGGGATGGTT GATGCGATTT CCAAGTGTTC TGGATTTGTA AAGCGTTTGA TATAGTTGAC	1920
ATTGCTGTTA AAGAAGGCTT CCAAGTCGCT ATCGCTTGTC TTAACAAGGA TGGTGATAGG	1980
CTTGCTGGT GCTACATTTA CTTCGACAG CGCATTCGA ACAGCACGAA TCAAGTCTTT	2040
GAGACTTTCC ACACCAGTGT GAGCCGCAAG GTCTTCAAAG GCTAGATTAA CAGTTGGGTA	2100
TGCAGCTGTC ACGATAGAAC CTCTGAGAT TTGTCCAAAG ATTTCTCTG TCACGAATGG	2160
CATGATTGGG TGAAGGAGAC GAAGGATCTT GTCCAGCGTA TAGAGGAGAA CAGATCGAGT	2220
AATGACCTTA TCGTCTTCAT TGTCGCTGTA TAGAACTTCC TTGGTCAACT CAACATACCA	2280
GTTGGCAAAT TCTTCCAGA TGAAGTTGTA AAGGATATGA CCAGCCACAC CAAACTCGAA	2340
CTTATCAAAG TTTTCAGTAA CTTTTCGAAT GGTTCGTTG AGATTGTGGA GAATCCAGCG	2400
GTCCGTCACA TTACCAGCCT CACCTGTTGC AACTTTTGTG ACATTGTCAT GCGCCACATC	2460
CAGCGTCAAA CCTTCATTGT TCATGAGGAT ATAGCGAGAA ATGTTCCAAA TTTTGTTAAT	2520



AAAGTTCCAT GAAGCATCCA TTTTCTCGTA AGAGAAACGA ACGTCTTGAC CTGGTGCGGA	2580
ACCGTTTGAA AGGAACCAAC GAAGGGCATC AGCACCGTAT TTCTCGATGA CATCCATTGG	2640
GTCAATCCCG TTACCGAGAG ATTTAGACAT CTTGCGTCCT TGCTCGTCAC GGATGAGACC	2700
GTGGATAAGC ACGTTTGGGA ATGGCTGACG ACCAGTAAAT TCCAAGGACT GGAAGATCAT	2760
ACGAGACACC CAGAAGAAGA TGATGTCGTA ACCTGTTACC AAGGTTGAAG TTGGGAAATA	2820
ACGTTTAAAG TCTTCTGAGT CGACTTCAGG CCAGCCCATG GTTGAAAATG GCCAGAGGGC	2880
AGAACTGAAC CAAGTATCCA AGACGTCTTC GTCCTGAGTC CATCCGTAC CTTCTGGAGC	2940
TTCTTCGCCC ACATACATT CACCATCAGC ATTGTACCAG GCAGGGATT GGTGACCCCA	3000
CCAAAGCTGA CGAGAGATAA CCCAGTCGTG GACATTTTCC ATCCATTGAA GGAAGGTATC	3060
GTGAAACGA GGTGGGTAGA ATTCGACCTT GTCCTCTGTG TCTTGTTAG CAATGGCGTT	3120
CTTAGCCAAT TGGTCCATCT TGACGAACCA TTGAGTAGAC AAGCGTGGCT CAACTACGAC	3180
ACCTGTACGT TCTGAGTGAC CAACACTGTG GACACGTTTT TCGATTTTGA CAAGGGCACC	3240
GATTTCTTCC AACTTAGCAA CGACTGCCTT ACGAGCTTCA AAACGATCCA TGCCTGAAAA	3300
TTCAAAGGCA AGCTCATTCA TAGTTCGTC GTCGTTTCATG ACGTTGACTT GTGGCAAAGT	3360
ATGACGTTGG CCAACCAAGA AGTCATTTGG ATCGTGGGCA GGTGTGATTT TCACGACACC	3420
AGTACCAAGC TCAGGATCTG CGTGCTCATC TCCAACGATT GGGATGAGTT TATTAGCGAT	3480
TGGAAGGATG ACGTTTTTAC CAATCAAGTC CTTGTAGCGC GGGTCTTCTG GATTAACCGC	3540
AACCGCAAGC TCCCCAACA TAGTCTCAGG ACGAGTTGTA GCAACTTCAA GGGCGCGTGA	3600
ACCATCTTCC AGCATGTAAT TCATGTGGTA GAAGGCACCT TCTACATCCT TGTGAATCAC	3660
CTCAATATCA GAAAGGGCTG TCGAGCTGC TGGGTCCCAG TTGATGATAA ACTCACCACG	3720
ATAGATCCAG CCTTCTTGT AAAGGTTTAC AAAGACCTTA CGAACAGCTT TTGACAAACC	3780
TTTATCAAGA GTGAAACGCT CACGAGAATA GTCTACAGAA AGCCCCATCT TGCCCCATTG	3840
TTCTTTGATG GTAGTGGCAT ATTCGTCTTT CCATTCCCAG ACCTTCGTCA AGAAAGACTC	3900
ACGACCTAGG TCATAACGCG TAATACCCTC ACCACGTAAG CGCTCCTCAA CCTTAGCCTG	3960
AGTCGCAATA CCAGCGTGGT CCATACCTGG AAGCCAAAGG GTATCAAAGC CTTGCATGCG	4020
TTTTTGACGG ATGATGATAT CCTGCAAAGT CGTATCCCAA GCGTGACCAA GGTGAAGTTT	4080
CCCAGTTACG TTTGGTGGTG GAATCACGAT TGAATAAGGC TTAGCCTTTT GATCGCCTGA	4140
AGGCTTGAAA ACATCCGCAT CAAGCCATTT TTGGTAACGA CCAGCCTCAA CCTCGGCTGG	4200
ATTGTATTTA GGTGAAAGTT CTTTAGACAT GTGTGTGTCC TTTCTCTATT TTGTTTATTT	4260

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TATTTTGAAT TTGCTTAGCA GCTTCTTCTG CAGACAAATT CGTATTATTT ATTTTAAAGT	4320
AGTGGTGCAA CTCATTCCGT TGATGTTGGG AATTTAATTG AAGTGTTTCA GCGGTCTCTA	4380
AAATTTCTCT TTCAGATACC TCAATATGTC GTTTTAAGGG TTTGTGCTTT AATCGATTCT	4440
CCGTTTCGATT TCGACGTATG CACTCTTCAA GACTTGTTTC CAATTCAACA AACAGAATCT	4500
CTTGATGAAA GTTATCCAAT AAATCCTGAA TTTGCTTTAA ATACATCAGC TGGTACTGAT	4560
TTGAAAAATC AATTACGTCT GTTAAATTA CTGATCGCTG ATTTCTTGCA CTGCTCCAA	4620
GGAAAGAAAA GGTAAATCCA CGAACAAATT CCCACATCTC CTCGGTATAA TCCTGATAGA	4680
TCTCTAGTGC AAAATCAATG GCTTGATGGT TATAAAATAG GGTAGCATCC GTCAGTCGAG	4740
ATAATCTTG ACCAATGGTC ATTTTCTCTG ATGCTGGAGC ACCAATGATG AAAAGATGCA	4800
TCAAATCACC TCCCACTCAC TCCTCAGCAA GCCATATCTC AAATCATCAC AGCAGTTGCC	4860
TTGAGCATCT TTGCGGTCTC TTATGCGAGC TTCGAGGGTA AAGCCAAGCT TTTCCGAGAC	4920
TCGTTGACTT TGAAGTTAT ATCCAAAGCA AGTTAGTTCA ATCTTGTAAG GACCAAGTTC	4980
TTTAAAGCT AGATCAATCA AGGAACACGC TGCTTCTGGA ACATAACCTC GACCCCAATA	5040
GTCTGGGTGC AAGGTATAGC CAAGCTCTAG CACATCATCC GCATGAAGAT GGTGAAGTC	5100
AACAGAACCA ATGACTTTAT CGGTTCTCTT GACGACAATC CCATAGCCAG CTGGGAGATT	5160
TTCCCTTTGA GTACGCTCCG GAAGAATGTG CTCCAGATAA TAAATCTCAT CTTCCAAGAT	5220
CTTGACTGGA GGAAACCTG CTGGATAGGC GACCTCTGGC AAACCTAGCGT AGGTATGGAT	5280
ATCCTCAGCA TCCACCACTG TGCGGACTCG TAAAACGAGA CGTTCTGTTT CGATTTTATC	5340
TGGCAGCTCA GTTCTTGCCA TCCTTCTTCC TCGCTTTTTT GATGAACTG CCCTTCATAT	5400
CTACACGCTT GTCCAGATAG CGATAAACGC GCTGATATCC ATCTCCCATG AAATAGGTTG	5460
GGGCAAACAG TTGATTTTTA AAATGTCCCT TTTCATCCAG GAGTTCTGGG GCAACAAGTC	5520
GCTCAAGAAT CTGGCAAAG ATGTGGCAAA TACCGTCTTC CTCACAATC CTATCTACCC	5580
GACAATCTAA AACAAGTGA CAGGCGTCTA AAATAGGAGT CTGAGTTCGT TCAGAAATTT	5640
CATAATGCAC TCCCAAACGT TCCAATTTCT CCTGATGACT GATAAAACCA GCCTGCTCCA	5700
TCGCAAGCAT AGAAGTTTCA TCAGAAATAT TCACAGTAAA TTTTGTATAC TGTTTGATCT	5760
GCTCTGCGGC ATTCTCTCTC GCAACGACTC CAATCACAAC CCAATCTCCT AGACTATAAG	5820
AGGAACTACA GGTCTGTATG TTATAGCCAA AATTCTAATC TTGATATCCT AAAATAAAAA	5880
CAGGAAAACC ATAATATAGT TTAATTTGTG TAAAAGATTG CTTATAACA ACCCCCTTTG	5940
ACTAAGACGT AAAAGAAAAG CCCTGCCATC TACATGACAG GGACGAATGT GTTTATCCGC	6000
GGGG	6004

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## (2) INFORMATION FOR SEQ ID NO: 28:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 5857 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 28:

TGTAGAATTC ACGACAATGC TTCGTTGATT TCTGGGTTGA TTTCGTCGCG TTCTGGCAAG	60
CGAGTCAATG AACCAAAAAT AGTACACAAT GTGGTATAAT CCTTTTATGG CATATTCAAT	120
AGATTTTCGT AAAAAAGTTC TCTCTTATTG TGAGCGAACA GGTAGTATAA CAGAAGCATC	180
ACACGTTTTC CAAATCTCAC GTAATACCAT TTATGGCTGG TTAAAGCTAA AAGAGAAAAC	240
AGGAGAGCTA AACCAACAAG TAAAAGGAAC AAAACCAAGA AAAGTTGATA GAGATAGACT	300
TAAAACTAT CTTACTGACA ATCCAGATGC TTATTTGACT GAAATAGCTT CTGACTTTGG	360
CTGTCAATCA ACTACCATCC ACTATGCGCT CAAAGCTATG GGCTACACTC GAAAAAGAA	420
CCACACCTAC TATGAACAAG ACCCAGAAAA AGTAGCCTTA TTCTTTAAGA ATTTTAATAG	480
TTTAAAGCAC CTAACACCTG TTTAGATTGA CGAAACAGGA TTCGATACTT ATTTTATCG	540
AGAATATGGT CGCTCATTAA AAGGTCAGTT AATAAGAGGC AAAGTATCTG GAAGAAGATA	600
TCAGAGGATT TCTTTGGTTG CAGGTCTAAC AAATGGTGAG TTAATCGCTC CAATGACTTA	660
CGAAGAGACG ATGACGAGCG ACTTTTTTGA AGCTTGGTTT CAGAAGTTTC TCTTACCAAC	720
ATTAACCACA CCATCGGTTA TTATTATGGA TAATGCAAGA TTCCATAGAA TGGGGAAGCT	780
AGAACTCTTG TGTGAAGACT TTGGGTATAA ACTTTTACCT CTTCTCCCT ACTCACCTGA	840
GTACAATCCT ATTGAGAAAA CATGGGCTCA TATCAAAAAG CACCTCAAAA AGGTATTACC	900
AAGTTGCAAT ACCTTTTATG AGGCTTTTTT GTCTTGTTCT TGTTTCAATT GACTATATAA	960
ATTGTCTAAG CGAAACAACC GATAAGAATT GGCACAAAAG CGACCGTATT TTTGTTACCA	1020
ATACAGGAAA AACAGTTCAT AGTTCTATCT TGAGCAAGTC TCTCCAGCGA GCAAACGAAC	1080
GCCTTAAAAA ACCAATTTCC AAACATCTGT CCCCTCACAT CTTCAGACAC ACCACTATTA	1140
GCATCTTATC AGAAAATAAA ATTCCTTTAA AAACAATCAC GGACAGGGTT GGTCAATCCG	1200
ACTCTGAAGT CACTACTTCC ATCTACACCC ACGTCACAAA GAACATGAAA GATGAAGCAA	1260
TCAATGTACT GGATAAAGTT ATGAAAAAGA TTTTAAAAA AGTTTGTGCC CTTTTTGCC	1320
CTCTAAATAC AAAAATAGCC CTTCCGATAA AATCCGAGGG GCTAGAAACG TTGTTAAATC	1380

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AACGGCCGAA CTTTGAATT TCATGTTTCG GGATAAAATA GTTCACTGAA CTATTTTATT	1440
TTTTAAGGTT ATCATAATAT CAAATAGTTC AATTAAATAC GCTAAATTAC TAATATACTT	1500
TTTACCTTTT TCATTCTAAA ATGTAAAGTA CAAACAATTA CAATATACTA GAGGGGGAGT	1560
AAAAAAGGTA TTAAATCGAT GAGTTCAGCA GGCAAGAAAA TAGCACCTTT ACGGGTGCTA	1620
TTTTTTAATT AACGCCACGT TAACTTTGA TTGATGAATT TTATTGTTTG GCACTTCTTT	1680
CATTTCACGG TAAACATCGA TGAAATTCIT TCCAACATTA TTTTGGAGT TAACTGCATT	1740
TATTTTGTGA TTAATAACTT TTTTAGTATC GAAAGAATGG TTTAAGAAAT CCATAACTAA	1800
CTCTCCTTTC TCATCCTGTA ATCAAGATTT TTATCAATGT CAAAATAGTA TTTTCTATCA	1860
ATCCAAATG GTCCTTCTCC TTTAGAAATA GCAAGTACAT CTACCGGACC TCCTACTGTT	1920
TCAAGAGTGT TGACAATTTT TCTCTTAAAT GAAGTTAATT CAATAAATGT TTTAGCTGTA	1980
CTCGCCATTT CATTAAGTGG TTGCATTCCA ATAAGGTCTA TTATAGGATT TATATAATAT	2040
TTTTGCTGTA TAGATGATAT ATTTTCAAAT ATATTCTCAA TTTTCATCACC CAATCCATTT	2100
TTCTCCATAA CTGATGATAC TTGCTCTGCG ATATATACAT TTAAGTTAGG ATCTATACCA	2160
TTCATAATCG TCTCAACCAT CTCTGACTGT GCAAAAGGGA TTATATGACA AGTTTATGA	2220
TGATTTATCA CACTTTCATT AATAACTTTC CAAATTAATC GTTTAGAAAA AATTCCATAT	2280
AATTCAAATTT GTCTTATAGA TGGAATATC TCGTCTGTAC CATAACCTGC TATAACTAAT	2340
CCAGTTATGT TTGTTGAGTC ATATCCAATG AAAATCGCTT TATATAAAGA TTTAGCAATA	2400
ACTTCAACCT CATCATCAGT ATGAGGAAAG GATTTAAAA CATCGTCTAC AATGCTTTTT	2460
ATTAACCTCTA ACTCAGCTTC AAAAAATCA AAATTACTTT CAGCTTCTAC TTTTGAAATT	2520
TCTAAACTAA AATTAGTTAT AGCATTTAAT AAAATTTTAT TAAAATCATC TAGAGTGATG	2580
GTTTCACCAT TAGAAACTCT TAAATCAGCT GTTCTCTGCG CTTTCATAGGC AATGCTGTCC	2640
AAAATACTTC TTGTACTTCT GACAATATAA TTTCTTAATA AATCCTCAAC TTGTAGATGT	2700
TTAAAGGAAA TTAAAAATTC TATTAGCTTT TCAACGTATT GGGCAGTATT ATCTAATAAA	2760
TCTGTGCCAA TAGCCTGCTT AACTCATTT AAAATTACCT CCCACGGAAT TTCCATAAAC	2820
GAAGCGTTCC CATATATCAT GATCCCCACG GAATGTTCTT TTGATAAAGT GAATAATTTT	2880
CGGGCGCTAT TAAAACTTT TGAATTTTTC CCGTCTGATA AGGTTACAGC GCTATCAGAA	2940
GCCAATACAA CACCATTTTT ATTTAATATT CCAATTTCTG CTGTCAAAT ATCACCTAAA	3000
CTTCTAAAC CTGCTCATGC TCTAATGGTA CAACAGCTAA GGTCTTACCA AGACTTGCCA	3060
ACACTTTTAA TACTGTATCA AGTTGTGGGC TTGTCTTTCC TGTTTCATT CTAGCGATAA	3120
CTGGCTGACT AACACCGCTC ATCTCCTCTA GTTCTTCTG ACTAATACCC TTTTCATTTT	3180

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TAGCCTCGAT AAGCTCACTC ATGATAGCCA CGCGCATATC ACTTTCCTCTT	3240
TGCTGAATAA TTCAGCTCTT ACATCTTTCC AGTTACTACC AATAGCATT	3300
TCTAAACCTC TTTCTTTTAA ATCTGCAAGT TCACGTTTAG CTTGCTCAAT	3360
GGTGTCTTCT GTGCTCTTTT CATAAAATGA TGCAGTAAAA CAAACTACC	3420
GCAACAAATA AAATCTATC TCTAAGTGGT CTCAGCTCCC AAATTTGAGC	3480
TTAATATATG GTTCGCCTGC GCGTGTCCA TGTGGGCTTA ACAACTCAAT	3540
ATTTTATTAA GCTTAATCTT GCTATCTTTC CCTTTTTTAC TGTAAGCTC	3600
TCAAAAACAG GCTCATTGCC GTTTTTATCC TTGTAAAAAT AGATATTATG	3660
ACCTCTTCCT AATAACAATT ATAACCTAAA AGTTATTGTT TGTAAACT	3720
TAAATAAAA AGCACCTAGT TTCCTAGATG CTAGCACAAT GACACGGATT	3780
CTACCTCTAT CAAGGTGTAC TCCTTCTATA CTATCCCTTG TGCTTTAGAA	3840
CACAATCAAC TAGATACCTA CCATCTCATG ATATACCCCC ATTTGGGCA	3900
GCTAAAAATC AAATCAGAAT AGATATTAAA CCACTTATTT AACTTATCAT	3960
TTGACTGATA AATAATATCC GCTGACAAGC TCCGATAACA TTCATGTGAT	4020
AACCTCTTTT ACAGCCTCTA AAATGTCAGC CTCACTTGTT TGTACCCTAA	4080
CTGCTTGATA GTTGCGTATT TTTGATAAGC TAGCATATCT TGATTTTAG	4140
CATTTTACGC TCAAGGACAC TATACTTAGG TTGTTCTTTA TCTCGCATGA	4200
GAGCCATAAA ATCTTTTCTC GGTGTATTAC AGAAATACGC TCAATTTTCT	4260
TGCTACCTCC TAAATCATCA ATTTAACAAT TCTAACCCT CACTTTTAGA	4320
TAGATCTTGT TCGATGTATG ATACAAAGGT TCTAAATCTT TTTCCACCT	4380
ATCTTATCCT CATGAGTAGG AAAGTATAGT ATTTCCGTTT CATCTCGTT	4440
TTGCACCAAT CATCAATAAT AACTGGCACT TCCCCTCAC GCCATTTTTT	4500
AAAAGTTCAT TATCACTAAA TAGCTCGCCA TCTATTTGGA AAAATTCCCC	4560
TTTCCTTCAA CAATAATAAA CTCTGGCATA TTTCTATTAC TTAATAACTC	4620
TGTAACCTCT TGATTTCTCT TAGATACTTC CTCAATTCC AACCTCAATT	4680
CCTTACTACT CCAAAAATTT CATGGGCTTT ATAAGATTGT TCAAGTATAG	4740
TTGAGTTCTT ATAAACGGGT TGACCTTACT GTCCATCATA ATATCATTGA	4800
AGCGTTAGAT GATGCTAAAT AAAGCATTTG AGTTGTTTTA TCCATCATCT	4860
TATCCTCAAT GTCTTTTTAA CCGCTGCAAC TTTTAGATAC TTATGACCTG	4920

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TACCCCTGCT TTTTGACATG CTTTGTCTAT CGTTGGCTCG GTAAGCATGG CATCTATGAA	4980
TTTAATTTGC TTGGACGTAA GGTATCATT TTCATTTCCCT GCCATCTATT ACCTCCTCAT	5040
TATCAAAATA AAGGGTTGCC CCTTTATTTT CCTATGCTAG ATAATTCTGC AATTCTGCAT	5100
CCATGCGCTC TGAATTGCCC TCAACAATCA TTTCATGCTG TACTAAATCA ATCTTATCTC	5160
CGTTAATAAG TAAACCACCG TGGAATAAT CAATTTTCT ATCAAGGAAA TGTACTAGCT	5220
TTTCAAGGCG TTGCTGTTGG CTGAATTGCT CCATGTCAAT TTCGATATAA GCAAGGGTAG	5280
TATCATTATC CATAATATCT TCTAATTTT TAAGAGCTAG AGGTTTATTT TTATATTTTT	5340
CTAGGTATTC TCTCATTCTT GCCACTGTTA ATTTGATACT AGATAATAAA CTTAGTTCAG	5400
CTGCATCATC TGCTGTAATA GGCTCTTCTT TTGATTTCATG GTTTGCTAGT TCAGCATTTT	5460
TCTCTTTTTC TAGTTGCTGA TACAATAGCT GAGCAGTATT TTGGGAATAG TTTTCGCCCT	5520
CTTTTATA TTTTAAAAGT TCTTGCTCTG CATACACTTT CCCGATAATC ACTTCCTTAT	5580
AAACTAATTG CCCATCTTGA GCTTTTAGCT TAATACTCCC ATGCTCTGGA ATTTCAATAT	5640
ACTTAATTAT ACCATTTTTT GAGTATAAAA CAAAGCCTTT CTCCATCATT TTTAATAATT	5700
TATCATCCTT GTTTTCAGTC ATGCTTTTCT CCTTTATTTT ATTTTATTAT AATCTGAATA	5760
CCCCTAGTCT ATTTATTTCA CTAGTTTTT AGGGTTCGTA TGCTAAAATA CTACCCTTTT	5820
TGTGTACCTT ATGGCTGACT TTCAAATTG GTTAGTT	5857

## (2) INFORMATION FOR SEQ ID NO: 29:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 10254 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 29:

AAAATGATAG CAGGAGAGTT TTCCCGTCCA TCAGACCCAG AACTGAGAGC CTTAGCTCAG	60
GCTTCTCGCC AAAACAGGC CGCCTTTAAC AAGGAAGAGA ACCCCTTGAA GGGAGCCGAA	120
ATCATCAAGA CTTGGTTTGC CTCAACCGGG AAAATCTTT ACATCAACAC TCGCTTGATG	180
GTGGACTACG GTGTCAACAT CCATCTAGGG GAAAATTTT ATTCTAATTG GAACTTGACC	240
ATGCTGGATA TCTGTCCCAT TCGTATCGGG GACAATGCTA TGATTGGTCC TAATTGTCAG	300
TTTTTGACAC CCTCCATCC ACTAGATCCA CAGGAACGCA ATTCAGGTAT CGAGTACGGA	360
AAGCCTATCA CAATCGGAGA TAATTTCTGG ACTGGTGGTG GCGTCATTGT CCTTCCTGGA	420
GTGACACTGG GAAATAATGT CGTTGCAGGA GCAGGGGCAG TAATTACCAA ATCTTTTGGC	480

GACAACGTTG TCCTAGCTGG CAATCCTGCG CGCGTGATTA AGGAAATACC TGTAAATAG	540
AAGTAAAAAG GAACAGCTGG GGTGTGTTCT TTTTGTAGG TTTCATCATT TTTTACCCAG	600
TTACATTTA CCTACTCTAT CTCTTAGCAA GTCTGTTTCA TTAAGCAAGT TCAAAGCATC	660
TCGTAAGTGG GATGTTTTTC TCCTCAGTTC ATCAGCTTCC TCCTTGACAC TCGGTCAGAT	720
TTTGATACAA TAGTACAAAA TTAGAGGAGG CAGGCTATGA TTCAGAAACA TCGGATTCCT	780
ATTTTAGAGT TTGATGACAA TCCTCAGGCG GTTATCATGC CCAATCACGA GGGGCTGGAC	840
TTGCAGTTGC CAAAGAAGTG TGTATTATGCA TTTTTAGGTG AGGAGATTGA CCGCTATGCG	900
AGGGAAGTAG GGGCGAAGTG TGTGGCGGAA TTTGTTTCTG CCACCAAGAC CTATCCAGTT	960
TATGTCGTGA ACTACAAGGA CGAGGAGGTC TGTCTGGCTC AGGCTCCTGT TGGCTCCGCT	1020
CCAGCAGCCC AGTTTATGGA TTGGTTGATT GGCTATGGTG TGGAGCAGAT TATCTCTACT	1080
GGGACCTGTG GTGTCCTAGC TGATATAGAG GAAAATGCCT TTCTAGTCCC TGTTCGCGCT	1140
CTGCGAGATG AAGGAGCCAG TTACCACTAT GTGGCACCTT GTCGTTATAT GGAAATGCAG	1200
CCAGAGGCTA TTGCTGCTAT TGAGGAAGTT TTGGAAGACA GAGGGATTCC TTATGAAGAA	1260
GTCATGACCT GGACGACAGA CGGTTTTTAC CGAGAAACGG CTGAAAAGGT GGCTTATCGT	1320
AAGGAAGAAG GCTGTGCTGT TGTGGAGATG GAGTGTCTG CTCTTGCGGC AGTAGCTCAA	1380
TTGCGTGGGG TTCTCTGGGG TGAATTGTTG TTCACAGCAG ATTCTCTAGC GGACTTGGAC	1440
CAGTACGACA GTCGTGACTG GGGCTCGGAA GCTTTTAATA AGGCGCTAGA ACTGAGTTTA	1500
GCAAGTGTTT ACCACCTTTA GTGTACTGG CAAAGGATTT GTTTTATCAT AAAATGTCTA	1560
GCTCATACTT TTCAAAAATA TGTTTAAACG AGGTCACCTT CCTCTGTCC TAGGCATGTT	1620
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CTCTTCAAAC CAGGTCAGCT TCACCTTGCC GTAGGTATAT GTTACTGACT TCGTCAGTCT	1800
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TATAATCAAA AAGAGAAATT TTCTCCTGAA AAGCATATAG AGTAGCTGGC GTTAAAAGCT	1980
CCTGTCTTGC TTTTGTGACC TATAGTCACA TCTATCAAGT ATTGTTCTTG CCTAAGCTAT	2040
CAATAAAAAG GTGGCATTTT TTAGGCTTGG TGTAGTAGA TTTTGCCCTA TCCTATCTAA	2100
GTCATTTGCA ACTTTTTATG GTACAATGGA AACATGTTAT TCAAATTATC TAAGGAAAAA	2160
ATAGAGCTAG GCTTATCTCG TTTATCGCCA GCGGTCGTA TTTTGTGAG TTTTGCCTTG	2220

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GTCATTTTAC TAGGCTCTCT TCTTTTGAGC TTGCCCTTTG TCCAAGTTGA AAGCTCACGA	2280
GCGACTTATT TTGATCATCT TTCACCTGCT GTCTCTGCAG TCTGTGTGAC GGGTCTCTCA	2340
ACCCCTTCCAG TAGCTCACAC CTATAATATC TGGGGTCAAA TAATCTGTTT GCTCTTGATT	2400
CAGATCGGTG GTCTAGGGCT CATGACCTTT ATTGGGGTTT TCTATATCCA GAGCAAGCAA	2460
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TCTTTGAGAA AGTTTGTCTA TTCTATTTTT CTCACGACCT TTTTGGTTGA GAGCTTGGGA	2580
GCTATTTTGC TTAGTTTTCG CCTTATTCCT CAACTTGGCT GGGGACGTGG TCTTTTGTAGT	2640
TCCATTTTTC TAGCGATCTC AGCCTTCTGT AATGCCGGTT TTGATAATTT AGGGAGCACC	2700
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TTTGAACAGC CAACTACTCT CTTTCTTGAG TGAACAATG CTGGAACGAT TGGCAATCTC	2940
CCTGTTGCCG ATAAGGTTTT AGTTAGCTTT TTTCAAACAG TGACGATGCG AACAGCTGGC	3000
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GTCTCTTGG TCTTTGCAGC AAGTGAGCTT CTAGGCTTGC CTCATGCCAA TGTGCGAGA	3180
CGAACGATCG CGCCGCGAAC GGTTCAAAA TCCTTTAGTG TCTTTATTAT CTTTTTGATG	3240
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CCTGACCTTG GGAAATTGGC TCTCAGTGT ATCATGCCAC TTATGTTTAT GGGACGAATT	3420
GGTCCCTTGA CCTTGTTTGT TAGCTTGGCA GATTACCATC CAGAAAAGAA AGATATGATT	3480
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GATTGGAATT TTGGGCTTGG GAATTTTTGG GAGCAGTGTC CTAGCTGCCC TAGCCAAGCA	3600
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GGTTATGCAC TGTAAGAGTT TGGGGGTACC GACTGTTATT GCTAAGGTCA AAAGTCAGAC	3840
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GGGGCAGTCT CTAGCACAGA CCATTCTTTT CCATAATAGT GTTGATGTCT TTCAGTTGGA	3960
TAAAAATGTG TCTATCGTGG AGATGAAAA TCCTCAGTCT TGGGCAGGTC AAAGTCTGAG	4020



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TTCCCCATTG GATGTTGAAT TTGGACCAGA TGACCTCTTG AAAGCAGATA CCTATATTTT	4140
GGCAGTCATC AACAAACAGT ATTTGGATAC CCTAGTAGCA TTGAATTCGT AAAGAGGGAT	4200
GACCCCTCTT TTTTGATGCC TAAGATGGCA AATAGAGACA GAAGCCCTT GTCTTCTAGT	4260
AAAAGTTCTT CAAAGGCTGG ACTTTATGGT AAAATAGAAA GAAGTGACAA GAGAGAGTAA	4320
TACTCAATGA AAATCAAAGA TCAAACTAGG AACTAGCTA CGGGCTGCTC AAAACACTGT	4380
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AGTCTTGCCCT GTTCGGCAGA TTTTGGGCTG GGACCAGGTC GGAAATTTCT CCAAAGGCCA	4980
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CAAGACCATG TACTATCTGC CTGTCGATTT CTATCGTTAT TTGATTGGGC GTGAGGACCA	5160
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GAATCATATT GAACTCACGA CGGTGATTTT CAGTACCCTG CTCAACCGAT CTGGAACAGC	5340
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CTTTCAGGCT ATTCGTAAGA CCATGTTGAG CCGTTTGACC AAACATTCTG TCTTGCCAGA	5460
TCGCAAACTG TCCAATGTCG TCTATCAAAT CACCAAATCT GTTTATGGAT TTAATTAATA	5520
TAAGTGTTTT ATAAGAGGGA TTTAAGAAAA ATTTTAACTT TTTCTTAGTC CTTTTTAATT	5580
TCAGGAGATT ATACTAGAGT CATCAAATAA AGAAAGACTC TAAGGAGAAT CCTATGAAAT	5640
TCAATCCAAA TCAAAGATAT ACTCGTTGGT CTATTCGCGG TCTCAGTGTC GGTGTTGCCT	5700
CAGTTGTTGT GGCTAGTGGC TTCTTTGTCC TAGTTGGTCA GCCAAGTTCT GTACGTGCCG	5760

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ATGGGGCTCAA TCCAACCCCA GGTCAAGTCT TACCTGAAGA GACATCGGGA ACGAAAGAGG	5820
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GCCCTTCTAG TCTGGATACA CTTTTTGAAA AAGATGAAGA AGCTCAAAAA AATCCAGAGC	6000
TAAACAGATGT CTTAAAGAA ACTGTAGATA CAGCTGATGT GGATGGGACA CAAGCAAGTC	6060
CAGCAGAAAC TACTCCTGAA CAAGTAAAG GTGGAGTGAA AGAAAATACA AAAGACAGCA	6120
TCGATGTTCC TGCTGCTTAT CTTGAAAAAG CTGAAGGGAA AGGTCCTTTC ACTGCCGGTG	6180
TAAACCAAGT AATTCCTTAT GAACTATTCG CTGGTGATGG TATGTTAACT CGTCTATTAC	6240
TAAAGCTTC GGATAATGCT CCTTGGTCTG ACAATGGTAC TGCTAAAAAT CCTGCTTTAC	6300
CTCCTCTTGA AGGATTAACA AAAGGGAAAT ACTTCTATGA AGTAGACTTA AATGGCAATA	6360
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TGCTACTAA AAATGTAGAC ATCAACATCA ATGGATTAGT TGCTAAAGAA ACAGTTCAAA	6540
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TGGACAACAT CGTAGCAACT AAAAAAGTCA CTATTAACAT AAACGGTTTA ATTTCTAAAG	7440
AAACAGTTCA AAAAGCCGTT GCAGACAACG TTAAGGACAG TATCGATGTT CCAGCAGCCT	7500
ACCTAGAAAA GGCCAAGGGT GAAGTCCAT TCACAGCAGG TGTCAACCAT GTGATTCCAT	7560

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ACGAACTCTT CGCAGGTGAT GGCATGTTGA CTCGTCTCTT GCTCAAGGCA TCTGACAAGG	7620
CACCATGGTC AGATAACGGC GACGCTAAAA ACCCAGCTCT ATCTCCACTA GGTGAAAACG	7680
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AAAAACAAGC GCTCATTGAC CAGTTCCGAG CAAACGGTAC TCAAACCTAC AGCGCTACAG	7800
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CTTCTAACTC TGGTTCTGGC GTGACTCCGA TGAATCACAA TCATGCTACA GGTACTACAG	7980
ATAGCATGCC TGCTGACACC ATGACAAAGTT CTACCAACAC GATGGCAGGT GAAAACATGG	8040
CTGCTTCTGC TAACAAGATG TCTGATACGA TGATGTCAGA GGATAAAGCT ATGCTACCAA	8100
ATACTGGTGA GACTCAAACA TCAATGGCAA GTATTGGTTT CCTTGGGCTT GCGCTTGCA	8160
GTTTACTCGG TGGTCTAGGT TTGAAAAACA AAAAAGAAGA AACTAATCA GCTAAGGAAA	8220
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TTCTTTCAAT AGCAGATTAA AATCATCGTA AAACAATAAA AATAGTGTTA TACTTAAAGC	8340
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ATTTACGGCC TGAGCTTGGG AGCAGATGAT TTTATTGCTA AGCCTTTTAG CCCACGTGAG	8700
CTGGTTTTGC GTGTCCACAA TATTTTGCGC CGCCTTCATC GTGGGGGCGA AACAGAGCTG	8760
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CGAGTTTTCT CCAAGACAGA CCTCTATGAA AAGATCTGGA AAGAAGACTA CGTGGATGAC	8940
ACCAATACCT TGAATGTGCA TATCCATGCT CTTGACAGG AGCTGGCAAA ATATAGTAGT	9000
GACCAAACTC CCACTATTAA GACAGTTTGG GGGTTGGGAT ATAAGATAGA GAAACCGAGA	9060
GGACAAACAT GAAACTAAAA AGTTATATTT TGGTTGGATA TATTATTTCA ACCCTCTTAA	9120
CCATTTTGGT TGTTTTTTGG GCTGTTCAAA AAATGCTGAT TGCGAAAGGC GAGATTTACT	9180
TTTTGCTTGG GATGACCATC GTTGCCAGCC TTGTCGGTGC TGGGATTAGT CTCTTTCTCC	9240
TATTGCCAGT CTTTACGTGC TTGGGCAAAC TCAAGGAGCA TGCCAAGCGG GTAGCGGCCA	9300

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AGGATTTTCC TTCAAATTG GAGGTTCAAG GTCCTGTAGA ATTCAGCAA TTAGGGCAAA	9360
CTTTTAATGA GATGTCCCAT GATTTCAGG TAAGCTTTGA TTCCTTGGA GAAAGCGAAC	9420
GAGAAAAGGG CTTGATGATT GCCCAGTTGT CGCATGATAT TAAGACTCCT ATCACTTCGA	9480
TCCAAGCGAC GGTAGAAGGG ATTTTGGATG GGATTATCAA GGAGTCGGAG CAAGCTCATT	9540
ATCTAGCAAC CATTGGACGC CAGACGGAGA GGCTCAATAA ACTGGTTGAG GAGTTGAATT	9600
TTTTGACCCT AAACACAGCT AGAAATCAGG TGGAAACTAC CAGTAAAGAC AGTATTTTTC	9660
TGGACAAGCT CTTAATTGAG TGCATGAGTG AATTTCAGTT TTTGATTGAG CAGGAGAGAA	9720
GAGATGTCCA CTTGCAGGTA ATCCCAGAGT CTGCCCGGAT TGAGGGAGAT TATGCTAAGC	9780
TTTCTCGTAT CTTGGTGAAT CTGGTCGATA ACGCTTTTAA ATATTCTGCT CCAGGAACCA	9840
AGCTGGAAGT GGTGGCTAAG CTGGAGAAGG ACCAGCTTTC AATCAGTGTG ACCGATGAAG	9900
GGCAGGGTAT TGCCCCAGAG GATTTGGAAT ATATTTTCAA ACGCCTTTAT CGTGTGAAA	9960
CTTCGCGTAA CATGAAGACA GGTGGTCATG GATTAGGACT TGCGATTCCG CGTGAATTGG	10020
CCCATCAATT GGGTGGGAA ATCAGAGTCA GCAGCCACTA CCGTCTAGGA AGTACCTTTA	10080
CCCTCGTTCT CAACCTCTCT GGTAGTGAAA ATAAAGCCTA AAACCCCTTT ACAATCCAG	10140
CTATTCATGG TAGAATAGAT TTTGTGTGAA ATATCAGCAG GAAAGCATGA AGCTCGTCAA	10200
CAGGTGTCTT ATGACAAGTA ACCTTGGCTG TTTAGGCGAA GGCATCTGC ACGG	10254

(2) INFORMATION FOR SEQ ID NO: 30:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 9769 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 30:

CCGGCGACTA TCGATAACAC TTGACTTGGT AGCCCCACAT TTTGGACAAC GCATCCTTTC	60
CCTCCTTATC GTTTTCTTTT CATTATACCA TTTTTTAAGC GATTCCTCAA ACAATTCTTC	120
TTTTTGCTTG ACAAGTTTTT TGTTTTGTG TATTATTAA TTAAGACAAC AAGGTAAAAG	180
AAAGGAGACT AAGATGTCCT GGACATTGA CAACAAAAA CCCATCTATT TACAGATTAT	240
GGAGAAAATC AAGCTTCAGA TTGTTTCCCA TACACTGGAA CCCAATCAAC AACTTCCAAC	300
CGTGAGGAGC TAGCTAGCGA GGCTGGTGT AATCCCAATA CCATCCAAAG AGCCTTATCA	360
GACCTTGAAC GAGAAGGATT TGTCTACAGC AAGCGAACAA CTGGACGATT TGTGACTAAG	420
GATAAGGAGC TAATCGCCCA GTCACGCAA CAATTATCAG AAGAAGAATT GGAACACTTC	480

GTTTCCTCCA TGACCCATTT TGGCTATGAA AAAGAAGAAC TACCAGGCGT AGTCAGTGAT	540
TATATTAAAG GAGTTTAAGC CTATGTCATT ACTAGTATTT GAAAATGTAT CCAAATCATA	600
TGGAGCAACA CCAGCCCTTG AAAATGTTTC TCTTGACATT CCAGCTGGAA AAATGTGCGG	660
CCTTCTTGGG CCAAACGGCT CAGGAAAAAC AACCTGATT AAATAATTA ATGGCCTCTT	720
ACAACCAGAT CAAGGACGTG TCCTCATCAA CGACATGGAC CCAAGCCCAG CAACCAAGGC	780
CGTTGTAGCT TATTTCCTG ATACGACCTA TCTCAATGAG CAAATGAAGG TCAAAGAAGC	840
CCTAACCTAC TTCAAGACCT TCTATAAGA TTGTCAGATC TTGAACGCGC CCATCATCTA	900
CTTGACAGCC TGGGCATTGA TGAAAATAGT CGTCTCAAGA AACTATCAAA AGGAAACAAA	960
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CCCATTGGTG GGTGGATCC AGCAGCCCGT GCTTATATCC TCAATACCAT TATCAACAAC	1080
TACTACCAA CTTCTACCGT TTTGATTTCT ACCCACTTGA TTTCTGATAT CGAGCCAATC	1140
TTGGATGAAA TTGTCTTCCT AAAAGACGGA AAAGTCGTCC GTCAAGGAAA TGTAGATGAT	1200
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GAACACCATA TCATCACAGC CAAACTAATC GGTGCCTTTA TCTGGTCATT GATTAGCACC	1620
GCTGTATTGG CTCTAAGTGC TGTATTATT CTGGCTTTAA CAGCTCCAGA ATGGATTCTT	1680
CTTTCTTATG TGATTACATT TGTAGAAACA CATCTCCCTC AGATCTTTCT TACAGGTATA	1740
TCCTTCCTAC TAAATACTAT TTCAGGAATC CTCTGCATCT ACCTGGCTAT TTCCATTGGA	1800
CAGCTTTTCA ATGAATACCG TACAGCACTC GCTGTTGCAG TCTACATTGG TATCCAAATC	1860
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GTAGGACTCA ATGACCATTT CTATATGGGA GCAGGTATAG CCATTGTTGA AGAACTCATA	1980
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TAAATAATTT TTACCTAGAT ATGTAACATA CTCATAGAAC AAAAGAGACC AGGCAAAAAG	2100
TCTTTAAAT TAGAAAAAGC ATAGTATCAG GTGTTGAATA TGTACTGCC CCCAAAAGTT	2160
AGATTTTTC TGTCTAACTT TTGGGGCAG TTCATAAGAA CCTTGTAAT ATGCGTTTTT	2220

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TTCACTTAC TATACAATTG AGTTTCAAG CAACCTGTTT ACATAATGTG TACATAATTA	2400
GGTTCGTGAT TCCACCTTT TCACCTTTAA AAACCTCGCT TTCGCAAGGC TCTTCTATTT	2460
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CGCATAGAAA TAGTGACTTG CCCTTATGCT AGAAAAACG ACTTCCATAA TTTTGGTGCC	3060
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TGACTCGACA TGTCGAAGAT AGGTTTCCTT GATTACAACC CACATATTTT TCATACTTCC	3660
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ATATATTGAC CTTGAGTCAA GATTGAGAAG AGTTCCTTC CAGCGCTCTC ATCCTCCAAA	3780
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ACATCTTGAA CTGGTCCGTG CAAGACCACA CGCCATCTC GGATCATCAG AATATCGTCA	3960
CAAAGTTCCT CAACATTGGT CATGACATGG TCAGAAAAGA TAATGGTTGT CCGCGCTCTT	4020

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TTTCCTGAAA AATGACTTGT TTGAGCAATT CTGTATTAAC TGGGTCCAAT CCACTAAAAG	4080
GCTCATCCAA GATAATCAGG TCTGGTTCAT GAATCAGAGT AATAATGAGC TGAATCTTCT	4140
GCTGATTTC TTTTGACAGA CTCTTGATTT TATCTGTCAG CTTTCCTTTC ACTTCCAACC	4200
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CCAAGTAGCG AACTTGTTCA AGAAGTGTCA ATTTAGGCAT GAGATGCGTT CTTCAGGCAG	4320
ATAACCAATC CGAGCATAGG TCTCCTGACG AATATCCTGA CCATCCAGAC CGATTCTCTCC	4380
CTGATATTCT AGGAATTTCA AAATACTATG GAAAATCGTT GTTTTTCCAG CACCATTTTTT	4440
TCCGACTAGT CCCAAAATAC GACCTGGTCG CGCTTGAAAG TCAATACCAA ACAAACCTTG	4500
CTTGGATCCA AAACCTTTCT CTAGACTTCT TACTTCTAGC ATCTTTCACC TCCGAAATTT	4560
CTTGCACTCA TTATACTCCT TTTTGATAGC CTTTACAATG TTTTTGTGCC ATTTTTAGAA	4620
GACTATTGCT GTGTAAATA TGGCCTGGAG CACTTTTATA CTCAATGAAA ATCAAAGAGC	4680
AAACTAGGAA GCTAGCCGTA GACTGCTCAA AGTACAGCTT TGAGGTGCA GATAAACTG	4740
ACGAAGTCgA CTCAAACAC TGTTTGAGG TTGTGGATAG AACTGACGAA kCfTAaCTAT	4800
ATCTACGGCA AGGCGAACTG ACGTGGTTTG AAGAGATTTT CGAAGAGTAT TAGTGATAAA	4860
TCCATTATAC AGCAGCAAAC TTAATTTATA CCTCCGCTC CTCAACTGTC TATTTTAAAT	4920
CCTGAATTGT TATTTGAGTA ACTCCTTTTT CCTCGTAAAG TTTTCTTCTCT CTAACCTTC	4980
TGGA AAAAGG CTAATAGTTT CAGACAACAT TTTTATAAGA AACAAGTTCA TCTGTCATTT	5040
CAAGAAGGAG TAATCCTTTA TCTACTAATG GACGGAACAG AATTCAACCG CTTGTCCGAT	5100
ATGTTTTCTA AGGATTATAT AGTAAATGA AATAAGAACA GGACAAATTG ATCAGGACAG	5160
TCAAATTGAT TTCTAACAAAT GTTTTAGAAG TAGATGTATA CTATTCTAGT TTCAATCTGC	5220
TATATCTATT ATGCACACCC CTATAGGATC TAATGAAAAT CACAACAGGC TCATTCATAG	5280
ATGGTTACCT AAGCCTAAGG GAACTAAGAA AACGACTACC AAGGAAGTCG CATTTCATCGA	5340
AAAGTAGATT AACAACTATC CTAAAAAATG CTTGAACTAC AAGTCCCCCA GAGAAGACTT	5400
CTGGATGACT AACTTGAAC TGAATTTAG CAATAATTAA TTCACTATCT AACTATATTT	5460
AGTAATTATT TCAGAACTGA TTAATATTAA AATTAACTAA CAATTCAAAG GATTTCATACT	5520
AGCCATAAAT TACGTCCATC AGAGAGAGAC TCTTACTACT TTTAGATTTT AGTCTTTCTA	5580
GCTTCAGAAT ACATCTAAAC TTTAGGGAAA ATGACTATTG GAAAGCGCGA ATGCCTCAAA	5640
ATTATCTCAG ATAAGCTATT CGAAACTTAG AATGCTTTTA AATTTATGGA ATTGCGATTA	5700
TTCGAAACCT AGAATGCATA TAACCTTTAG TTGACAGACC TATTCTAAGT CTGAAGGGC	5760

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TATTTACTTT CTATTCCTTA TCAAAAAAGA CTCATTCCCC CTTTCTCCTC CAAAATATGG	5820
TATAGTAGAA ATATACTATC TATGAGGAGT TTACATGTCA CAGGATAAAC AAATGAAAGC	5880
TGTTTCTCCC CTTCTGCAGC GAGTTATCAA TATCTCATCG ATTGTCGGTG GGGTTGGGAG	5940
TTTGATTTTC TGTATTTGGG CTTATCAGGC TGGGATTTTA CAATCCAAGG AAACCCCTCTC	6000
TGCCTTTATC CAGCAGGCAG GCATCTGGGG TCCACCTCTC TTTATCTTTT TACAGATTTT	6060
ACAGACTGTC GTCCCTATCA TTCCAGGGGC CTTGACCTCG GTGGCTGGGG TCTTTATCTA	6120
CGGGCACATC ATCGGGACTA TCTACAATA TATCGGCATC GTGATTGGCT GTGCCATTAT	6180
CTTTTATCTA GTGGCCTAT ACGGAGCTGC CTTTGTCCAG TCTGTCGTCA GCAAGCGCAC	6240
CTACGACAAG TACATCGACT GGCTAGATAA GGGCAATCGT TTTGACCGCT TCTTTATTTT	6300
TATGATGATT TGGCCCATTA GCCCAGCTGA CTTTCTCTGT ATGCTGGCTG CCCTGACCAA	6360
GATGAGCTTC AAGCGCTACA TGACCATCAT CATTCGTACC AAACCCTTTA CCCTCGTGGT	6420
TTATACCTAC GGTCTGACCT ATATTATTGA CTTTTCCTGG CAAATGCTTT GACACGTAAA	6480
AAATCCGTTT GGTTCCTCAA GTGGATTTT AAAGCGTAGA TTAATATAG CTTGATACTA	6540
AATATACTTT GGTATGGAAA TCATGCATAT TTTTCGATAG TGAGGCGAGG ACTTACCTAG	6600
CCTTTCGCC GTGATAGAAA CACCTGAAAT CTAATGGTTT CAGGTATTCG GAACTTTGA	6660
GCCTAGTGTC TCAAAGTTTA GGTATGGAAT TTTGAAGAAA GTCGCTACCG TCCGTAATCA	6720
CTTAAGGAAA GGCTCAAAAA TATTGTTTTC AACCACAAAA TCCGTTTGGT TTCCCAAGCG	6780
GATTTTGTC TTTATTTTGA AACTTCTTTT GCAAGAACAA AGTTCCCAAG TGTGGCAGAA	6840
CCATTTCTCTG CGACTGCTGG CGTCACGATA TAGTCACGCA CATCTGGTAC TGGTAGGTAA	6900
CCATTAAGAA GAGATGTAAA TTTCTCACGG ACACGGTCCA GCATATGTTG TTGAGCCATG	6960
ACCCCTCCAC CAAAGACAAT CACGTCTGGG CGGAAAGTCA CTGTCGCATT AACCGCAGCT	7020
TGAGCGATAT AGTAGGCTTG AACATCCCAA ACAGGGTTGT TGAGTTCAAT AGTTTCCCCA	7080
CGTACACCTG TACGAGCTTC CAAACTTGGA CCAGCTGCAT AACCTTCTAG ACATCCCTTA	7140
TGGAAAGGAC AAACACCCTT AACTCTTTT TCAATATCCA TTGGGTGTCT AGCAACATAA	7200
TAATGACCCA TTTCAGGGTG ACCCACACCA CCGATAAACT CACCACGTTG GATGACGCCT	7260
GCACCGATAC CTGTACCGAT TGTGTAGTAA ACCAAGTTT CGATACGACC ACCAGCATTG	7320
TTACGGGCAA CCATTTCAAC GTAAGCAGAG CTGTTTACGT CTGTTGTGAA GTACATGGC	7380
ACGTTTAGGG CGCGACGAAG GGCACCAAGC AAGTCTACAT TTGCCCAGTT TGGTTTGGGA	7440
GTCTGCTGA TAAAGCCATA AGTTTTTGAG TTTTGTCAA TATCAATCGG CCCAAATGAA	7500
CCAACGTCAA GACCAGCAAG GTTATCGAAT TTTGAGAAGA ACTCAATGGT TTTATCGATT	7560



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GTTCGATTG GAGTTGTTGT TGGAAATTGT GTTTTTTCTA CAACGTTAAA GTTTTCATCA	7620
CCGACAGCAC AGACAAACTT TGTACCGCCC GCTTCCAAGC TTCCATATAA TTTTGTCTATG	7680
ATAAACCTCT TGTTTTTATT TTCTTTATTA TAGCATACTT CGAAAGTCTA AATGTCTCTA	7740
TTTTTTAGAT TTTCTCTGT AAATCTTACT ATCTAATAAA AACGAACAAA CATGTCATTT	7800
GTTCGTTTTT ACATTAGAGA GGATTGATTA GATTTTCACT TCGATCACAG CATCCCCCTT	7860
AGCAACTGAA CCTGTTGCGA CTGGAGCTAC TGAAGCGTAG TCACCTGTAT TTGTAACGAT	7920
AACCATTTGT GTATCATCAA GTCCAGCTGC AGCGATTTTG TTTGAGTCAA ATGTTCCAAG	7980
AACATCGCCA GCTTTCACCT TATTACCTTG AGCAACTTTT GTTCAAAAC CGTCACCGTT	8040
CATAGATACA GTATCAATAC CAACATGAAT CAAAACCTCA GCACCATTTT TGTTTTCAA	8100
ACCAAAAGCG TGCCCTGTTG GAAAGGCAAT TGAACCTCA GCATCAGCTG GTGCATAGAC	8160
CACGCTTGG CTTGGTTTCA CAACGATACC TTGTCCATA GCTCCACTTG AGAAGACTGG	8220
GTCATTGACA TCAGCAAGAG CGACAACATC ACCGACGATA GGAGTTACAA GTGTTTCATT	8280
TTGAAGAGCT GCTGGCGCAA CTCTTCTTT TTCTTCAGCC ACTTCAGCTC GTTTTGCAGC	8340
TGCAAGTTGCG TCTACTTCAT CTTGTAACC AAACATGTAA GTAAGAGCAA AACCAAGGGC	8400
AAATGATACA GCTACCATAA GAAGGTATTG TGAAGTTGT CCGTTACCAA CATAAAGCAT	8460
TGTACCAGGG ATGATGGTGA TACCATTACC AGTACCAGCA AGTCCAAGGA TAGAAGCCAA	8520
TCCACCACCG ATTGCACCAG CAATCAATGA AAGGAAGAAT GGTTTACGGA AGCGCAAGTT	8580
CACCCCGAAG ATAGCAGGCT CTGTAATACC TAGGAAGGCA GAAAGAGCAG CCGGGAAAGC	8640
AAGTGTTTTC AGTTTGGAT TTTTGTGTTT AACACCAACC GCAACAGTAG CAGCACCTTG	8700
AGCTGTCATA GCAGCTGTGA TGATAGCGTT GAATGGGTTA GCATGGTCAG CAGCAAGTAA	8760
TTGCACTTCA AGCAAGTTGA AGATGTGGTG CACACCTGAC ACGACGATCA ATTGGTGAAC	8820
CCCACCAATC AAGAAACCAC CAAGACCAA TGGCATGCTA AGAATCGCTT TTGTAGCAAT	8880
AAGGATGTAG TTTTCAACAA CGTGGAAAAC TGGTCCAATG ACAAAGAGTC CAAGGATAGA	8940
CATGACCAAA AGTGTCACGA ATGGTGTTAC CAAGAGGTCA ATGACATCTG GAACAACTTG	9000
CGGACAGCTT TTTCAAATTT AGCTCCGACA ACCCCGATGA TGAAGGCTGG AAGAACGGAA	9060
CCTTGCAAAAC CAACAACAGG GATGAAACCA AAGAAGTTCA TCGCTGTTAC TTCACCACCT	9120
TGAGCAACTG CCCAAGCGTT TGAAGTGAG CCAGAGACAA GCATCATACC AAGAACGATA	9180
CCAACGGCAG GATTTCCACC AAATACACGG AAGGTTGACC ACACAACCAA ACCTGGCAAG	9240
ATGATGAAGG CTGTATCTGT CAAGATTTGT GTGTAAGTTG CAAAGTCACC TGGAAGTGGC	9300

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ATTTC AAGAG CGTTG AAAAG ACCACGCACA CCCATGAAGA GACCTGTCGC TACGATAACT	9360
GGGATGATTG GAACG AAAAC ATCACC AAAA GTACGGATAG CACGTTGGAA CCAGTTCCCT	9420
TGTTTAGCAA CTCTGCTTT CATGTCATCC TTAGATGATG TTGGTAATCC AAGTACAACA	9480
ACTTCATCGT ACATTTTGT AACTGTACCT GTACCAAAGA TAATTTGGTA TTGCCCTGAG	9540
TTAAAGAAAG CACCTTGAAC TTTTCCAAG TTCTCAATCA CTCTTTTATT GATTTTCTCT	9600
TCATCTTTGA CCATGACACG TAGACGAGTC GCACAGTGGG CAACACTATT GACATTTTCA	9660
CGTCCGCCCA AGGCATCGAT GACTTTTTTT GCAATTCCT GATTGTTTAT TTGCAAAAAT	9720
CTCCTTATAT AACATTTTGT TCTGTTTGA AAGCGATTTT ATTCGCCGG	9769

(2) INFORMATION FOR SEQ ID NO: 31:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 3149 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 31:

CGCTTGAGTG CTAATTCATA GTTCTATTGT ATCACTTGGT CAGAAATAAT CAAGAAAAAA	60
GTCTGACTTT CTCAAGATAA AAAGCCTGAG ACCAACTCAG ACTTTTAAAT TCTTAAATG	120
GCAATTCCTC CTCTTCCAAG ACCAAATCTG CCAAATCTTG GCCTGCATTA TTTTCACGCA	180
TAGCAGCTTG GGCACGACTT TCCAAGAGTT GGAATCCTGT GACAAGTACT TCGGTCACGT	240
AGTTCATTTG GCCATTTTTC TCAAAGCGAC GGGTACGCAA TTCTCCATCA ACGGAAATGA	300
GACTACCTTT GGTGCGTAC TTGCCAAAGT TTCTGCTAGT CTGCCCCATA GGACCATATT	360
GACAAATCA GCTTCAGTT CACCGTTTGT GTCTTGTAA CGACGGTTCA CAGCGATAGT	420
TGCTCGCGCT ACCGACTTGT CATTGTTGGT TTGTGCAAT TCTGGTGTAG ACGTTAAACG	480
TCCAATCAAG ATAACCTTAT TATACATATT TTCTTCCTCC TACTTATCTA TTCGTAGGAA	540
ATCAAAAAA GTTACAGAAA TTTGTAACCT TTCGAGAAAA TTTTATTATT TTTATGAACC	600
ATGAAACCTG TCGCCTGTTG APTGGCCATA ATGGTCATAT CTGTAATCTG AACACGACGA	660
GGTTGACTAG TCACATAGAC TACTGTATCT GCAATATCCT GAGCTTGCAA AGCTTCTATT	720
CCTTGGTAAA CGGACGCAGC TCGTTCTTTA TCACCATGAA AACGCACTGT AGAAAAATCT	780
GTTTCGACAA TTCCAGGCTG AATGGTCGTC ACCTTGATAT CCGTTGCGAT GGTATCAATT	840
CGCAGTCCAT CTGAAAAGGT CTTAAGTCCC GCCTTGGTGG CTGAGTAAAC AGCTGCACCA	900
GCATAGGCAT AAATTCCTGC GGTGACCCC ATATTGATAA TATGACCTTG ATTGGCTTTT	960

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ACCATTGCTG GCAAGAAACA GCGAGTGA CTTCATCAAAC CTTTGACATT GGTATCCAAC	1020
ATGGTCAGCA TATCCAAC TCATAGTCT TGATAGGGAG CTAAGCCAAG AGCCAGTCCT	1080
GCGTTATTGA CCAGGATGTC AATCTGACCT ATCGTTTCTA AAATATCAGA GCAGACAGTC	1140
TTTACCATTG TCATATCCGT GACATCTAGG AGAAAAGTCC AAAGTGTGTTG ATTTGGAAAA	1200
GTTTCTGCAA ACTCCGCTT AAGAGCTTCT AGTCTGTCTA TCCGTCTGTC TGTTAGAAGC	1260
ACATCCTCAC CCTGCTCCAG ATAAGCACGC GCAATCGCTT CACCGATTCC TGATGTCGCT	1320
CCTGTAATCA CAACATTTTT TGCCATCTTA TTTCCTTCTA GCTGGTCTAT CAGATATTAA	1380
CAACTTCTTA GGCAGTCCAG TGTTCGCTG GGTGGAACGG TGTTCGACA ACTTGGTCTT	1440
CTGATAATTC AAGCACCCCA CGTTTTTGTG GAGCATTGAG CAGATGCAAT TCACGAGGAC	1500
TGCACATCAT ACCAAAAC TCCTTCCAC GAAGTTCACC TGGGAAAATG AGATTCCCTT	1560
TTGGCATCAT AGCTCCAGGA AGCGCGACAA TGGTTTCAA CCCACACGC GCATTGGGAG	1620
CTCCTGCAAC GATTTGTACA GTCTTATCAC TTGCGACTGC AACTTGGCAG ATGTTGAGGT	1680
GGTCACTATC TGGATGGCT ACCATCTCAA CAATTCACC TACAACAAAC TTAGGTTCTT	1740
TATCATTAAC AATTTCTTCT GTAAAACCTT CCGCCTGCAA CTCTTGGTTC AAACGAGCGA	1800
CTTGCTCATC TGTCAAAAAG ACTTGACCGC GCTCTGCAAT TTCAATAAAA CTTGAACTT	1860
CGAAAAATTT CCAAGCCACT GTTCCCAT TATCTTTGAG AAAACACCG GCTACCTTGC	1920
CTTTGCGCTC CACATCCAGT TTGGCATCTC CGTATTTTT CACGATGACC ATAAGGACAT	1980
CACCGACATG TTCTTTATTA TATGTAAAA TCATTGTTTC CTTTTCTCC TATTTAGTC	2040
CTGCTAAAA GTCAATGATT TGTGCTTGC TTTTACGGTC GCGATTGACA AAACGACCGA	2100
TTTCCTTGTC CTTTCTAGA ACAACAAGGC TAGGAATTCC GTAAACATCC CAGAGTTTGG	2160
CCAAATCCAT ATACTGATCT CGGTCCATTC GAATAAAGGT GAACTCTGGA TTGGTCTCCT	2220
CAATCTCTGG TAAGGCAGGA TAAATATAAC GACAATCGCT ACACCACTCT GCCACAAAA	2280
TGAAGACCTT CTTGCCGCT TTTTCCACTA AAGATGCTAA TTCTTCTAAA CTTGCTGGCT	2340
GTATCATAAG ACTTCTCTCT CATAGACTAG GTCTTCATTT TCATAGACAA AGGTATAATG	2400
ACGGCCATCC TCAAAAATGA CGCCACCAAC CAAGCTCTCC AGACTGCTTT CGTAAACTTG	2460
AACATAAAGG GTCGCAATTT CCCCCATGTC GGAAAAATGG TCTCGCACAA TCTCTGTCAA	2520
CTCTTCTGA GTCTTCATGA GCTTACGGTC ATCTGCAACT TTTTCTGTAG CAAGAGCAAG	2580
GCTTCCGATA CCTAGCAGAG CCAAGCCTGC CATCCACATT TTTTGTAGTT TCATACCATT	2640
CATTTTAACA CAAAAAGGC TTCAGGACAA ATGAGGAAGC AGCAGAAAAG CAAGTAAAAA	2700

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GCCTCTTCCT TTAAGGAAAA GGACTTCTTA TACTCAATGA AAATCAAAGA CCAAAC TAGG	2760
AAGCTAGCCG CAGGCTGCTC AAAGCACTGC TTTGAGGTTG TAGATAGAAC TGACGAGTCa	2820
CTCAAAACAC TGTTTTGAGG TTGTGGATGA AGCTGACGTG GTTTGAAGAG ATTTTCGAAG	2880
AGTATTATTC TTATTGCCAG GCACCTAAGT TGCCAACGTA GTAACATCA GGTGTGTAGG	2940
TATTGCGAGC ATCTTACCTG ATGAAGCCAG ATAATACTAC TTGCCATTGT CTTTGACCCA	3000
ATCATTCGCA ATCATGGAAC CAGAAGAACT TACATAATAC CATTCCTCCCT TGTCATAAAC	3060
CCAAGTACTG ACTTTCATGG TTCCTGAGCA ATTAAAGGCA AAAAACTGT CCAATAACAT	3120
TCGTTTTTTA AAAGCATTTG AACTACAT	3149

## (2) INFORMATION FOR SEQ ID NO: 32:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 10240 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 32:

CCAAAAATTC AACCTTTAAG GGGAGTCCAG AGAGACTCAC AAGGTGTCAG ATAAAAGAAT	60
GGTGCAATTT TCTAGAGGAG ACTTTTGTAG TGTGCTCTCT TGTGTTGTAC GATTTTAACT	120
GAGGCGTTGC ACTAGCAAGG TCTTTTCTTT ATCTGGTCCC CTTAAAAATT AAGGAGGAAA	180
AGTTATGAAT CCCACATGTA AGAAGCGTTT GGGTGTCAAT CGTTTGGAAA CCATGAAGGT	240
GGTTGCACAA GAGGAAATCG CGCCACAATC TTTGAATTAG TCCTAGAAGG AGAAATGGTT	300
GAAGCCATGC GAGCAGGCCA ATTTCTTCAT CTGCGTGAC CGGACGATGC CCATCTCTTA	360
CGTCGTCCTA TTCAATTTTC GTCTATTGAC AAGGCAAACA AGCAGTGTC CCTCATTTAT	420
CGGATTGACG GAGCTGGGAC TGCAATTTTT TCAACCTTAA GTCAGGGAGA CACTCTTGAT	480
GTGATGGGGC CTCAGGGAAA TGGTTTTGAC TTGTCTGACC TTGATGAGCA GAATCAGGTT	540
CTCCTTGTTG GTGGTGGAT TGGTGTCCA CCCTTGCTTG AGGTGGCCAA GGAATTGCAT	600
GAACGTGGAG TGAAAGTAGT GACAGTCCTC GGTTTTGCTA ATAAGGATGC TGTTATTTTG	660
AAAACGGAAT TGGCTCAGTA TGGTCAGGTC TTTGTAACGA CAGATGATGG TTCTTATGGC	720
ATCAAGGGAA ATGTTTCCGT TGTATCAAT GATTTAGACA GTCAGTTTGA TGCTGTTTAC	780
TCGTGTGGGG CTCCAGGAAT GATGAAGTAT ATCAATCAAA CCTTTGATGA TCACCCAAGA	840
GCCTATTTAT CTCTGGAATC TCCTATGGCT TGTGGGATGG GAGCTTGCTA TGCTGTGTT	900
CTAAAAGTAC CAGAAAACGA GACGGTCAGC CAACGCTCT GTGAAGATGG TCCTGTTTTT	960

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CGCACAGGAA CAGTTGTATT ATAAGGAGAA AATTATGACT ACAAATCGAT TACAAGTTTC	1020
TCTACCTGGT TTGGATTTGA AAAATCCGAT TATTCCAGCA TCAGGCTGTT TTGGCTTTGG	1080
ACAAGAGTAT GCCAAGTACT ATGATTTAGA CCTTTTAGGT TCTATTATGA TCAAGGCGAC	1140
AACCCTTGAA CCACGTTTTG GGAATCCAAC TCCAAGAGTG GCAGAGACGC CTGCTGGTAT	1200
GCTCAATGCA ATTGCGTTGC AAAATCCTGG TTTAGAGGTT GTTTGGCTG AAAAGCTACC	1260
TTGGCTGGAA AGAGAATATC CAAATCTTCC TATTATTGCC AATGTAGCTG GTTTTTCAAA	1320
ACAAGAGTAT GCAGCTGTTT CTCATGGGAT TTCCAAGCA ACTAATGTAA AAGCTATCGA	1380
GCTCAATATT TCTTGTCCTA ATGTTGACCA CTGTAATCAT GGACTTTTGA TTGGTCAAGA	1440
TCCAGATTTG GCTTATGATG TGGTGAAAGC AGCTGTGGAA GCCTCAGAAG TGCCAGTTTA	1500
TGTCAAATTA ACCCCGAGTG TGACCGATAT CGTTACTGTC GCAAAGCTG CAGAAGATGC	1560
GGGAGCAAAG GGCTTGACCA TGATCAATAC TCTGGTTGGA ATGCGCTTTG ACCTCAAAAC	1620
TAGAAAACCA ATCTTGGCCA ATGGAACAGG TGGAATGTCT GGTCCAGCAG TCTTTCCAGT	1680
AGCCCTCAAA CTCATCCGCC AAGTTGCCCA AACACAGAC CTGCCTATCA TTGGAATGGG	1740
AGGAGTGGAT TCGGCTGAAG CTGCCCTAGA AATGTATCTG GCTGGGGCAT CTGCTATCGG	1800
AGTTGGAACA GCTAACTTTA CCAATCCTTA TGCCTGCCCT GACATCATCG AAAATTTACC	1860
AAAAGTCATG GATAAATACG GTATTAGCAG TCTGGAAGAA CTCCGTCAGG AAGTAAAGA	1920
GTCTCTGAGG TAAACTGCAA TCAATCTGTT CTTGATTTTT TATTAGTTTG TAATATGAAT	1980
TTAGGAGAAT TTTGGTACAA TAAATAAAT AAGAACAGAG GAAGAAGGTT AATGAAGAAA	2040
GTAAGATTTA TTTTTTTAGC TCTGCTATTT TTCTTAGCTA GTCCAGAGGG TGCAATGGCT	2100
AGTGATGGTA CTTGGCAAGG AAAACAGTAT CTGAAAGAAG ATGGCAGTCA AGCAGCAAAT	2160
GAGTGGGTTT TTGATACTCA TTATCAATCT TGGTTCTATA TAAAAGCAGA TGCTAACTAT	2220
GCTGAAAATG AATGGCTAAA GCAAGGTGAC GACTATTTTT ACCTCAAATC TGGTGGCTAT	2280
ATGGCCAAAT CAGAATGGGT AGAAGACAAG GGAGCCTTTT ATTATCTTGA CCAAGATGGA	2340
AAGATGAAAA GAAATGCTTG GGTAGGAACT TCCTATGTTG GTGCAACAGG TGCCAAAGTA	2400
ATAGAAGACT GGTCTATGA TTCTCAATAC GATGCTTGGT TTTATATCAA AGCAGATGGA	2460
CAGCACGCAG AGAAAGAATG GCTCCAAATT AAAGGGAAGG ACTATTATTT CAAATCCGGT	2520
GGTTATCTAC TGACAAGTCA GTGGATTAAT CAAGCTTATG TGAATGCTAG TGGTGCCAAA	2580
GTACAGCAAG GTTGGCTTTT TGACAAACAA TACCAATCTT GGTTTTACAT CAAAGAAAA	2640
GGAAACTATG CTGATAAAGA ATGGATTTTC GAGAATGGTC ACTATTATTA TCTAAATCC	2700

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GGTGGYTACA TGGCAGCCAA TGAATGGATT TGGGATAAGG AATCTTGGTT TTATCTCAAA	2760
TyTGATGGGA AAATrGCTGA AAAAGAATGG GTCTACGATT CTCATAGTCA AGCTTGGTAC	2820
TACTTCAAAT CCGGTGGTTA CATGACAGCC AATGAATGGA TTTGGGATAA GGAATCTTGG	2880
TTTTACCTCA AATCTGATGG GAAAATAGCT GAAAAAGAAT GGGTCTACGA TTCTCATAGT	2940
CAAGCTTGGT ACTACTTCAA ATCTGGTGGC TACATGGCGA AAAATGAGAC AGTAGATGGT	3000
TATCAGCTTG GAAGCGATGG TAAATGGCTT GGAGGAAAA CTACAAATGA AAATGCTGCT	3060
TACTATCAAG TAGTGCCTGT TACAGCCAAT GTTTATGATT CAGATGGTGA AAAGCTTTCC	3120
TATATATCGC AAGGTAGTGT CGTATGGCTA GATAAGGATA GAAAAAGTGA TGACAAGCGC	3180
TTGGCTATTA CTATTTCTGG TTTGTCAGGC TATATGAAA CAGAAGATTT ACAAGCGCTA	3240
GATGCTAGTA AGGACTTTAT CCCTTATTAT GAGAGTGATG GCCACCGTTT TTATCACTAT	3300
GTGGCTCAGA ATGCTAGTAT CCCAGTAGCT TCTCATCTTT CTGATATGGA AGTAGGCAAG	3360
AAATATTATT CGGCAGATGG CCTGCATTTT GATGGTTTTA AGCTTGAGAA TCCCTTCCTT	3420
TTCAAAGATT TAACAGAGGC TACAACTAC AGTGCTGAAG AATTGGATAA GGTATTTAGT	3480
TTGCTAAACA TTAACAATAG CCTTTTGGAG AACAAGGGCG CTACTTTTAA GGAAGCCGAA	3540
GAACATTACC ATATCAATGC TCTTTATCTC CTGCCCCATA GTGCCCTAGA AAGTAACTGG	3600
GGAAGAAGTA AAATTGCCAA AGATAAGAAT AATTTCTTTG GCATTACAGC CTATGATACG	3660
ACCCCTTACC TTTCTGCTAA GACATTTGAT GATGTGGATA AGGGAATTTT AGGTGCAACC	3720
AAGTGGATTA AGGAAAATTA TATCGATAGG GGAAGAACTT TCCTTGGAAG CAAGGCTTCT	3780
GGTATGAATG TGGAATATGC TTCAGACCCT TATTGGGGCG AAAAAATTGC TAGTGTGATG	3840
ATGAAAATCA ATGAGAAGCT AGGTGGCAAA GATTAGTACT ATAAGTGAAT ATGATTTGAG	3900
TGAATAGTAA GTTAAAAATC CTGATTTCAA GTAAAATCAG GATTTTTTCA TGGATGCAAT	3960
TTTTTTGGAG TCTGGTGTGA CGCGGAGGGT CTTTTGTCCT GTGTAAGTGA CAAAGCCGGG	4020
TTTTCCACCA GTTGGTTTAT TGAGTTTTTT GACTTCAATC ATATCTACCT GCACCAGATT	4080
CGACAGGCGC CCTTGAGAGA AGTAGGCAGC TAACTCTGCT GCGTCTGTCT TGA CTGCATC	4140
AGATGGGTCA AGATTTCTCTG AGATGACAAC ATGGCTTCCA GGAATGTCCT TAGCATGGAA	4200
CCAAAGTTCC TCCTTGCGGG CCATTTTTAA GGTCAATTCC TCATTTTGAA GATTGTTTCG	4260
TCCGACATAG ATGATGGTTT TGCCATCGCT TGCTAGATAT TGTTCAGTT TTTTGCCTTT	4320
CTGGATTTTC TCCCCTTGTC TTCTGCGGAT AAAACCTGTT TGAATCAATT CTTACGGAT	4380
TTACGCGATT TCTTCCAGTC CAGCTTGGTT GAGGACGGTT TCTACACTTT CCAGATAGAG	4440
AATAGTGGCT TTGGTTTCTT CAATCAAATC AGTCAAGTAT TTGACAGCTT CTTTGAGTTT	4500

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CTGATACCGT TTAAATAGC GTTGGGCATT CTGGTTGGGA GTCAGAGCCT TATCAAGCGC	4560
AATCATGATA GGTGGTTGG TATAGTAGTT GTCTAGGATA ACCTGGTCTT GGTCGTTAGG	4620
CACCTGGTGG AGGAAGGTTG TCAGCAATTC TCCTTTTGA CGAAATTCTT CAGCGTTGTC	4680
TGTCGCCAGT AACTCTTTT CCTGTTTTT GAGTTTGTGT CGGTTTTCTT GAAGTTCATT	4740
TTCAACACGA CGAATCAGTT CACTGGCCTG CTGTTTGACG CGGTCGCGCT CAGCCTTATC	4800
CTTATAGTAG GTGTCCAACA AATCAGAAAG ATTTGCAAAA GGCTCTCCA CCTGATTGTC	4860
AAAAGGAAGT GGACTGAAGG AAGTCTCAGT CAAGCATGGC TTGGTTTCTT GATTGAAAA	4920
ATTTGCAAAA GCGGAAAGTT TTCTACTAAC CAGTATCCTT TCCAATTCAT TTGCCGTATC	4980
GCGTCCCAGA CCTTGAAAGA GGCTTTGAAG ATTTTGTGCT GTTAGTTCTT GGGTTTGACG	5040
GATTTCAAAG AGCTTTTCAT CCTTGATAGT AAAAGGATTG AGAGATTTTG TACTTGGCGG	5100
AGCGATATAG GTCGATCCTG GAAGTAAGGT GCGGTAGCTA TTTTGTGAAA AGCCGACGTG	5160
TTTGATAACT TCGAGGATTT TATGACTGCT TTTATCGACC AGTAGAATAT TACTGTGTTT	5220
CCCCATAATT TCGATAATCA AGGTAGCCTG GATATGGTCT CCAATCTCGT TTTTATTGGA	5280
AACTGTAATT TCCACAATAC GGTCAATTTT CACTTGCTCA ATCGACTCAA TCAGGGCCCC	5340
CTGCAAATAC TTTCTCAAAA CCATGATAAA GGTAGAAGGT TGAGCTGGAT TTTCAAAAGT	5400
CGTTTGGGTC AGCTGAATGC GTCCAAAAC TGGATGGGCA GAAAGGAGCA GGCGATGGCT	5460
TTGGCGATTG CTGCGGATTT GCAAGACCAA CTCTTGTTCA AAAGGCTGAT TGATTTTCTG	5520
GATGCGACCA TTCCTAATT CGCTTCGCAA TTCCTCAACT ATGTGGTGTA AAAAAATCC	5580
GTCAAATGAC ATCGTCTCTT CCTTGTGATT GTATTCCATA GTATTATATC AAAAAGGTAG	5640
AATAAAATCA TGGAAATGTG GTATAATAAA GCCAAGTAAA GAGAAACGAG AAGCACATGT	5700
ATATTGAAAT GGTAGATGAA ACTGGTCAAG TTTCAAAAGA AATGTTGCAA CAAACCCAAG	5760
AAATTTTGGG ATTTGCAGCC CAAAATTAG GAAAAGAAGA CAAGGAGATG GCAGTCACTT	5820
TTGTGACCAA TGAGCGTAGT CATGAACCTA ATCTGGAGTA CCGTAACACC GACCGTCCGA	5880
CAGATGTCAT CAGCCTTGAG TATAAACAG AATTGGAAAT TGCCTTTGAC GAAGAGGATT	5940
TGCTTGAAAA TTCAGAATTG GCAGAGATGA TGTCTGAGTT TGATGCCTAT ATTGGGGAAT	6000
TGTTTATCTC TATCGATAAG GTCATGAGC AGGCCGAAGA ATATGGTCAC AGCTTTGAGC	6060
GTGAGATGGG CTTCTTGGCA GTACACGGCT TTTTACATAT TAACGGCTAT GATCACTACA	6120
CTCCGGAAGA AGAAGCGGAG ATGTTGCGTT TACAAGAAGA AATTTTGACA GCCTATGGAC	6180
TCACAAGACA ATAAACGAAA ATGGAAAAAT CGTGACTTGA TATCCAGTTT AGAATTTGCT	6240

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TTGACAGGTA TTTTACTGC TATCAAGGAA GAACGCAATA TGCGAAAACA CGCAGTGACG	6300
GCTCTAGTGG TCATCCTTGC AGGTTTGTGT TTTTCAGGTGT CACGAATCGA ATGGCTCTTT	6360
CTCCTATTGA GTATTTTCTT GGTAGTAGCC TTTGAGATTA TCAACTCTGC TATTGAAAAT	6420
GTGGTGGATT TGGCCAGTCA CTATCACTTT TCCATGCTGG CTAAAAATGC CAAGGATATG	6480
GCGGCCGCG CGGTATTAGT GGTTCCTCTT TTCGCAGCCT TAACAGGCGC ATTGATTTTT	6540
CTCCACGAA TCTGGGATTT ATTATTTTAA ACAGTAAGAG GAAATTATGA CTTTTAAATC	6600
AGGCTTTGTA GCCATTTTAG GACGTCCCAA TGTGGGAAG TCAACCTTTT TAAATCACGT	6660
TATGGGGCAA AAGATTGCCA TCATGAGTGA CAAGGCGCAG ACAACGCGCA ATAAAAATCAT	6720
GGAATTTTAC ACGACTGATA AGGAGCAAAT TGTCTTTATC GACACACCAG GGATTCACAA	6780
GCCTAAAACA GCTCTCGGAG ATTTTCATGGT TGAGTCTGCC TACAGTACCC TTCGCGAAGT	6840
GGACACTGTT CTTTTTCATGG TGCCTGCTGA TGAAGCGCGT GGTAAGGGGG ACGATATGAT	6900
TATCGAGCGT CTCAAGGCTG CCAAGTTCC TGTGATTTTG GTGGTGAATA AAATCGATAA	6960
GGTCCATCCA GACCAGCTCT TGTCTCAGAT TGATGACTTC CGTAATCAA TGGACTTTAA	7020
GGAAATTGTT CCAATCTCAG CCCTTCAGGG AAATAACGTG TCTCGTCTAG TGGATATTTT	7080
GAGTGAAAAT CTGGATGAAG GTTCCAATA TTTCCCGTCT GATCAAAATCA CAGACCATCC	7140
AGAACGTTTC TTGGTTTCAG AAATGGTTTCG CGAGAAAGTC TTGCACCTAA CTCGTGAAGA	7200
GATTCGCGAT TCTGTAGCAG TAGTTGTTGA CTCTATGAAA CGAGACGAAG AGACAGACAA	7260
GGTTCACATC CGTGCAACCA TCATGGTCGA GCGCGATAGC CAAAAGGGA TTATCATCGG	7320
TAAAGGTGGC GCTATGCTTA AGAAAATCGG TAGCATGGCC CGTCGTGATA TCGAACTCAT	7380
GCTAGGAGAC AAGGTCTTCC TAGAAACCTG GGTCAAGGTC AAGAAAACT GCGCGGATAA	7440
AAAGCTAGAT TTGGCTGACT TTGGCTATAA TGAAAGAGAA TACTAAGTAG AGGTAGGCTC	7500
ATGCCTGCTT CTGTGTTTTA CAGAAGGAGG ACTTATGCCT GAATTACCTG AGGTGAAAC	7560
CGTTTGTCGT GGCTTAGAAA AATTGATTAT AGGAAAGAAG ATTTTCAGTA TAGAAATTCG	7620
CTACCCCAAG ATGATTAAGA CGGATTTGGA AGAGTTTCAA AGGGAATTGC CTAGTCAGAT	7680
TATCGAGTCA ATGGGACGTC GTGGAAAATA TTTGCTTTTT TATCTGACAG ACAAGGTCTT	7740
GATTTCCCAT TTGCGGATGG AGGGCAAGTA TTTTACTAT CCAGACCAAG GACCTGAACG	7800
CAAGCATGCC CATGTTTCT TTCATTTTGA AGATGGTGGC ACGCTTGTTT ATGAGGATGT	7860
TCGCAAGTTT GGAACCATGG AACTCTTGGT GCCTGACCTT TTAGACGTCT ACTTTATTTT	7920
TAAAAAATTA GGTCTGAAC CAAGCGAACA AGACTTTGAT TTACAGGTCT TTCAATCTGC	7980
CCTTGCCAAG TCCAAAAGC CTATCAAATC CCATCTCCTA GACCAGACCT TGGTAGCTGG	8040



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ACTTGGCAAT ATCTATGTGG ATGAGGTTCT CTGGCGAGCT CAGGTTTCATC CAGCTAGACC	8100
TTCCCAGACT TTGACAGCAG AAGAAGCGAC TGCCATTTCAT GACCAGACCA TTGCTGTTTT	8160
GGGCCAGGCT GTTGAAAAAG GTGGCTCCAC CATTTCGACT TATACCAATG CCTTTGGGGA	8220
AGATGGAAGC ATGCAGGACT TTCATCAGGT CTATGATAAG ACTGGTCAAG AATGTGTACG	8280
CTGTGGTACC ATCATTGAGA AAATTCAACT AGGCGGACGT GGAACCCACT TTTGTCCAAA	8340
CTGTCAAAGG AGGGACTGAT GGGAAAAATC ATCGGAATCA CTGGGGGAAT TGCCTCTGGT	8400
AAGTCAACTG TGACAAATTT TCTAAGACAG CAAGGCTTTC AAGTAGTGA TGCCGACGCA	8460
GTCGTCCACC AACTACAGAA ACCTGGTGGT CGTCTGTTTG AGGCTCTAGT ACAGCACTTT	8520
GGGCAAGAAA TCATTCTTGA AAACGGAGAA CTCAATCGCC CTCTCCTAGC TAGTCTCATC	8580
TTTTCAAATC CTGATGAACG AGAATGGTCT AAGCAAATTC AAGGGGAGAT TATCCGTGAG	8640
GAATCGGCTA CTTTGAGAGA ACAGTTGGCT CAGACAGAAG AGATTTTCTT CATGGATATT	8700
CCCCTACTTT TTGAGCAGGA CTACAGCGAT TGGTTTGCTG AGACTTGGTT GGTCTATGTG	8760
GACCAGATG CCCAAGTGA ACGCTTAATG AAAAGGGACC AGTTGTCCAA AGATGAAGCT	8820
GAGTCTCGTC TGGCAGCCCA GTGGCCTTTA GAAAAAAGA AAGATTTGGC CAGCCAGGTT	8880
CTTGATAATA ATGGCAATCA GAACCAGCTT CTTAATCAAG TGCATATCCT TCTTGAGGGA	8940
GGTAGGCAAG ATGACAGAGA TTAAGTGAAG GGATAATCTG CGCATTGCCT GGTTTGGTAA	9000
TTTTCTGACA GGAGCCAGTA TTTCTTTGGT TGTACCTTTT ATGCCCATCT TCGTGGAATA	9060
TCTAGGTGTA GGGAGTCAGC AAGTCGCTTT TTATGCAGGC TTAGCAATTT CTGTCTCTGC	9120
TATTTCCGCG GCGCTCTTTT CTCCTATTTG GGGTATTCTT GCTGACAAAT ACGGCCGAAA	9180
ACCCATGATG ATTCGGGCAG GTCTTGCTAT GACTATCACT ATGGGAGGCT TGGCCTTTGT	9240
CCCAAATATC TATTGGTTAA TCTTTCTTCG TTTACTAAAC GGTGTATTGT CAGGTTTGT	9300
TCCTAATGCA ACGGCACTGA TAGCCAGTCA GGTTCCAAAG GAGAAATCAG GCTCTGCCTT	9360
AGGTACTTTG TCTACAGCG TAGTTGCAGG TACTCTAACT GGTCCCTTTA TTGGTGGCTT	9420
TATCGCAGAA TTATTTGGCA TTCGTACAGT TTTCTTACTG GTTGGTAGTT TTCTATTTTT	9480
AGCTGCTATT TTGACTATTT GCTTTATCAA GGAAGATTTT CAACCAGTAG CCAAGGAAAA	9540
GGCTATTCCA ACAAAGGAAT TATTTACCTC GGTAAATAT CCCTATCTTT TGCTCAATCT	9600
CTTTTAAACC AGTTTGTCA TCCAATTTTC AGCTCAATCG ATTGGCCCTA TTTTGGCTCT	9660
TTATGTACGC GACTTAGGGC AGACAGAGAA TCTTCTTTT GTCTCTGGTT TGATTGTGTC	9720
CAGTATGGGC TTTTCCAGCA TGATGAGTGC AGGAGTCATG GGCAAGCTAG GTGACAAGGT	9780

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GGGCAATCAT	CGTCTCTTGG	TTGTCGCCCA	GTTTTATTCA	GTCATCATCT	ATCTCCTCTG	9840
TGCCAATGCC	TCTAGCCCCC	TTCAACTAGG	ACTCTATCGT	TTCCTCTTTG	GATTGGGAAC	9900
CGGTGCCTTG	ATTCCCGGGG	TAAATGCCCT	ACTCAGCAAA	ATGACTCCCA	AAGCCGGCAT	9960
TTGAGGGTC	TTTGCCTTCA	ATCAGGTATT	CTTTTATCTG	GGAGGTGTTG	TTGGTCCCAT	10020
GGCAGGTTCT	GCAGTAGCAG	GTCAATTGGG	CTACCATGCT	GTCTTTTATG	CGACAAGCCT	10080
TTGTGTTGCC	TTTAGTTGTC	TCTTTAACCT	GATTCAATTT	CGAACATTAT	TAAAAGTAAA	10140
GGAAATCTAG	TGCGAGTAAA	AATCAATCTC	AAATGCTCCT	CTTGTGGCAG	TATCAATTAC	10200
CTAACCAGTA	AAAATTCAAA	AACCCATCCA	GACAgATTGA			10240

## (2) INFORMATION FOR SEQ ID NO: 33:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 13206 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 33:

CGCTTTATCG	TGGACGTGGT	CAAGCCGAGA	ATTTTCATCAA	GGAGATGAAG	GAGGGATTTT	60
TTGGCGATAA	AACGGATAGT	TCAACCTTAA	TCAAAAACGA	AGTTCGTATG	ATGATGAGCT	120
GTATCGCCTA	CAATCTCTAT	CTTTTCTCA	AACATCTAGC	TGGAGGTGAC	TTCCAAACTT	180
TAACAATCAA	ACGCTTCCGC	CATCTTTTTC	TTCACGTGGT	GGGAAAATGT	GTTCGAACAG	240
GACGCAAGCA	GCTCCTCAAA	TTGTCTAGTC	TCTATGCCTA	TTCCGAATTG	TTTTCAGCAC	300
TTTATTCTAG	GATTAGAAAA	GTCAACCTGA	ATCTTCCTGT	TCCTTATGAA	CCACCTAGAA	360
GAAAAGCGTC	GTTAATGATG	CATTAAAGAA	CAGTCGAGAT	GAAAAAATCG	TGTGACGCAC	420
CAAGGGAGGA	GTCTGCCCTT	TTGAGGAAAT	CTAGCGAGGA	AAAACGATAC	TGGAACAGCA	480
GAAAGTAAAA	CTGACCTCAT	GAGGAGGAAG	AAAGTGGCTC	ATGAGGTCAG	GGGTTTGTAA	540
AGTTACATCT	AGTTGAGAGA	GGTATGAATG	ATTTGGGATT	AATCATTTCT	TGTTTTAAAT	600
CAGGAGAATA	GTAACGATTT	TTTCCTTTT	TGACGAACTC	TATTCCGTAA	CGATCAATCA	660
ATTTAATCAT	GTACCTAATA	TTAGAATTGT	TTATCCCAAA	TTTATTTGAA	AGCTTCTCTA	720
AGCTATATCC	TTGTTTTCTA	AGTTCATAGA	TCTGAACTTT	ATCATCATAA	GTTAGTTTCA	780
TAATAAAAAC	ACCCCAAAAG	TTAGATTTT	TCTGTCTAAC	TTTGGGGGGG	CAGTTCATTC	840
AACACCTGAT	ACTATGCGTT	TTTCTTATTT	GAAATACTTT	TTACTCAACC	TCTTTTACT	900
CAATGAAAAT	CAAAGTGCAA	ACTAGAAAGC	TAGCCTCAGG	CTGCTCAAAA	CAGTGTTTTG	960

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AGGTTGCAGA TGGAAGCTGA CGTGGTTTGA AGAGATTTTC GAAGAGTATT ACTTAATCTT	1020
CTTGATACTT TGACTAAGAA TAAATCCTAC AATCATCCCT ACCATATTTT GCATAAAATT	1080
CGGTAGAATT TCTGGGAGGG CTGCTGCCCA GCCATTTCATC AAAGCAGAAC CCAAGGCGTA	1140
GCCTCCTACC ATGGCAATAG TTGCTAAAAT AAGGCCTAAC CACTGACTTT TTCCTTTAAA	1200
TCCTGCGAAA AATCCCTGCA AGCCATGGTT GACCAAGCTA AAGAACATCC ACTGAGGGTA	1260
GCCTGATAAG AGGTCAATCA AGAACTTGC TAGTCCTCCG ACTACCGCTC CTTACGACT	1320
ACCAAAGTAA AAGGCCGCAA AGAAGACACC AGCATCTAAA AGAGTTAGAA TTCCTGTAGG	1380
TGTTGGGATT TTTAAGAAAT AACCTAGAAC CACAGAAAGG GCGGTTAATA GGGATACAAG	1440
GGCGATTTTA GTTGTTTTGG TTTGCTTCAT ATTGTCTTAC TCCATACTGA TCTGCTTGTC	1500
CAATAGCACG ATAAACGAAA GCCTTAGAGC TTTCTACTGC TGGCAAAAGT TTATCACCTT	1560
TAACCAAGTG ACTGGCAATG CTAGAGsCAA AGGTACAACs TGCACCAGCA TTTTGGCCTT	1620
GGATAACTGG ATTTTCTAGG ATAGTAAAGG TCTGTCCATC ATAAAAGACA TCCACAGCCT	1680
TGTCCTGACT AAGACGATTG CCTCCCTTGA TAATGACTGt GCGCTCCTA AATCATGCAA	1740
TTTCTGCGCT GCAGTTTCA TGTCTTCCAA GGTTTTAATT TCCTGACCGG ATAATAATTC	1800
TGCTTCTGGG AGATTAGCG TAATCACACT GACATAAGGG AAAAAGCGAA TCAACTCTTG	1860
GCAGAGCTCA CTGACAGCTA CATCATGCGT TTCCTTGCAg ACCAAGACAG GATCCAACAC	1920
CACAGGTACT CCTGGGCGTT GTTTGATAAA GTCCAAGGCC TTCTCAGCCA CGCTGACAGT	1980
AGGGAGAAGA CCAATCTTAA TTCCCCCAA TTCCACATCA CGCAAGCTAT CTAATTCATG	2040
TTGAAAAATG GTATCATCAG TTGGAAAGAC TTCAAATCCT TTTTCTGTCA AGGCTGTCAA	2100
ACAAGTCACT GCTACAAACC CATGCAAGCC GTTCAAGGTA TAGGTAGCCA AATCAGCTGA	2160
CAGTCCACCA CCACTAAAAA TATCATTTCC AGAAAGTGCT AAAATACGAT TATTCTTCAT	2220
AACGAATCTC CTTTAAATAC AAACCATTTG GTGCTGCAGT GGGACCTGCA AGTTGCCTGT	2280
CCTTCTTCTC CAAGATGAGA TCAATCTGCT CTACTGGCAT GCGGTTGTTA CCGATTTTGA	2340
GAAGAGTCCC CACCATATTG CGAATCTGTT TATACAAGAA ACCATTTCTT GAAAAGGTAA	2400
AGGTCAAAAA TTGTCCTGTC TCATCGACTA TTAAACTAGC TTCTGTGATG GTGCGAACCT	2460
TATCCTCTAC ACTAGTCCCA GAGGCTGTAA AACCGGTAAA ATCATGGGTT CCCTCTAGCT	2520
TTTTGATTGC AATCTGCATT CGTTCCACAT CGAGTGGGTA GGGAAAGTGG GTGGCATAGT	2580
GACGGCGCAT CGGATTTTGG GGACGTCCTC TATCCACAGT AAATCATAG GTCTTGCTAT	2640
GCTTGGCATA ACGGCAATGA AAATCATCTG CCACAAGCTC AATCGAAATC ACATCAATAT	2700

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CTTCAGGAGA CTGGGTATCC AAGGCAAAAC GGAGTTTCTC CTCATCCATC TGATAAGGCA	2760
GGTCAAAATG AATCACCTGT CCCAGGGCAT GAACCCCACT ATCTGTCCTA CCAGCACCGT	2820
GAACAGTAAT GGCTTGCCCT TTATTTAATC TGGTCAAGGT TTTTTCATTT TCTTCCTGAA	2880
CGCTACGCGC ATGAGGCTGG CGCTGAAAGC CAGCAAAGGC ATAACCATCA TAGGAAATAG	2940
TTGCTTTATA TCTCGTCATA GCCTCTATTT TATCAAGAAA TTAGTCTGTA AACAAGGACC	3000
TAAACAAAT ATTGTATGGG TATAAAAATC TCATACTCTT CGAAAATCTC TTCAAACCAC	3060
GTCAGTTTCC ATCTGCAACC TCAACACACT ATTTTGAGCA ACCTGCGGCT AGCTTCTAT	3120
AGTAGATTGA AATAAGATAT GAACAACTCT ATTAGGAAAG TCAAATTAAT TTCTAGAAAT	3180
ATTTTAGCAG CTACAGCGTA CTATTCCAAA CTCAATCAAC TATAGTTTGC TCTTTGATTT	3240
TCATTGAGTA TCAAAAGAAA AACTTAGGAA TCAATCCTAA GCTCTCTTCT GAAGTAGGTA	3300
CATGACAAAG ATAGAGATTA CAATCAACCA ACCTCCTAAG ATACTAAAGA CCAACATCCC	3360
ATTGTGAGTT AGTAAGCCAA TTGCACCTAG AACGAATGGG GTCGTAAAGG CTCCGAAACT	3420
ACAGCCTAAT ACAGCAAATG AAGTTGCTTG ATTGAGGAGT TTAGCTGGAA TTCGTTTCTA	3480
GACAAGTTGA AAGACCGTCG TCAAGACTAC ACTATAGGCA AATCCAGCCA GAACACTTCC	3540
TGCTACTACC ACCCACAAGG ATGAAGACAA GGCAATCAGG ATTTGCCCA AGCCAAAGGT	3600
AATACCAGAC CAGAGGAGCA GTTCTCTTT AAAGATAGAA ATCAAGAAAG AAAAATCAG	3660
CCCAGCCACA ATCCCGATCA ACTGCATGAT ACTAAGAACA AACTAGATA ACTGGGCATC	3720
CCCCAATCCT CTTTCCACCA TCAAACTTGG AATACGGATG GTAATAGCTG TATTGGTACA	3780
AACTACAAT GCCGCTTCGA TAGCTAAGGT AAAAATCAAG CCTTTCATTT CTCGAGTTAA	3840
ACGACTTGCT TCCTTCGCTC TTTCTTTGAC TTCTTTCTTT GATTTTCCAT AAGGGACAAA	3900
GAGCAGATAA AGGGGACGCA CCAAAAATCC AGCACTATAG GCTAGAAAGA TAGCTGTCCA	3960
ACCAAAGGCC AACAACTGAC CGACGGCCAA GGTAATGAGA GAAGCTCCAA CGACCTCTGC	4020
AGAAGCGCGT AGCCCTAACA TCTGAATTCG CCTTTTCCT TGGTAGCGTT CACTGATAAT	4080
AGAAATGGCC TTGGCATTGA TCATCCCAAG ACCCAAACCA AAGAGAAGCC GTGTTCCAAA	4140
GACAAAGGGA TAGGCTTGGT ACCAGAAGGG AGCTGTACCG CTCAATGATA AAATCAGCAA	4200
GCCCAAACTA ATCTGTAAGC GCTCAGGAAA TATTTTCTT AAGAAACCAT TTAGCAGTAA	4260
CATCATCATG ATTCCAAAGG AAGGCAAGCT CACCAAGAGC TCAATTTGTT CCTTAGAATA	4320
ACCCTGATAA TAGTCAAACA TGGCTGGTAG GGCACCTGAA ATGGAAAAGG AGGTAATCAA	4380
AACGAGGGAG AGAGCCAAAA TGCTGGCCCG TTCTAAAAAT TGTTCATGA AATCTCTTTC	4440
TATATTTCTC TTAATCTTCT ACTTTTTTGA TAGTTATCAA ATAAGCAAGA AAAGAAGAAG	4500

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CCTCATTGGT	TGTTAGACTC	CTTCTTAAAT	TCGAAAATGA	ATCCCTTGTA	TCTTATACTC	4560
AATGAAAATC	AAAGAGCAAA	CTAGGAAGCT	AGCCGCAGGT	TGTTCAAAAC	AGTGTTTTGA	4620
GGTTGCAGAT	GGAAACTGAC	GTGGTTTGAA	GAGATTTTCG	AAGAGTATTA	GGATGACTTT	4680
CTCTTGATTT	GCTTGATAAA	GTAGAAAATA	AATCCTGCTA	CCATATAGGC	AACAAAGATA	4740
ATCAGACACC	ACTTAAACAC	AACATTCCAA	CCCTTGTTCA	CATTCAAAAA	GAAGTAAGGG	4800
AAAGGATTAT	CCTTGGCATT	TGGAATATTG	AGTTTTAGAA	CCAAGCCATT	AAAAAGAGCA	4860
AACATCATAT	ACAGAAAGGG	TAAATGGTC	CACACTGCTG	GATCCCAAAT	CTTGTATTGA	4920
CCCTGTTTGT	CAAAAAAGAG	GGTATCCGCT	AAAAACCAGA	TGGGAACGAT	ATAGTGGCAA	4980
AGGAAATTTT	CTAGGGTATA	GAAATTAGTC	GCAATGGGCG	CCAAGAGGAA	ATGGTAAATC	5040
ACACAGGTAA	TCATGATACT	CATGGTGACC	CCACCTTTTA	AGCGCAAGAG	ACTTGGCCTT	5100
TGCCAATTTT	CACCTACACG	GCTCATAACC	TTTAGAAGAT	AAAGGGTAAA	AATAGTTACC	5160
AAGAGGTTGG	ACAGAACCGT	GTAATAGAGA	AGCATCCCAA	AACCACCATG	CTTAGTAATT	5220
TCAAGATAAA	TCCCCGTAAA	AGCCGCTAGA	AACAAGAAGA	TACGGCTATA	AAATACAAGT	5280
TTATAGTGTT	TTGACATGCT	TAAATCTTCC	TCACAACTC	TGATTTAAGT	TTCATGGCAC	5340
CAAAACCATC	AATCTTACAG	TCGATATTGT	GGTCGCCTTC	TACGATGCGG	ATATTTTTC	5400
CGCGCGTCCC	TTGTTTCAAA	TCTTTTGCGG	CACCTTTTAC	TTTCAAGTCC	TTGATGAGAG	5460
TTACTGTATC	ACCATCAGCC	AATTTATTTC	CGTTGGCATC	GATAGCGACA	AGACCTTCTT	5520
CTACTTCTGC	AACTTCAGCA	GGATTCCACT	CATGAGCACA	CTCTGGGCAA	ACCAGTAGGG	5580
CACCGTCTTC	GTAGACATAC	TCTGAGTTAC	ATTTTGAGCA	ATTTGGTAAA	TTGTTTCATGG	5640
TTTCTCCTTA	TCATCATTC	CTATTCTTTG	AAAATCAAAA	TTTCTCGAAC	AGCAACTATT	5700
ATACCCATAA	ATCAGCATTT	TGACAAATTT	AGAAAAAAC	CGATATCAAT	CTATCGGCTT	5760
TTCTACATTT	ACATTCTTTT	TTGAGCTTCT	GCTTTGATTT	TTTCAACTAC	TTCTTGAATG	5820
TTCAAACCA	TTGTATCAAG	GTAGACAGCA	TCCTCTGCTT	GTTTGAGAGG	AGAAGTCTCA	5880
CGATGACTAT	CCTTGATGTC	ACGCGCAGCA	ATTTCCCTTT	TTAGGGTTTC	AAGGTCTGTT	5940
TCAATTCCCT	TGGCAATATT	TTCTTGTA	CGACGCTCTG	CTCTCTCATC	AACAGAAAGCT	6000
ACTAGGAAAA	TTTTCAATTC	TGCTTGTTGGC	AATACAACAG	TTCCAATATC	GCGACCATCC	6060
ATGACAATCC	CGCCTTGCTG	GGCAATTCTT	TGTTGGAGAG	AAACCAGTTT	CTCACGCACT	6120
TGAGGAATTG	CTGCAATAGC	AGAAACATGA	TTGGTCACTT	CATTTTCACG	GATAGGATGG	6180
GTAAATATCCA	CATCTCCTAC	AAAAACAAGC	TGGTCTCCAG	TTTCTGAACG	TCCAAAGCTG	6240

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ATTGGATGCT GGTCCAACAA GGCTAGAAGG GCTTCGACTT CTTCAACTCC TAATTGGTTC	6300
TTAAGAGCCA TATAGGTGCG TGCACGATAC ATAGCTCCTG TATCAAGGTA GGTGAATCCA	6360
AAATCCTTAG CAATAATCTT TCGGACCGTA CTCTTACCGC TGGAAGCAGG ACCATCAATA	6420
GCAATTTGAA TTGTTTTCAT ATCGGCTCCT ATTTTATTTT TATAACATCA CCTGGATTAG	6480
CAAACCAAGA TCCTGTAGCC ATGTGCCAG GATTCAAGGC CTCTAACTGA GCAATGGAGA	6540
TTCTGTCACG AGCGGCAATA GCTGCTTCCC CTCTCCTGC GAGAACTTTA ATCGTTCCTT	6600
CAGGATTAGC AGCTTCTTCT GAACTACTAG AAGTAGATTG TGGCTCTGAA CTCTGCTCAG	6660
GCTGAGAACT ACTTGAAGAT GAGATTTGTA CTACACTGGC ATCAGAATCA TGAAAGCCTT	6720
TTAAGGCTGC TGTGCGATTA CTCCCCCG ATGATAGATA GATGAGAAGC ATGACCATCA	6780
CCACCACAAT TACAAAGAAA ATACTAGCTA GGATCGTCAA AATACGATTA GCCATCCTAT	6840
CAGCCCCTCC GTGGTTTGA TGCCGACGCT CTGCTCTGA TTCTTCTGA TCATAGATAT	6900
CTTCTTGCCA CGGTCTTTT GCCATACCTT ACTCCTTGT TTTTCTTACT TTTCTTATTA	6960
CAATATAAAT ATGAACATGA AAATCACACT TATACCTGAA CGATGTATCG CCTGTGGGCT	7020
TTGCCAAACT TATTCTGATT TATTTGATTA CCACGATAAT GGAATCGTGC GTTTTACGA	7080
TGACCCCTGAC CAACTGGAAA AAGAAATTC TCCTAGTCAG GATATCTTAG AGGCTGTAA	7140
AAATGCCCCA ACTCGCGCCC TGATTGGAAA CCAGGAAGCC TAAATCAATG GCGATAATCC	7200
ACTCCCTCTA GTTTAGCACA TTCCCATGTA AAATTATAGT CTTTCACTT TATTTTTC	7260
TGTAAAATCA GGAAGGTCAC TTTTCTTTT GATAAGATA AGTGGTCTTT TTTTAGTCTC	7320
TAAATAAATC TTAGTGATAT ACTTGCCGAG AATCCCAATG GTCAAGAGTT GAATGCCTCC	7380
AAGAAAGAGA ATAACAGCCA TCAGAGAGGT CCAACCAGAT GTCGGATTGC CCAAATGAG	7440
GGTCCGAACC ACAACAAAA AGGTCATCAG CAGAGAAAGA AAACAAGATA GGAGACCAGC	7500
TACAAAGGCT ATAATCAAGG GAAAATCTGA AAAATTAATA ATCCCTTCAA TGGAGTAGAA	7560
AAAGAGTTGC CTAAACTCC AACTTGTCTT GCCAGCCTGC CTTCGACAT TTGGATAGTC	7620
CAATAGTAG GTTTGAAAC CCACCCAGGC GAAGAGCCCC TTGAAAAAC GATTGGACTC	7680
GGTCAAGCTT AAAATGGCAT CGACTACAGA CCTTCTCATC ATACGAAAA CACGGACACC	7740
CGACGGCAGA GCTACTGGGC TGATTTTGTG CATGAGGCGA TAAAAGAGAA CAGCACAGAA	7800
ACTGCGAAAG AAGGGTTCTC CCTCCCGACT AGTTCTCCGT GTCCCAACGC AGTCCAAGTC	7860
TACATTTTTC TCTAATACAT TTTTCATCTC AAACAACATA CTAGGAGGAT CTTGGAGGTC	7920
TGCATCCATC ACCACCACCA AATCTCCTGT CGCATATTGC AAGCCTGCAT AAAGGGCTGC	7980
TTCTTTGCCA AAATTCGAG AGAAAGAAAT ATAATGGACT GCCGGATTTT GCTCCCGATA	8040

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GGCCTTTAAG AGTTCCAAGG TCCCATCACT TGATCCATCA TCGACAAAGA CATACTCGAT	8100
TTCTGTTTCC AAATCTGGAA GTAAAGCTTC CAGAGCCTGA TAAAAAAGAG GAAGTACTTC	8160
CTCTTCGTTT AAACAAGGGA CGATGATTGA AATCATCATC TTAGTCTTCA AATCCATTG	8220
GATGCTTGCT TTGCCAACGC CATGCGTCTT CACACATTTG GGTGATGTGC AGTTCTGCTT	8280
CCCAACCGAG TTCTGCTTTA GCTTTTGCCG GGTCTGAGTA GCAGGCAGCG ATATCACCTG	8340
GGCGACGTTT TACGATGCGG TAAGGAATAG GACGGCCAC CGCTTTTTC ATGTTTGGGA	8400
TAATTTCAAG AACTGAGTAA CCTTTACCAG TTCCAAGGTT ATAAACGTTT AGTCCTGAAC	8460
CTTTTGGAT TTTTTCAAA GCTGCAACGT GACCCTTAGC CAAATCGACA ACGTGGATAT	8520
AGTCACGAAC ACCTGTTCCA TCTTCCGTAT CGTAATCGTC TCCAAACACT TGCACCTGCT	8580
CTAATTTTCC AACGGCTACT TGAGTCACAT ATGGCAAGAG ATTGTTTGGGA ATACCGTTTG	8640
GATTTTCTCC CAAATCACC CTCTCATGGG CTCCGATTGG GTTAAAGTAA CGAAGCAAGA	8700
CAACATTTCCA TTCTGAGTCT GCTTTGTAAA TATCAGTCAA AATTTCTCT AGCATGAGCT	8760
TAGTACGACC GTATGGGTG GTCACTGAAA GTGGGAAATC TTCCAAGATG GGCACGTGT	8820
GCGGATCCCC GTAACTGTC GCAGAAGAAC TGAAGATGAT GTTTTACAG TTGTTTCTT	8880
CCATGGCTTT CAAAAGGCTG ACAGTTCCAG CGATATTGTT GTCATAGTAG GCAAGAGGGA	8940
TACGTGTTGA TTCGCCAACA GCCTTCAAAC CAGCAAAGTG AATGACACCA GTCGGTCTT	9000
CCTGCTTGAA AATATCTCTG AGGGTATCTG TGTCACGAAT ATCTGCCTCA TAGAAAGGAA	9060
TCTCACTCC TGTGATTCCT TCAACAACCT CTAACTCTT ACGATTGCTA TTGACAAGAT	9120
TATCCACCAC AACAACCTGA TGACCTGCTT GGATCAATTC AATAACAGTG TGGGTCCAA	9180
TAAAACCGGC ACCACCAGTT ACCAAAATCT TTTCTTGCAT CTTTTTCTT CGATTCTCAG	9240
ATTATTTTTT CTTATTTTAC CATTTTGGAC AGGGAATGTC ATTTGCCATC CTAACTACC	9300
TGATAAAAT TCAGTAAAT GCTTATACTC TTCGAAAATC CAATTCAAAC TACGTCAACG	9360
TCGCCTTGCC ATGGGTATGG TTACTGACTT CGTCAGTTCT ATCCACAACC TCAAACAGT	9420
GTTTGGAGCT GACTTCGTCA GTTCTATCCA CAACCTCAA GCAGTGCTTT GAGTAACCCG	9480
CGGCTAGTTT CCTAGTTTGT TCTTTGATTT TTATTGAGTA TTATTCGCTT TTTACTCGTT	9540
TGACATAGTT TTCAATTGGG TAATTTAGAG GGTCCAAGGT CAACTCCTTG TCTTGGATCA	9600
GTGGGCTAG ATGGTAACCA ATGATAGGAC CAGTTGTGAG GCCTGATGAA CCTAGTCCAC	9660
TGGCTGCATA GACACCAGTT AAGTCAGGCA CCTGCCAAA GAAAGGAGAG AAATCACTGG	9720
TGTAGGCACG GATTCCAACA CGCTCAGATT TTGAAGTAGC TTCAGCCAAA ATCAGATAGT	9780

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GAGTCAAGGT GGCCTCCTCC ATTTGTTGGA GCAAGGTTTC ATCTACCGTC AAATCAAATC	9840
CCATGTCATT TTCGTGGGTA GCGCCTAAGG ATAATTTCCC ACCTGCAAAG GGAATCAAAT	9900
CCCACTCCCC TTCTGGCATG ACAACAGGGT AATCTTCCAT GTCTTGGGCA AGCTGATAAT	9960
CTCGTAGTTG TCCTTTTGA GGACGGACAT CCACTTCATA ACCTAAAGGC TCTAACATGT	10020
CCCCAACCA AGCTCCCGTC GCCAAAATAA CCTGCTCAAA CTCCTCTTCA CCAATCTGGT	10080
AGCCTGATGC TAACGGTGTC AGAGTCACTT TTTCTTTGAC CAGCTTGACA TGACTGACTT	10140
CCAGCAAACG AGTCACTAAA AGTTGGCCAT CTACTCTCGC TCCACCAGAA GCATAGAGCA	10200
GGCGGTCAAA TCCCTGCAAA CCAGGGAATA ATTCATTAGC TGAGGCTTGG TTCAGAAATGG	10260
CTAATTGCCC TATCAAGGGA GATTCTTCTC TGCGCTGGAG GGCCAGTTGA TAAAGTTCTT	10320
CCAAATTGGA TTCATCCTTT TTCAAGAGAA AGACTCCCGA ACGCTGGTAA AAGTCGATTT	10380
CTTGTCCTGA TTTCTCTAAA TCAGCTAATA AATCCACATA AAAATCAGCC CCCAAGCGCG	10440
CCATCTTGTA CCAGGCTTTA TTACGGCGTT TGGAAAACCA AGGACTGATA ATTCTGCTG	10500
CGGCCTTGGT GGCTTGACCT TGCTCATGGT CAAAACGGT CACCTCTAGG TCACTTTCTC	10560
TCGAGAGGTA GTAGGCAGCT GTTGCTCCCA CAATTCCTGC TCCAATAATG GCAACTTTTT	10620
TCATTGTCTT CACTTTCTAA CTAGATATGA TGGAAAGGAT TGGTTGATGC CTGACTAGGC	10680
AAGATATCAA TAGACCACCC CTTATCTTCC TTCCATTGAC TAAGAAGTGC TGCGATTTTT	10740
TCTACAAAA TCACTTCGAT ATAGTGACCT GGGTCCAATG CAAGCAACCC ATCAGATAGC	10800
ATATCCTGAG CAGTATGGTA GTAGATATCA CCAGTGATAT AGACATCTGC CCCCTTTGCC	10860
AAAGCATCCT TATAGAAAGA CTGCCCCTT CCACCACAAA TTGCTACTCT TGAAATAGGC	10920
TTCTGCAAAAT CATCCTCTTG ATAATGCACC ATTGGAAGGC TATCTAGGTC AAAGACTGTC	10980
TTGACCTGTT GGGCCAATTC CAAAATGTC TGAGGCTGAA TATTCCCAAT ACGTCCAATT	11040
CCACGTTCTG GACCTGTTTC CTGCAGATAA GTCGTCTCCT CGATTCTTAG CATCTGACAA	11100
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ATATCATGCT TAATCAGGTC GATGTAAATC TGATTTTGCG GACGGCTGGC AAGCAAGTCC	11220
TTGATAGGAC GAAAGATAGG CGCGTGCTTG ACGATAATCA AGTCCACACC CTTTCAATG	11280
GCCTCTGCCA CTGTCTCTTC ACGAATATCG AGGGCAACCA TGACCCCTTG GATACCCCTG	11340
TCTAAAGTGC CAATTTGCAG ACCACGGCTG TCTCCCTCCA TAGAAAATTC CTGAGGGCAA	11400
AAGGCTTCAT AAGCTTGGAT CACTTCACCT GCTAACATGG AGCACCTCCT TGATAGCTTG	11460
AATCTTATCT ACTAGAACTT GACGTTCTTC CAGATTTTTT TCTGGGATTT GTCCGAGGGC	11520
GAACTCTAGC TTCTCAGCTT CTTTTTGCCA TTTTGGACA AATACTGGAC TGACTTCTTT	11580



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GGACAAGAAG GGACCAAAGC GAACATCACT GGCTGATAGC TTCATTTGTC CTGCTTCCAC	11640
CACCAAAATC TCATAAACT TTCCAGCTTC TTCTAAGATG CTTTCTGCTA CAATCTGGAA	11700
TCCATGATCC TGTAGCCAGA TACGCAAGTC GTCTTCACGA TTATTGGGCT GGAGGATCAA	11760
ACGCTCTACA TTAGCTAACT TCCCCAAACC TTCTTCTAAA ATCCTAGCAA TCAAACGACC	11820
ACCCATGCCA GCAATGGTAA TGACAGACAC TTGGTCAGTC TCTTCAAAAG CTGCCAAGCC	11880
ATTGGCTAAA CGGACTTGGA TTTTCTCCTT TAGGCCGTGA GCCTCAACAT TTTTAACCGC	11940
AGACTGATAG GGACCTTCCA CCACCTCACC TGCAATAGCG CTTTGTATTT GGCCTCTCTC	12000
AACCAACTCG ATAGGCAGAT AAGCATGGTC ACTTCCCACA TCTAGTAAA TAGCCCCCTG	12060
TGACACAAAG GAAGCTACCA ATTCTAATCT CTTTGAAATC ATCTTCTCTC ACTTTCCAAA	12120
ACTCTATTAC CTCTATTAT ACCACATTC AATCTTCAAC TTCCAGTAA TATAAGCACC	12180
TCTGGCGAAA GAAGTTTCAA TGTCTTAAAG TAATAAGTGA ATCCAATTGA AAGATTTTAA	12240
ACAATTTGCA AAAATGTCAA AAAATAAAAA ATAAACAGTT TATTCAGAAA ATTCTTGACA	12300
TATAAAAACA CATGGTAGAA TATAATTAGA AAGTTAGAAA AAATAAAGT TTGACTAAAA	12360
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TTAGAACTAC TTCCAGAGGA AGATATCATT GTCACAGTC TCCCTAAGTA TTGTTCTTTT	12540
ACTTGTTTAA TTACAGGTCG CTAGTTATAT TTTATATAAA ATAAGTAGCT TTACTTACGG	12600
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TAGAGAAAGA ATGTTTAAAA TGTGATAAAA ATTTCCAACA GGGTGATATT TGAATTACT	12720
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AAGACGCTGT AAATATTTTT AAGATTGTGT ATAACTATC CCAACTAAAT AATTGTAGCT	12840
TTAAAGTTGT TAAAAATTTA GAGGAATTAA AAAAAATTAA TTCCCTAGG GAAATGAGCC	12900
CTACTGCTAA CAAATTTATA ACTCTATATC CTAAGTCAGA ATCTGAAGCT AAGAGTATGA	12960
TTTGTAATCT TACGAATAGA CTGTCAGAA TTAAGGCTCC AAAAATACTA TCTGACTATC	13020
AATGTGGAAT GCATTCTCCA GTTCATTATA GATATGGGGC TTTTTTAAAA AAACAAGCTT	13080
ATGATGAAAA AAATAAAAAA GTCATCTATT TATTGCTAGA TGAAAAAGG AAGAACTATG	13140
TAGAAGATAA GAGACAAAT TTCCTAGTC TTCCTAGCTG GAAAATGGAT TTATTTTCAG	13200
AAGAAG	13206

(2) INFORMATION FOR SEQ ID NO: 34:

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- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 13104 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 34:

CCGGATCCAG CGAAAAATAT GCTCTTTGAT GCTGTAAGTG GTCAAAAAGA TGCTAAAACA	60
GCTGCTAAGC ATGCTGTAAC ATTGATCAAA GAAACAATCA AACAAAAATT TGGTGAATAA	120
AAAATTGTGTT CAAGGGGGGT GGAAATCAAA TCCCCTTTG AATTTATCAA TAGAGACACA	180
AATAATTTAG CTTTCTTATA AAAAAGTAGT ATCCTATGAA AGGAGTTAAT ATGGAAAAGC	240
AACAACCTAG TAAAGCAGCC CTGCTGTCTA TCATTCCTGG GTTAGGACAG ATTTACAATA	300
AACAAAAAGC CAAAGGTTT ATCTTCCTTG GTGTAACCAT CGTATTTGTC CTTTACTTCC	360
TAGCACTTGC AACCCCTGAA TTGAGCAACC TCATCACTCT TGGTGACAAA CCAGGTCGTG	420
ATAATTCCTT CTTTATGCTG ATTCGTGGTG CCTTCCATCT AATCTTTGTA ATCGTTTATG	480
TACTCTTTTA TTTCTCAAAT ATCAAAGATG CACATACGAT TGCAAAACGC ATTAACAATG	540
GAATTCAGT TCCACGCACA CTCAAAGACA TGATCAAAGG GATTTATGAA AATGGCTTCC	600
CTTACCTCTT GATCATTCCA TCTTATGTTG CCATGACCTT CGCGATTATC TTCCCAAGTTA	660
TCGTAACTT GATGATCGCC TTTACCAACT ACGACTTCCA ACACTTGCCA CCAAACAAGT	720
TGTTGGACTG GGTGGTTTG ACCAACTTTA CAAACATTTG GAGCTTGAGT ACCTTCCGTT	780
CTGCCTTTGG TTCTGTTCTT TCTTGGACTA TCATTTGGGC TTTGGCAGCT TCTACTTTAC	840
AAATCGTAAT TGGTATCTTC ACAGCTATCA TTGCCAACCA ACCATTTATC AAAGGAAAAC	900
GTATCTTTGG TGTTATTTTC CTTCTTCCTT GGGCTGTCCC AGCCTTCATC ACTATCTTGA	960
CATTCTCAAA CATGTTTAAC GATAGTGTG GTGCTATCAA CACTCAAGTA TTGCCAATCT	1020
TGGCTAAAT CCTTCCTTTC CTTGATGGAG CTCTTATTCC TTGGAAAACA GACCCAACIT	1080
GGACTAAGT TGCCTTGATT ATGATGCAAG GTTGGCTCGG ATTCCCATAC ATCTACGTTT	1140
TGACCTTGGG TATCTTGCAA TCTATTCCTA ACGACCTTTA CGAAGCAGCT TATATTGACG	1200
GTGCCAACGC TTGGCAAAAA TTCCGCAACA TCACTTTCCC AATGATTTTG GCTGTTGCGG	1260
CACCTACTTT GATTAGCCAA TACACCTTCA ACTTTAACA CTTCTCTATC ATGTACCTCT	1320
TCAATGGTGG AGGACCTGGT AGTGTGCGAG GTGGAGCTGG TTCAACCGAT ATCTTGATCT	1380
CATGGATCTA CCGTTTGACA ACAGGTACAT CTCCTCAATA CTCAATGGCG GCAGCTGTTA	1440
CCTTGATTAT CTCTATCATT GTCATCTCAA TCTCTATGAT CGCATTCAG AACTACACG	1500

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CATTTGATAT GGAGGACGTC TAAGATGAAT AACTCAATTA AACTCAAACG TAGACTGACT	1560
CAAAGCCTTA CTTACCTTTA CCTGATTGGT CTATCAATTG TAATTATCTA TCCACTGTTG	1620
ATTACCATTa TGTCAGCCTT TAAAGCAGGT AACGTCTCAG CCTTTAAACT AGATACTAAT	1680
ATCGACCTCA ATTTTGATAA CTTTAAAGGC CTCTTCACTG AAACCTTGTA CGGTACTTGG	1740
TACCTCAACA CTTTGATTAT CGCCTTAATT ACCATGGCTG TTCAAACAAG TATCATCGTA	1800
CTTGCTGGTT ATGCTTACAG CCGTTACAAC TTCTTGGCTC GTAAACAAAG TTTGGTCTTC	1860
TTCTTGATCA TCCAAATGGT GCCAACTATG GCCGCTTGA CAGCCTTCTT CGTTATGGCG	1920
CTTATGTGA ACGCCCTTAA CCACAACCTGG TTCTCATCT TCCTCTACGT TGGTGGTGGT	1980
ATCCCGATGA ATGCTTGGCT CATGAAAGGC TACTTCGATA CAGTGCCAAT GTCTTTAGAC	2040
GAATCTGCAA AACTAGACGG TGCAGGACAC TTCCGCCGCT TCTGGCAAAT TGTTCACCA	2100
CTTGTTGCCC CAATGGTTGC CGTACAAGCT CTCTGGGCT TCATGGGACC TTTGGGGAC	2160
TACATCCTCT CTAGTTTCTT GCTTCGTGAG AAAGAATACT TTACTGTGCG CGTAGGTCTC	2220
CAAACCTTCG TTAACAATGC GAAAACTTG AAGATTGCCT ACTTCTCAGC AGGTGCTATC	2280
CTCATCGCCC TTCCAATCTG TATTCTCTTC TTCTTCCTAC AAAAGAACTT TGTTTCAGGA	2340
CTTACAAGTG GTGGCGACAA GGGATAATT ATCCCGCCA CCCTTTTCA TTTTATACTC	2400
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AACCTGTGGC TAGTTTGAC TTTGATTTTC ATTGATTATT AGCAATTGTC ACTGTAAATA	2520
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ATAATACTCA TATAGAAAAC ACCTTTTAGA AAGATACCTA TGCTTCATA TCCATTTTCC	2640
TATTTTCAA GTATTGGGG GGTTCGTAAG CCCCTGTCCA AACGTTTGA GCTCAACTGG	2700
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CTGACAGATA AGGTGTGCTA GGATCTCTCT GAACATGCTA CAATGTGCGA TGGCACATTA	2880
ACTTATACTG GAACAGCTAG TCAAGCCCCT TCTGTTGTGA TTGGTCCAAG TCAAATCAAG	2940
GAATTACCTA AGGACTTGCA ACTGCATTTT GATACAAATG AGCTAGTCAT CAGCAAGGAA	3000
AGCAAGGAAC TGACCCGCAT CTCTTACCGA GCCATTGAGA CTGAGAGTTT CAAAAGCAAA	3060
GACAGCTTGA CCCAAGCAAT TTCTAAAGAC TGGTACCAAC AAAATCGTGT CTATATCAGC	3120
CTCTTCCTAG TTCTCGGTGC GAGCTTCCTC TTTGGTTTGA ATTTCTTTAT CGTCTCTCTT	3180
GGAGCTAGCT TTCTCCTTTA TATCACCAAA AGATCACGCC TCTTTTCATT TAATACCTTT	3240

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AAAGAGTGCT ACCATTTTAT CTTGAACTGT TTAGGATTGC CGACTCTGAT TACACTTATT	3300
TTGGGATTAT TTGGCCAAAA TATGACAACC CTGATTACTG TACAAAATAT TCTTTTGT	3360
CTGTATCTGG TCACTATCTT TTATAAAACA CATTTCCGTG ATCCAAATTA CCATAAATAG	3420
GAGATTTTAA TGCCCGTTAC GATTAAAGAC GTGGCCAAGG CTGCTGGTGT TTCGCCTTCA	3480
ACCGTAACCC GTGTTATTCA AAATAAATCA ACCATTAGCG ACGAAACAAA AAAACGTGTT	3540
CGCAAAGCTA TGAAGGAAC TCACTACCAC CCAAACCTCA ACGCTCGTAG CTTGGTAAGC	3600
AGCTATACTC AGGTTATCGG ATTAGTTCTT CCTGATGACT CAGACGCCTT CTACCAGAAT	3660
CCTTTCTTTC CATCGGTTCT ACGTGGCATC TCTCAAGTCG CATCTGAAAA CCACTATGCC	3720
ATTGAGATAG CAACAGGAA AGATGAGAAG GAGCGTCTCA ACGCTATTTT ACAAATGGTC	3780
TACGGCAAGC GTGTAGATGG GCTAATTTTT CTCTATGCCC AAGAAGAAGA CCCTCTCGTA	3840
AAACTCGTCG CAGAAGAACA GTTCCCTTC CTTATCTTAG GTAAATCTCT ATCTCCTTTC	3900
ATCCCACTTG TCGACAACGA CAATGTTCAA GCTGGTTTTG ATGCGACTGA ATATTTTCATC	3960
AAAAAAGGCT GCAAACGCAT TGCCTTTATC GGAGGAAGTA AAAAGCTCTT CGTGACCAAA	4020
GACCGTTTAA CAGGCTATGA ACAGGCGCTT AACATTACA AACTTACCAC TGACAACAAT	4080
CGCATCTACT TTGCCGACGA GTTCTTGAA GAAAAGGGCT ATAAATTTAG CAAGCGATTA	4140
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GTTTGTAAGT ATATTGCCAA ACACCAGCTG GATGTCCTG TTCTCAGCTT TGACTCGGTT	4260
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AAAGACTGCG TCTGTACAC GGCTAGAGAC AAAGATGGTA ATCATAGAAT AAAGAGCCTA	5040

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ACTACCGACA TTCTTACCCG TTTTCTTACG AATAGTCAGG CTGACGATAT CCGTCCCACC	5160
ACTGGAGATA TTGTTTCGAA GAGCAAAACC AATCCCCAAA CCCATAACAA CACCCCCAAA	5220
AAGGGAATTG ATAATGGGAT CCTCTGTCAA GGTGACCACA GGGACAAACT GGATAAAGAA	5280
GGAACTCATA GATACCGTGA TAAAGGTAAA GACGGTGAAC TTATGGCCAA TCTGATACCA	5340
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ACCAAACCAG TGATTACTCA AGGCAGAGAT AATCTGTGCC AGACCTGTTG CACCACTCGA	5460
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CAGAGAGGCC GAAATCTTCT CATCATACTT TTCTCGAGAG ATACTTTGTA AGACACGTAA	5580
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GGATATTTTC TTCTCCAGCA AGCAACATGA CAAAACGGTC AAGCCCGATA GCCAAACCAC	5820
CGTGTGGTGG GAAACCATAG TCCATGGCTT CAAGAAGGAA ACCAAACTGG TCATTGGCTT	5880
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GAAGGTACC ACCACCAAGC TCATAACCGT TCAAGACGAT ATCGTAAGCA ATGGCACGAA	6000
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GGTGGGCGCT CATGTAGCGG CCTTCTTCTT CAGACCATTC AAACATCGGC CAGTCAACCA	6120
CCCAAAGGAA GTTGAACCTA TCATTATCAA TCAAGCCAAG CTCTTTAGCA ATACGTCCAC	6180
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CAACTGGTCC GTTTAATTCT CCATCAACCA CCTTGACCCA AGCAAGACCT TTGGCACCAT	6360
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CGTAAAGAGC CATAGCATCA TCGTATTCA TACGAGGGAA TGGTAGCGTT ACTTCGATGC	6600
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AGTCCTCGTC ACGGAAACAT TTAACGATTT GGTAGTAACG GTCAAAACCA GCATTTCATCA	6780

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GAGACGGCAC TAAATAATCA CGCGCCCCCT CAGGCGTTGA CTTAGAAAGG AATGGTGTCT	6900
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TTACCGGTCA CGAAGATCGA TAAAGATCAA ACCACCAAGG TCACGACGAC GGCCAACCCA	7320
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AAATAAATCG ATTAAGCCG CTCTTCTCAA TATGAACAGG AGCCTTCTGA TACCATTGTT	8460
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GATTAAACCA GCTTAGGTCC ATCCCAATCA GTAGAAATAC GCTGACTAAT AAAGCTATGA	9540
CCACTACATA ATAAATCACT TTATACTTGT TCATCACTCG TCCTCCTCCA AACGAAATAC	9600
CGATTGCACT GTTTCGTTGA AAATTGAGA TATTTTCAGG GCAATGATAA TGGATGGGGT	9660
GTAATCATCC CGTTCTAGTA GGCTAATGGT CTGTCTGGAA ACCCCTGCCA GTTTGGCTAG	9720
GTGGGTTTGA TTGAGACCAT CGCGAGCTCG AAGCTCTTTT AGACGATTTT TTAGTTGCAT	9780
GTTACACACC TACTCTCCGT CAAATTCAAC GGTTCGGATA TCCTCAATAC GTTGCAACTT	9840
GAATTTTCT TTTCCCGTAT TATCTACACG TCGTAGCTTT ACCCATTCCT CATCAACATC	9900
CACAACTTCC CAGTTATCTG GCCCAATATA CACTCCCGTT ATAATTGGTT CCTTTCCAAT	9960
CATTTCTTGT AATAATCTCG ACATTTCTGC GTTTCCTTTC TCTTTTCGCT CAAGTCTTTT	10020
GATTTTATTC TCTAGTTTCT TGATTTTTTT AGAATTATTA GAATAAAAGA AAATCATAAA	10080
TAGTATAAAT CCTAGTACCC ACATTATAAC TCCTTCTGTC TTCCTATTTT TTAACCTGAA	10140
TTCAATGTAA CATATCTTTT TCTTTTGTAC AAGTATAGTT GTCAAAAAAA TTATGATTTT	10200
TGTCAATTTG CAAAAGAAAA AGGTCAGGAG TAGGTTCTCG ACCACTTTAT CTATCATTAA	10260
TACTCTTCTA AAATCTCTTC AAACCACGTC AGCTTCACCT TGCCGTAGGT ATGGTTACTG	10320

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ACTTCGTCAG TTTCATCTAC AACCTCAAAA CCATGTTTTG AGCTGACTTC GTCAGTTCTA	10380
TCCACAACCT CAAAACCATG TTTTGAGCTG ACTTCGTCAG TTCTATCCAC AACCTCAAAA	10440
CCATGTTTTG AGCTGACTTC GTCAGTTCTA TCCACAACCT CAAAACAGTG TTTTGAGCAA	10500
CCTGCGGCTA GCTTCCTAGT TTGCTCTTTG ATTTTATTTG AGTATAAAAT CCTAGTTTTT	10560
CAAAGATTTC TGAGAAGTTT TGGCTGATTG TCTCAAGTGA CACTTGCACT TCTTCTCGGG	10620
TTTGTTTGT CTTGACCGTC ACTTGTCCGC TTTGCACTTC GCTCTCTCCT AGGGTGATGA	10680
GGGTCTTAGC CGCAAAGACA TCGGCTGACT TGAAGTGAAG TTTTAGTTTA CGGTTGAGGT	10740
AATCACGCTC TGCTTTGAAA CCTTGTGGC GAAGAGCCTG TACCAATTCC AAGGCCTTGA	10800
TATTTGCCCC TTCGCCAAG ACTGCGATAT AGACATCTAG GCGGTTTTCG ATAGGGAGGG	10860
TCACACCTTG CTTTCAAGG ATGAGAAGCA GCGGCTCTAC ACCAAGTCCA AAACCAATC	10920
CAGCAGTTTC AGGGCCTCCA AAGTAAGCAA CCAAAACATC GTAGCGACCA CCCGCACAGA	10980
CGGTCAAGTC ATTTCCCTCA ATCTCTGTGA TAAACTCGAA AATGGTGTGG TTGTAGTAGT	11040
CCAGACCACG CACCATATTG GTATCGATGA TGTAACTAC TCCAAGATT TCCAACATCT	11100
GACGCACAGC ATCAAAATGA GCTTGGCTTT CTTTCATCAAG AAAGTCCAAG ATAGACGGCG	11160
CATTCTCTAC TGCCACCTTG TCTTCTTTTT CCTTAGAGTC CAAGACACGA AGAGGATTTT	11220
CCTCCAAGCG ACGTTGGCTA TCCTTAGACA AGGTCTCCTT GAGCGGTGTC AAATAGTCAA	11280
TCAAGGCTTG GCGGTAGGCT GCACGGCTCT CAGGATTTC AAGAGTGTG AGGTGCAATT	11340
TGACACCTTG AATACCGATT TCCTTCAAAA AATGGGCTGC CATAGCGATT GTTTCACAT	11400
CGGTAGCTGG ATTGCTAGAG CAAAACACT CAACACCAAT CTGGTGGAA TGGCGCAAGC	11460
GCCCTGCCTG TGGACGCTCA TAACGGAACA TAGGTCCCAT GTAGTAGAAC TTGCTTGGCT	11520
TTTGCACTTC TGGGGCGAAA AGTTTATTTT CCACATAGGA ACGGACAACG GGTGCAGTTC	11580
CTTCTGGACG GAGGGTAATA TGACGGTCAC CCTTGTGATA AAAATCGTAC ATTTCCTTGG	11640
TTACGATATC CGTTGTATCT CCGACAGAGC GACTGATAAC CTCGTAATGC TCAAAAATAG	11700
GCGTGCCGAC TTCTGCATAG TTGTAGCGTT TGAAAATCTC ACGGGCAAAG CCCTCAACGT	11760
ACTGCCACTT AGCAGACTCA GCAGGTAAAA TATCCTGCGT TCCTTTTGGT TTTTGTAAAT	11820
TCATAGGGAA TCCTCTTTAA ACTTAATAGT CTTATTTTAC CATAAATAGA GGGATTAAAA	11880
CAGTAAGAAA AAAATTAGGA TTTAGATATC ATTTTGTAGA TTAAGAATTG TCAAAAAAAT	11940
AGCTAGCAAG GAAAGACCAA CAAATAGCAT CCAAGTCAAC TGTATATTCC ATACGGCTAC	12000
TAGTGAAAA CAAGCTGTTT CCACAGGTAT GGATAAGGTA AACAATAGAC CTAAAAAATT	12060
ACTAGTACGA GCTAGAACCT CTGGAGCTAG ATTTTTCATG AGCATGGCAC TAATCTTTGG	12120



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TTGAACTTTA CCAGACACAT ACAGAGTAAA GAAGAGAAAT AGCAAACCAA GCACGACTTG	12180
ATTGAATAAA TTAGCCAAAC CAACTAGACT AAGTCCTACG GTCTCCACCA TCATCAATCT	12240
AGGCAAGGAC TGCTTCCCAA AATAATCATT GCCCGTAAGG CTA CTGATGA TGACTGATAC	12300
TAAACACAG AATTGATTGA TAAATAGTGC CTCTGTATAA GAAAAATTCA AGAGAGAATG	12360
GCTCAAAAAG AAGATATTAT AAATTCCACC CAAAGCGCCA CCCAAGGAAT TAATAAGCAA	12420
GACAGCAAAG AGCATAAAAC CAAAGTTTTT CTGTCCACTT TTAAGAAAAA CGAGACGTAA	12480
ATTTGCGTAA ATTGTTAGGA ACTGGTCTTT GATAGAAAGC TTCTCATTTT TTAAGTTTTT	12540
ACCATCAGCA GATGACATTG ACAGGCTCAA TTGCTTTTTT CCTAAAAAGA GGATAGTGGC	12600
TGATACTAGG AAAAAGCAGG CATTGATTCC CGCAACGAGA GAAAAATTGT TGACCGATAG	12660
AGCTAAGAGC CAGACTCCGA AAGCTTGACC ACCAATAGCT GAAATATAGG TGATGAACTG	12720
TGAAAAAGAA TAAGCCTCCA TCAGATCATC TTCAGCTACT TTTTCCTTAA TAAGAGGCAT	12780
ACGCAGGCCA CTGCAAAAT CACTGATGAT ATCACTAATG ACATTGATCA AACACAGGCT	12840
AGAAAAGGCA AAGAGACTAG CTTGCTGAAC AACTAGGGCT GCTAGAAAAA ATAGAACCGC	12900
CTGAAACAAA CCGCTATAGA CCATCCATTT GACCTTGTC CTGCTGTAAT CTGCCCGAAT	12960
CCCTGCAAAA ACTGTAAAGA GGGTCGGAAG AATCATGACA ATATTGCGCA TAGCAACAGC	13020
AAAAGATGCT TGTGACAAGG TCGATGCATA GACGATAAAG ACCAGGTTGA AAATCGAAAC	13080
ACCAAAAGCA TTGAAGAAGC GTGG	13104

(2) INFORMATION FOR SEQ ID NO: 35:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 19250 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 35:

CCGGGCAAAT AGTTTGAAC TTTTCATCAT TTTCTCCTTT AAAACTTTCT CTCCATTATA	60
GACTCTTTTC AGAAAGTTGT CAACAGAATT TTCAGAATTT TTGAAAATTA TTTTTCAAAC	120
AACATCTTTG CAAAAATAT GAATATCGTA AGCGCGTCAT AACAAAGGTAT CTATCATTCA	180
TGGAGCTCCT CCTGTATACT ATTAGTAAAG TAAATATTGG AGGATATTTT AATGCCACAA	240
CCTATTGTTC CTGTAGAGAT TCCACAATCT CGTCGTTTGG ATTCTAAAAA GAGAAATGAT	300
ATTCTTCTTA AAATTCGTAT TGGCAAGCTT GAAGTAAGTT TTTTTCATC TCTCAATCTC	360

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GAAATGATAG AACAGCTTTT GGATAAGGTG TTGCTCTATG ACAATTCATC TATCTAGCCT	420
AGGGCAGGTC TATCTCGTGT GTGGGAAAAC TGATATGAGA CAAGGAATCG ATTCACCTGGC	480
TTATCTCGTT AAAACCCACT TTGAATTGGA TCCTTTCTCC GGTCAAATCT TTCTCTTTTG	540
TGGTGGACGT AAAGACCGCT TTAAAGTCCT TTAAGTGGAT GGTCAAGGAT TTTGGCTACT	600
ATATAAACGC TTTGAGAACG GCAGACTGAC TTGGCCCAGT ACAGAAAAGG ATGTCAAAGC	660
TCTCGCACCT GAACAAGTAG ATTGGCTGAT GAAAGGCTTT TCTATCACTC CAAAAATATA	720
GTAGATTGAA ACTAGAATAG TACACCTCTG CTTCTAAAAC ATTGTTAGAA ATCGATTTTA	780
CTGTCTGAT CGATTTGTCC TGTATTATT TCATTTTACT ATAAATCCAT CAGAAAGTCG	840
TGATTTCTAT TGAAATGAGG ACTTTCTTTT TATACTCATC TGCTTTCAAA AAGCACTCTA	900
GTCCATCTCC GATTAACGAT GGACTTTATC ACCTCCTTCT CCAGTCCTTG TATAACATCT	960
TGAAGTTGAT TCATGACATC TTCCAAAGTT CGAAAGGCTT TATTCTTAAA TCCACGTTTA	1020
CGAATCTCTT TCCACACTTG TTCAATGGGG TTCATCTCTG GTGTGTATGG AGGAATAAAT	1080
GCAAAGCCAA TATTAGTCGG AATCTTTAAG GTACTTGATT TATGCCATAT AGCATTTGCC	1140
ATAACGAGTA AAAGATAATC ATCTGGATAA GCTTGTGAAA GCTCCTATTG CTAAAGCCCC	1200
TTTATAACCT CTTCGAGAG AGACTATTGA CTCAGCCCTT ACTTCATGCG GATGAAACCT	1260
CCTATCGGGT TCTAGAGAGT GATAGCCATC TGACCTACTA TTGGACTTTT TTGTCAGGTA	1320
AAGCAGAGAA ACAAGGGATT ACGCTTTACC ACCATGATCA GTGTCGAAGT GGTTCAGTAG	1380
TACAAGAATT CCTAGGAGAT TATTCTGGCT ATGTTCAATTG TGATATGTTG CGGCAGTAAC	1440
TTAGGACTTT AGTCCTCTAG TTCTGCCTAT GCGATAGCAG TCCAAGGTTT AGGAGTAAGG	1500
CGACGCTAAG CTTGGTAAAC TGCGAACAGC TAGAAGCTTA TCGTCAACTG GAAGAAGCTG	1560
CACCTGTGG ATGTTGGGCG CATGTGAGAA GGAAGTTTTT TGAAGTGCCC CCCAAGCAAG	1620
CAGATAAATC ATCCTTAGGA GCTAAAGGTT TAGCCTATTG TGATCAGTTA TTTTCCTTGG	1680
AAAGAGACTG GGAGGCTTTG CCAGCTGATG AACGGCTACA GAAACGTCAA GAACATCTCC	1740
AACCCCTACT GGAAGACTTC TTTGCTTGGT GCCGTCGTCA GTCAGTTTTA TCGGGTTCAA	1800
AACTAGGAAG GGCAATTGAA TACAGCCTCA AGTATGAAGA AACCTTTAAG ACCATTTTAA	1860
AAGACGGACA TCTGGTCCTT TCCAATAATC TAGCTGAACG CGCCATTAAA TCATTGGTTA	1920
TGGGACGGAG TAAAAGAGTC CAGTGGACTC TTTTAGCCTA AGCTCAGTTT AAAAAACGA	1980
GGGTGGTTAT TTTTAAAAA GCGAGGGTGG TTATTTTCTC AAAGTTTGA AGGAGCTAAA	2040
GCAAGAGCTA TTATTATGAG TTTGTTGGAA ACAGCTAAAC GTCATCAATT ATAGTGCATT	2100
GAATCTATAA CAGTACGCAT CGACTGCTAA AATATTTCTA TAAATCAATT TTCCTTTCCT	2160

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AATCGATTG TTCATATCTT ATTACAATCC ATTATAAATA GCGAGAAATA TCTATCCTAT	2220
CTTCTAGAAT GTCTTCCAAA CGAGGAAACT CTCGTAAACA AAGAGGTTTT AGAGGCCTAT	2280
TTACCGTGA CTAAAGTTGT ACAAGAAAAG TGCAAATAAG AAATCTCCAG ATTAGGAACT	2340
ATATATGAGT TCTCTAGTCT GGAGATTTTT CAATAGACTT CGTTATTGGG CGGTACTTTT	2400
CGAAACTTTG AAAACTTCAA AAAACGGATT TTTATCGCTC TGAACATCAA AAAAGAAAGG	2460
ACGAAATTTG TCCTTTCTCA AGCTTAGCTT TTCTTCAACC CACTACAGTT GACAAAGAGC	2520
CCTTTATCT ATCAAACATG AAGCGCAAAA ACAAGCCAAA AATCCGATAG AATGGCTATC	2580
CCTCGACTAT CAAGTAAGAC ATTPCCATCA AATACGTCA ATTTACTCT TGTCTACTA	2640
AGAATTAATC ATCTCGTTTT GATTTATTAA AAATATACAA TTCAGCTTTT CCTCCAACT	2700
ATTTTATCCA CTATCCCTGT ATAGCTCTGT ATTATCTTAA CAACTTTAGT AGAGACATTT	2760
TCCTCAACAT AATCCGAAC CGGTAATCCA AAATCCTCAT CTTGTGCCAA GCTAACAGCA	2820
GTTTCAACTG CTGAAGAAG AGAATTTTCA TCAATGCCTG CCAAATAAA TCCTGCCTTA	2880
TCTAAGGACT CAGGACGTTT TGTACTTGTA CGAATACATA CAGCGGGAAG AGGATAACCT	2940
TGACTAGTAA AGAACTACT TTCTCCGGT AAAGTCCCCG AATCAGATAC TACAACAAAT	3000
GCATTCATCT GTAAACAATT ATAGTCATGG AATCCTAGTG GCTCATGCTG AATCACACGT	3060
TTATCTAGTT TAAACCGCT CTCTGTAGC CTTTCTTTG ATCTAGGATG GCAAGAATAT	3120
AAGATTGGCA TATTATACTT TTCAGCTAAT TGATTAATTG CTGTAAAGAG AGAAATAAAA	3180
TTTTTATCTG TATCAATATT TTCCTCACGG TGAGCTGAAA GTAAGATATA ACCTCCTTTT	3240
TTCAATCCCA AACGTTTCATG GATATCTGAA GACTCAATAG CAGATAAATT TTTATGTAAC	3300
ACTTCTGCCA TAGGAGAACC AGTTACATAT GTGCGCTCTT TAGGTAAACC AACTCATGT	3360
AAATACTTAC GTGCATGTTT AGAGTATGCT AAGTTAACAT CTGAAATAAC ATCAACAATC	3420
CGACGATTAG TCTCTCCGG TAGGCACTCA TCTTTACAGC GATTGCCAGC CTCCATATGA	3480
AAAATTGGAA TATGTAAACG CTTGGCAGCA ATAGCTGATA AACAAGAATT TGTATCCCCT	3540
AAAATCAATA AAGCATCTGG TTAAATTGTA TTCATCAATT TGTATGAAGT ATTAATAATA	3600
TTCCCTACAG TAGCACCAAG ATCATCTCCA ACAGCATCCA TGTATACGTC CGGAGTGTCT	3660
AACCCTAAAT TATCAAAGAA AATACCATTT AAATTGTAAT CATAGTTTTG TCCAGTATGT	3720
GCCAAAATAA CATCAAAATA CTTTCGACAT TTAGTGATAA CACTACTTAG ACGTATAATC	3780
TCTGGACGTG TTCCACAAT AATCAATAAC TTAAGTTTGC CATTATCTTT AAAGTGAATA	3840
TCACTATAAT CTGTCTTAAT TTTCATTTAT TTCTCCACTT GTTCAAAAAA AGTATCTGGA	3900

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TGTCTAGGAT CAAATGACTC ATTAGCCAC ATGACAGTAA TTAGATTTTC TGTATCAGAA	3960
AGATTAATAA TATTATGTGC ATAGCCCGGT ATCATATGTA TTGCTTCAAT CTTATCGCCC	4020
GACACTTCAA AGTTCAGAAT AGGATACTCT TGACCGTTTT CATCCAGCCC TATCCTACGC	4080
TCTTGATTA AAGCAGACC AGAAACAACC ATGAAAAATT CCCACTTAGA ATGATGCCAA	4140
TGTTGCCCTT TGGTAATGCC AGGTTTAGAA ATATTAACAG AAAATTGACC CGTATTTTCT	4200
GTTTTTAATA ATTCGTAAA ACTACCTCGT TCATCTATAT TCATTTTTCAG AGGAACTTA	4260
AACTTATCTA CTGGTAAATA AGATAGGTAG GTAGAATACA ATTTCTTTT AAACGATCCC	4320
TGAGGAATT CAGGCATAAC TAAACTATCA GGCTGTTTT TAAATGTTTC TAATAGAGAG	4380
ACAATCTCTC CTAAGGTGC ACGATGAGTC GTTGGTACGT AGCAGTAGTT TCCTGATGGG	4440
CTAGGTAAGA TTTGTAATCC ATCTAGATTA CAACGATGAG GATTTCCTTC CAATGCAGTT	4500
AGACACTCTT GTATCAAATC ATCAATATAC AGCAACTCCA ATTCACACT TGGATCATTT	4560
ACTTGAATAG GTAAATCGTG AGCTAGATTA TAACAGAAAG TTGCTACAGC AGAATTGTAG	4620
TTAGGACGGC ACCACTTCCC ATAAAGATTC GGGAAACGGT AACTAAGAC AGGTGCTCCC	4680
GTTTTCTTTC CATATTCAAA GAAGAGTTCT TCCCCTGCTA GCTTAGATTG TCCATATATA	4740
GAGTTTGAAA ATCGGCCTTC TAACTAGCT TGAGTAGAAC TTGAGAGTAG AACAGGACAA	4800
GTGTTTTCAT ACTTTCTAA AATCTCCAAT AATCTACTTG AAAAACGTA ATTTCCCTCC	4860
ATGAATTCAT CAGGATTCTG TGGACGATTG ACACCAGCTA AATGGAATAC GAAATCGGCC	4920
TTCTTACAAT ATTCATCTAA TAAATCGGA TCTGTATCAC GATCATACTG AAAATCTCT	4980
CCAACTCTA AATTAGGACG AGTCCTATCT CGTCCATCTT TCAAAGCTTC CAGAGTACAG	5040
ATAAGATTTT TTCTTACAAA TCCTTTCGCT CCTGTGATTA AAATATTTT AATCATGCCC	5100
CCTCCTTATT TTATATGCTG TTTAATAGT TAACTCTCTC GACAATACAT GATACATTAT	5160
ATATCCTTGA TAATTTTAAT GTATCTTAAA AGATTTTACA TCTCTTCGTC TGCTACCATA	5220
TCACGAATTG CTGTCTGTAT TTCATCTAAT TCTAGCAACT TTCTTTTAAC TTGCTCTACA	5280
TCCATCAAAT CGGTATTATT ACTATTGAAT TCTGTCAACA AATTTCTATT CGTACTACCA	5340
TCTTTGAAAT ACTTATCATA GTTAAGATTA CGATTATCAC TAGGAACTCT ATAAAAATCA	5400
CCCAAATCAA TTGCATTGTC GCACTCTTCG TTAGTTAATA GTGTTTCATA CCTTTTTTCT	5460
CCGTGTCTAA TACCTATAAT CTTAATATCT TGTCTGAGG CAAAAATTTC TGATACAGCC	5520
TTAGCCAACA CTTCATCGT ACATGCTGGT GCTTTCTGAA CTAGTATATC TCCAGATTTT	5580
CCTTCTTCAA ATGCAATAA AACCAAGTCT ACTGCTTCTT CCAATGTCAT CAAAAACGT	5640
GTCATGCTAG GTTCAGTAAT TGTAAGAGCA TTTCCTTGCT TAATTTGCTC AATCCAAAGA	5700

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GGAACGACAG ATCCACGGCT ACACAGAACA TTCCCATAGC GAGTCACACA TATCTTTGTA	5760
TGCTCAGGAT TTACCGTCCT GGAAGTAGCA ACAGCAATCT TTTCCATCAT AGCCTTGGAT	5820
GTTCCCATAG CATTGACAGG ATAAGCCGCC TTATCTGTAG AAAGACAGAT AACTTGCTTT	5880
ACACCAGCTT CGATAGCCGC AGTGAGGACA TTCTCCGTTC CAAAATGTT AGTTTTTACC	5940
GCTTCTACAG GGAAAAATTC ACAAGAAGGT ACTTGTTTAA GAGCAGCAGC GTGAAAAACA	6000
TAATCCACAC CATGCATAGC ATTTTTTACC GAAGCTAAGT CACGCACATC TCCAAGGTAA	6060
AAACGGATTT TCCCAGCCAC TTCTGGTACT TTTACCTGAA ACTCATGACG CATATCATCT	6120
TGTTTCTTTT CATCTCGCGA AAATATACGA ATCTCTGAGA CATCTGTTTC TAAAAACGC	6180
TTGAGAACCG CATTCCCAA TGAACCTGTC CCTCCTGTAA TTAGGAGAGT TTTTCTGTAA	6240
AATGTGACA TATATTACAC TTCTCCTTCT AGTATGTCTG CAATTTTCTT ACAAGCCGTT	6300
CCATCTCCAT ATGGATTGA AGCTTGACTC ATTGCTTGAT AAAGTGAATC ATTTTCTAAT	6360
AATCTTTTAA AATGCCTATA AATATTATTT TCATCAGCAC CTACAAGTTT CAAAGTCCCT	6420
GCTTCAATTC CCTCTGGACG TTCAGTTGTA TCTCTCATAA CAAAACAGG TTTTCTTAAA	6480
CTTGAGAGCT CTTCCTGAAT ACCACCACTA TCTGTAAAA TTAATAACT TCTTGATAAA	6540
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ACATCTGAAT ATTCTTCAAT AATCCTTCTA ATTGCTCTAA ACATATGTCT CATCGGTTCA	6720
CCAAGATTTT CACGACGATG AGCTGTAATT AGAATAAAC TGCTTTCTCC TATCCATTCT	6780
AACTCAGGAT GCGTATAGTC CTCTGAATT GTAGTTTGTA AAGCATCAAT CGCCGTATTA	6840
CCTGTCACAA ATATGCTCTC TGGAGTTTTT CCTTCTCTTA AAAGATTATC TTTTGAAAGT	6900
TGTGTTGGTG TAAATGATA CTGAGCCAAA ACCCCAAGT CTGACGATT AACTCTTCA	6960
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TGTAATAAAA AGGCCGCCAG TGAAGTAGCG AAGGTCGTAC TTGTATCCCC ATGAACTAAC	7080
ACCAAATCAG GTTTTTCTGA CTCTAAATA GCCTTCATTC CTCCAAAAT GCCAATGGTC	7140
ACATCAATAA AAGTTTGTTC ATCTTTCATA ATAGACAAAT CAAAATCGGG AATAATCCCA	7200
AATGTGTCCA AGACCTGATC CAACATTGA CGGTGTTGGC CCGTAACGCA AACTAATGTT	7260
TCAATATTCT TACGTGTCTT TAACTCTTTG ACCAAAGGAC ACATCTTGAT GGCTTCTGGA	7320
CGAGTTCCAA ATACTACAAC TACTTTTTTC ATATATTAC TTAATCTTAA CAAATAATGA	7380
ACGGTTCTTA AAATAAATTA GATAACGGCT AATCCATAAC ACCACCTCAG ACATACTTGA	7440

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ACAAATAGCT AATGTTACTA AACTAAAATT ATCAGACAAG ATAAATATTC CTAATCCCAA	7500
AGTTTGGACA ATCGAAGCTA ATATAGTTGT CATTGTAGTT TCTTTCACCT TATCAATAGC	7560
TCCTAAGACA GGCCATCCGT AAATCATAGA ATAAAACTA GCAACAAAAG CGGGTAATAA	7620
GTACTTAAGA AAATCTGCTG AAACGGTATA TTTTTCACCA CCAATTATAG AAAGAATTTG	7680
ATTTGAAAAG AATAAACTA TCAAACTCC AAAGATAATA GGAATAACA TAATCCGATT	7740
AATACTCTTA ACCGATTGTA TATCTTTAGT ACGTATCATA TGCGGATATA AACTATTCGC	7800
TATAGGATTA TACAATGATT TTGCTGCTGA AAGCAGTTGC ATTGCTATCC CCCAAAAGGC	7860
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CAGATAAGAA AATGATAATT TAATTCATA ATAATGAAG AATCTATAAG AACTACTGC	8040
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TACTACAATA AATGTCAAAA TTGTAATGAT AGTTTTAGAA ATAATATAAG GAATTGCAAC	8160
TGCATGCATC TTTTCAATTC CACGAAATAA AAAGTCAAAG ATAAAAATAT TGGTCACTGT	8220
AGCTAACAAA TAAAAACTG AAAAAAGAAT ATTCTCTCTC ATTATTGGGA TTGCCCACAT	8280
CAATATGGTG TAAATTAGAA TCGAAATGAT AGATAAAAT ATTTTTTCAA CTAGAGTATC	8340
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TGATATCATG AAACCAAAAT CAATCACCAG TTGAACATAA GCTATTAACG CTTTAACATA	8460
AATAACCATT CCATACGCGT CTAGCGAAAG CACCCTTGTC AAATACGGGA GTGTTAATAA	8520
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AATCTATCA ACTTTCACGA ACTAGTCCTT CCAAAAAAG ATCTAAATAG TCCAACTAC	8640
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GTTTCTTTAC AATACTATTA ACACTTGAAT CAAATAAAGA TTCACAACGT TGTAACCTC	8760
CAATTGCTCC ATAATAACGT GCTGTTTTTT CTGGATGGCA TGCAATGGCA ATCAGAGATT	8820
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ATTTTCAAG AGCTTTTTTG GAATGATTAT AGTGAACAAG AATTATCTTC TTATCTTTAG	9120
CTTCTTTTT CAATTGACAC AGCTGCTCTG TTTTTCTTC TCTTAATTTA CTTGAAATAA	9180
TTAAATCAAA GGTTCATGC ACTGGAGCCG AAGGCGACAA ATGCTTCAAA GAATCAAATG	9240

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ATTCTCGATC ACGAACTGTA ATAAATTGAG CATGATTAAAT AATCTCTTTT ATACCATAAT	9300
TCATCAAAGA ATCGTTATTA GGCCCTGCAC CAATACCTAA TACTCCTATA GGCTTTTAA	9360
AATATGAAGC CCAAATCCC AAAGGTAAAA ATCGTTTAAA TTGGATTAAA TTATCACGAA	9420
AACGTGCATT ATGCCCTTCC CCAAATATC CTCCCGGAT ATACAAAATA GCATCTGCTT	9480
GTTTTTTAGT AAAACTTTGT TTTTGGCGAT ATTCTTTCAA GTACATTGA AAGAAATCTG	9540
ATGGATTATA AAAAGAACT TCATATCCTT TAGATTCTAA TAAATCATAG ACAATCTCAC	9600
CGTAAAGATA ATCACCCTAA TTACTTGAAC CATAATCCGT TGCACCATGT AACATAATTT	9660
TTTTCAACCAC TATTTTTCA ACCTCCTAAA AATAAATATC ATAATCAAAC TATACATAAT	9720
AGGACGATAA ACATCTATTG AACTACTTCT CACTAAAAGC AATAGTTGAG AAATTACCGA	9780
AAAATAAATA ACTTTTGAGA TTTTACTTGT TTGAAAAGCT CTGAAATTTA ATCGCCATCC	9840
ACTAAATATT CCAAAAACAA AACTCCAAA AACACCACCA TAGTAACCAA AGTTCCAAA	9900
TAATCTTCC ACAAAGAAG AGCCTACAGG TAACCCCAA AATTATTAA TAACAACCGT	9960
CGCTGATGCT TTATCAAAA AATCACCAAC TAACCATCCA ATAGGAAAA TTGATAGGAT	10020
AGTGCCTAGA AATGTCATCC CATATTCATA TGGAAATGCTA CTAGGCACAA CAGTTACAGC	10080
AGAAGCTACT GTTAGGCTGG TCAGTCCCGA CTCTGAAAT ACTTCCCCTA GTATATCTT	10140
TACAAAATCT AATGAAGAAA AGGAATCAA TAAGTATATA CCTATAGTAT TCAAGTCGAA	10200
ACGGTGCCCC CTAATAACAA CTAATACATT TAATAGAAAT ACAGTTACTA TTAATAATAC	10260
AAGTACTCTT TTCTTCGAAA AAGTAATCCC TAAAGATTGT GTGTATACTA AAACCAACGC	10320
CAAGATTGAA AACACCTGGA TTTTACGACT TCCTGTTAGG ATCATTATCA AAATTAGGTA	10380
AAACAACATT ACCCAAAAA TAGTACGCTT TATAACTCGG GACAGCTTAT CTGAATAAAA	10440
CAAGGAGAAC ACACCAGGAA GCATAAGTAC TCCTAAATCA TCTATTATTC CTGAACTAGC	10500
TGCCTCTGAA TATGCTGAAT AGCTATTCGC CGCTCTAACT GCTAGTACTG TTTTGAATC	10560
AGTTATTACC CTAGAAATAA AGCCCACTCC TGTTAAAATC CTACCCGCAT TGTACAAAAT	10620
TTTCTCTCA TTTCTCTGAT AATTTGTAC TTCTGAATGA TAATGTACCT TTCCATCACT	10680
ATAAAAAAT AAATAGCCTA CAGAATAAGA AAACAAAATC CAAATTATAA AAATATATGA	10740
ATGAAATAAT TCTTCATTAT TATAGAAGTT ACTAGGGCTC CACAGCAGAG TTGTTTGAAA	10800
CCCCATATAC TCATTGAAA TTAATCCAAA CATAAAAA TAAGATAAAA TCAGATACCA	10860
TACAGAAAA TCATATATAC TAACTTTTG TAAAAA CCAGTAATTT GAAAAATAAT	10920
TAGAAAGCAA ACCCATATA ATATAGACGG AACATAATTA GATATAAGAA AACCATTATT	10980

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CCAATTATCG AGAGTCCAGA ACAAGTAACA GAAAGCAAAT ATAAACTTA ATGTCAC TAG	11040
TGTCACCTCTA CAAATATACT TTGTCTGCAT CTATATCTCC TTTATTACAC ACATTTCTTG	11100
ATAACGATTC AATAATTTAC TAGCTTGATA ACAAATATCA TAGAGTCCAT CTGTCATACT	11160
GTTATTTTATT TCAAAACGAT TGCAATTCCTC AGATGTTAAA GACAGTACTT TATCTTTCCA	11220
TAGCAACACA GACTCTTCGT TGATAGGTAA GTAACATAATG TTTTGGTCA CATCTACTTC	11280
TTGCGTCACT GTATCTGACG ATAAATTTG TAATCCGAT GCCTGAGCCT CTACTAGAGA	11340
AACAGGCAAC CCCTCATATT TAGACGGAAG CAAAAACA TCCATCGCAG ATAATAATC	11400
AGAAATATCA GTCCTTCTCC CTAAAAATAG CACATATGGG GTCAGATTTA GTTCTAAAGC	11460
TTTCTGTTTT AATTTCTGCT CATCCTCACC ATTACCACT AGGAGTAAAA TAACATTTGG	11520
TTTGATTAAT ATGAGTCTT TTAACCGTT AAATAAATAA CTTTGGTTTT TTTGATCTGA	11580
TAGGCGAGCT ATATTTCTTA ATACGAACTT ATTTGACACA TCTAATCTC TACGACATTT	11640
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AATTTTCCG TCTTTATACG CTTTCTCTCC ATATAACCAC TTAGCCGAAT CTTCCCCACA	11760
TGCAAAACCA TGAGTTGCTA AGATTTTAC CAAATTTGT ACTAATTTAC GCAATACTTT	11820
TTGAAAAC TGTTCTGTTA CATAAGCCAT ATGACTATGA ATAATCTAA TTTTACAACC	11880
AATTATTTTA GATAAGATCA GACCAATTGC AGATTTATAG CCATGGCAAT GAACTATATC	11940
ATAATCTCCT TTCTTTATTA TTCTAGCAAG AGAGAGAAAC TGATGTAGAG GCTTTTCTCT	12000
TAATAGAGGC ACATGATAAA CCTTGCACC CAATCTTTC ATTTATCCT CTAAAAATCC	12060
TTGTCTTTT CCAGGCACAA TAAATCAAA TTGAATTTT TTTCTATCA TGTGAGAATA	12120
ATAGTTGAAT AGAAACTTT CTACTCCACC ACTATCTAGT GTTGTAATA GATGTAATAC	12180
TTTAATCATT CTTCTTCCTT AAGCTTAAGA TTCGCTTCTC TAATCTATT TCTGTTTTTT	12240
GTTTCTCTAA ACTAATCTG TCCATGAAGT TATCACAATT CTTAATTAGC TGTTCCTGT	12300
CAAGGTTTG AATATACAAA GCCAAACAAT CTTTTCCTGA TTCATCCTTC ATAGGTAAAA	12360
CGAAACCAA ACCATTCTCT ATTGACACTT TTTCCATATA AGTATCTCA CAACTAAAA	12420
TAGGTTTATA CAACAATGCA GCAAAGTAGA GTTTATTAGA CAAAGCATAG TCTAGTAAGG	12480
GAGTGTGATT CCCGTATAAA TTCAAACAA CATCTGTATT CTTATAAAAA GACATGGTAT	12540
CTTTAGGCTG GAATGTGTCC ACCAAGTTAA CATGCTGAT ATTTTCTCT TGACAAAAT	12600
CCCTTAATTC TCCTGCATTA GTACCTATAA AATTCAACTG AAATCGACTG TCATTTGCAA	12660
AAAAATCGAT TATTTTTTA TTTGTCTCT GAAACGAAT TAAACCAATG TAGGAAAGTT	12720
GAATTGGAAA CGTACTATTA TTTTAACT GCTTACCTC GTTAAATCT ATCATATTGG	12780



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GTAGGTTATG GGTAGTAAAA TACTCTCCCA TTGGTAAAAA AAATTTATAG CCGTCTGAAG	12840
AAACGATATT CATTAAAGAA TTTTTCACCA ATTGPTTCTG AACCAAACGA TAAACCAAAA	12900
ATTTTTCATA ACTGTAATCA CGAATATCAT AAATATATCT ATTTTAAAT GAAAAGAGAA	12960
GAAAATCTAC TAAAATGAAA GACACAATAC TATGTAACGG CAATATCATA TCATAATCAT	13020
TTTCTTTTAG CTTCTTTTA ATTTCTTTTC TGAATTTTAC ATAACCTAAT ATCTTACTTA	13080
ATTTTCCTTT ACCAGAAAAA GAAATACGAT AGTAGTTTGT TTTTGTAAATA ATCTCGTTAA	13140
TATTCATTATC CCAATATATA ACATCGTAAC TAATAGACAG TTTCTTCAAT AATTCTTTAT	13200
AAAAATGAA GTAAGGAGTT AGATATATAT TATCAGATAG TATAAACAGT ACTCTCATTA	13260
AATTATTCTT TCTTACTTTC CCTCTCTAAA CATGTCTCCA GTTCGAGCAT AAACGTCTCT	13320
TTTGAAAAGT GATTTTCATA GTAACAACGA GCTTTCTTTC CTAACCTCTT TGTCTCTTTA	13380
ATAGATAACA TACTAAATTT ACAAATATTT TTGCCAATT GTTTTACATC TCGTTCCGGA	13440
CTAACATATC CACAATTTGC TTCTTCTACA ATTATTTTAG CATCTCCTGA AATTGCACCT	13500
ATAATTGGTT TGCCTGCCGC CATATAAGAG TGTACCTTCC CAGGTATAGT ACGAGAACT	13560
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TCCTCCAAAG AACGTCTTCC ATAGAAGGAA ATATTCTTTA ACTCCAATTC ATGAGCTAAT	13680
GCTTTCATGC TTAACAATTC CGTACCATCT CCAACAAAAT GAAATGAAT TTTCTTGGGT	13740
AAATGGTAT TCTTCTCTAT CAACTGGCA GCTTTCAAAA TAGTTTCCAA ATTTTGTGCT	13800
TTGCCAATAT TACCAGCAAA AGTTAGGTCA ACACTTTCTT TATTAATAT AGATTTCATCA	13860
GGGATAAAAA GATCTTCTGC ATATTGTGGC AAATATGTAA TCTTTTGTTC GGATATGTCA	13920
AATTGCTTCA CAAAATAATT TTTAAATGAT GGAAGTGA CAAATATATA ATCACTAGCT	13980
CGGTAAACTT TTTTGTAGAT AAATTTAAAC AGCTTGAAAA TCAAGCCATC TTGTTTCACT	14040
CCACCTACGG TTAAACTATC TGGCCAAACA TCCATACAAT ATAGAAACAT CGGTTTCTTA	14100
TATTTTTTTT TATAAGCCAT ACCAGCCCAT GCCATCATAA CTGGAGACAA TTGGTTAACG	14160
AATACACAGT CAAAATTCGA TCCATCTTTC GTTTTATACC TCCCAATAA AACTCCTAAA	14220
GTAGAACTAA TTGCAAGCT AAAATAATTC AACAATCGAA ATACAACACT TTTTCTTCTA	14280
GGGATTGTAT AAGAACGATA TATCGTAACA CCTTCTATAA TCTCACGTCT TTTTCTTATTA	14340
TGACGATAAT CTGCATATAT CTTCCTTCA GGTAAATTAG GAATCCCAGC CAAAACAGAG	14400
ACTTCATGCC CTTTTCGAAC TAAATCTTCA CAAATATCTG ACAACCTGAA TGGTCTGGC	14460
TTATAATGTT GGCAACAAA TAGTATTTTC ATTGTCCAAT TTAACCTTCT TTCTTACCAC	14520

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TACCCCTCTAC AATACCTTTT CGTTTCAGTA CGTAAGGTAT TGTCTTAACT ATACATCTAA	14580
TATCCATTAT CAAAGACAGA TGTTTAACAT AGTAGCCATC TAACTCCGTC TTCATCTCAA	14640
CAGACAAAAGT ATCACGCCCG TTAATTTGTG CCCATCCAGT TAACCCCTGGC AAGATATCAT	14700
TTGCTCCATA CTTATCTCTC TCTGCAATCA AATCTAGTTC ATTTATACCC GCTGGTCTAG	14760
GACCTACAAT ACTCATATTA CCAACAAGAA TATTAAACAA TTGTGGTAGT TCATCCAAAG	14820
ATGTTTTTCG CAAGAAAGCC CCTACTTTTG TAATCyATTG CTCTGGATTA TATAAGTTTC	14880
GAGGCGCCAC ATTTTGTAGT GCATCTATTT TCATAGACCT AAATTTCAAA ATATAGAAGT	14940
ATTCTTTATG AATACCAAAG GGTTTTTGCT TAAATATAAC CGGACCTTCT GAATCAAGTT	15000
TAATCGCAAT TGCAATTATC ATAAAAACCG GACACAATAT TATTATCCCT ATTAAAGATA	15060
ATAATATATC ACCTAATCGT TTTATTATAC CGTACATAAA CAACCTCCAA CTATAAATTC	15120
TATTTCCATT TTTCAATTCTA TTTCCATTGG ACAAATTAAA TCAGGCAGTA CATGCAACTA	15180
CAGAAACTCA ATATATATTT GGTCACTCAA TGATTTTCAG AAATATAATT CTTTATCCT	15240
CTACGTCAGA TAAACTTTT CTCCATCTAA ACAAATTTA TTTGTTTCAG TAATATATGA	15300
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TTTGAAGACA TATCGGTTTC TGAAATTGCA ATCAGTACAT AAGCTAATAA ACTGATAAGT	15420
ATGCTCTGTA AGAATGCCAG AGTTATATTG TAGTCCCTT CCATACTATA TTCATTTTAT	15480
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TGAGTGATAA TTGCCGCATC AATAACAATT CCAATAGGCG GTGTATCAAT AATGATATAA	15720
TCAAAATATT TACGCAATGT TTCAATCATA TCATTAAAAT TTTTACTTTG TAACAAGGCT	15780
GTAGGGTTTG GTGATACAGA TCCCGATTGA ACTACAAATA AATTTTCAAT ATTTGTATCA	15840
CATAAACCGT GAGATAAATC AGCTGTCCCA GATAAAAATT CTGTTAGCCC TGTAAATTTT	15900
TCACGAGATT TAAAACTCC TAACATAACT GAATTTCCGAG TATCGCCATC GATCAAAAGA	15960
GTATTATAGC CTGCACGCG AAACGACCAT GCTATATTTA TGGAAGTAGT TGTTTTTCCT	16020
TCCCCAGGGT TAACAGAAGT AACGAAATT ACTTTTAGTT TATCTCCGCT CAACTGTATA	16080
TTTGTACACA AGGCATTGTA ATATTCTTCT GCCTTCTTAA TGAACCTCAG TTTTTTTTGT	16140
GCTATTTCTA ATGTCGGCAT CCTTCTCTCC TATTTCAACT TACCCAAGTT TGGCACAACT	16200
CCCCAAAAGT TCATCTGCAA TGTATTTTCG ATATCTTCCG GACGTTTCAC ACGAGTATCC	16260
AAAAGTTCAA GATGAAGAAC TATAACACTA GTTCCAATCA CCCCTGCCAA AAAACCAATT	16320

AGTGTATTGC GTTTAATATT TGGCGAAGAC GGGGATATCG CCGGCCTTGC CTCCTCCAGT	16380
GTTGTCACGT CAGAAACACG AGTAATACTG ATAATTTTTT GAGCAGCTAC TTCTCTCAAA	16440
GAGTTAGCGA TACGGCTTGC CTCTTCAGGA ACTCGATCAT TAACTGAAAT AGAGACAATA	16500
CGGGTATCAA CTGGTACTGT CACTTTAATT TTATTAGCCA AACCTTTTGG CGTCAAATCT	16560
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TGATTGCGAT TCACTACGTA AATTCGCGTG GTACTCGTAT ATTCCTGGCTT AACAATAAAA	16740
GTGCTATATG CAAAAGCCCC CGCACCTGTC ACAAGTGCCA CTATTAAAAT CATTAGCTTG	16800
CGTTTCCACA AGCTTTTAAC TAATTGAAAT ACATCGATTT CTATCGTATT TTGTTCTTTC	16860
ATCATTTCTC CTAATTAGT TGATCCATTA CAATTTTTCG AGGATTGTCT ATAAAAAGTT	16920
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CTATCAAGGC ATAACGACTA TCATTGAGGG TCGGAATCCG CTTTTTTTCC AGCTTATCCA	17340
GAACATCTGG TGTGTAATAA ATTTAGCCC CGTAAGCAAT GACCAAGTCA CTCGCCACTT	17400
CCTTAGCTAT TTCCCGAACC TGAAGAAAGT TTTCTGCTAT CTTCTCTTCC GGAGTTTCAA	17460
ACATGCCCTT GCGACGGTGA GAGGTAGAAA CAATGGTTTC CACCCCTGT CTGTAGGATT	17520
CTGCCAAGAG AGCCTTGCTT TCCTCTCTTG ACTTGGGACC GTCATCTACA TCAAAAACGA	17580
TATGCGAATG GATGTCTATC ATTTTCATCTA CCCTCCATCA CATCCTGTAT AGCTGCTTTA	17640
ACTACAGCTA AACTACTATC ATCTATTTCC ATCACATAGA GGTACTGTTC TGGCATTGCA	17700
TAAGAAGGAA GATCCATCCG ACCTGTCCCT TTTAAATCTT GAGAATTAC TTTATAATTC	17760
CCTCCACTTT CTAAGTGGC ATTGACCAAA TTTATCATGG TCTCAAGTGG CATATTTGTT	17820
TGGATAGAAT CTTGCAAGCT ATTAATGATC GTACTATAAT TTTTCAGCAC TTCGGTTGAC	17880
GTAAATTTTT GAAGGATAGC CACAATCACC TTTTGTGTAT GGCGCCCGCG GTCACGATCG	17940
CCATCTGCTA GGGAGTAGCG CTCACGAACA AAACCGAGAG CTTGTTCTGA ATCAAGATGA	18000
ACATTGCCTG CAGGGTAATA CTTTCCATTC GTATGGGCAG TAAATCTTG ATCATTATAA	18060

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ACATCAATTC CACCCAACAA ATCAATCAAT TTCAAAAACG AAGTGAAGTT CAATCGCACA	18120
TAGTAATTGA TATCCACTCC ATAGAGATTT TCTAAGGTGT GAATGGACGA ATCAACTCCA	18180
TAAATGCCCG CATGAGTCAA TTTATCTTTT TGATTATTTT CACCATCTGC GATTGGTACA	18240
TAGGCATCAC GTGGCGTTGT GGTCAAGAGG ATTTTCTTGG TATCTCGATT GACAGTCATC	18300
AGGATGTTGA CATCTGATCG CGACACCGAA CTAATAGGAC CATAGGTGTC AATTCCACTA	18360
ACATAGATAT TGAAAGACTG ACTCTTAGAC GTCTTAGGAG CTTCTACTTT TTTAGTGAAT	18420
CCCTTAGTAT AAATCTTTTT TATCTTCGAT GCGTAGTCTG GATACTCTGA CTCGATGATG	18480
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TCAGCTAGTA ATTTCTGAAT ATTTTCATTA TTAGTCCCAG TCGGTGCTGT CACACTCGTC	18660
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GAGTAATTAG AAGTCGCATT TAAACGATTG GTCAGTCCAA CAACTGCTG TACTGCAAAG	18780
AGCGACACAG AGCTGACAAG GATAGAGAAC ACCAACAGAA AAATAGTAAA CTTTTCAGCT	18840
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ACTAGATTAA GATATCTAAA AGCAAGGATA TTGTACTTAA AGATTAAAGAA CAATAAAAAA	18960
CAAACTAACA ATAAATAAAT AGTCAGCAAA ACTATATTAA CACTTCGCTT CACTTTCGT	19020
GAACGTGATT TTTTAAACG TCTACTCATG ATTAATACCT ATACATTGAA CATTATACGA	19080
TTATATCACT TTTTACGGT AATGTCTACA CCTTTATTTT TACTATCTGC ATCTTTAAGT	19140
ATCTTAGTAG ACTTCCCGCG AAACAAAAAT ATAGTAAAAT GAAATAAGAA CAGAACAAAT	19200
CGTTCAGGAC AGTCAAATCG ATTTCTAACA ATGTTTTAGA AGCAGAGGTG	19250

(2) INFORMATION FOR SEQ ID NO: 36:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 21706 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 36:

AAAGTTGAAA GACTGCTAGC TGTTTTTGAT ACCAATCGTT TCCAACTACA GAGCAAACAG	60
TATACAAAGT TTGTTTTTGG ATGTAAGCTT CTGATGGAC AATTCCAAGA AAATCAAGAA	120
ATTGCTGACC TTCAATTTTT TGCCATTGAC CAACTGCCGA ACTTATCTGA AAAACGCATT	180
ACCAAGGAGC AAATAGAGCT TCTTTGGCAG GTTTATCAAG GTCATAGGGG GCAATATCTT	240

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GACTAAGAAG ATGATTATCG TATTTCTAAA TCCATTTTTA ACAACTAGCA TGGTATAATA	300
ATATGCAGGA AAATTTTGAA TTATGAGGAA GACTAGATGA ATTTATGGGA TATTTTCTTT	360
ACGACTCAGG CAACCGAGCC GCCCAAATTT GACCTTTTTT GGTATGTTAG CCTATTTACG	420
CTCTTAGCCT TAACCTTTTA TACAGCCCAT CGCTATCGTG AAAAGAAGGT TTACCAACGA	480
TTTTTCAAA TCTGTCAGAC TGTTCACTTA ATCCTTCTTT ATGGTTGGTA CTGGGTCAAT	540
CATATGCCAC TGTGAGAAAG CCTACCTTTT TACCATTGCC GTATGGCTAT GTTTGTGGTA	600
CTCTTGCTTC CTGGTCAATC CAAATATAAA CAATACTTTG CATTATTGGG AACATTGGG	660
ACATTAGCAG CCTTTGTTTA TCCAGTGCCA GATGCTTACC CTTTTCCACA TATCACCATT	720
CTATCCTTTA TCTTTGGTCA TTTAGCACTC TTGGGGAAC CTCTAGTTTA TCTATTGAGA	780
CAGTATAATG CGCGATTGCT GGATGTGAAG GGAATTTTTC TCATGACCTT TGCCCTAAAT	840
GCCTTGATTT TTGTGGTCAA TTTGGTGACA GGTGGCGATT ACGGATTTTT GACAAAACCG	900
CCATTGGTTG GGGATCACGG TCTAGTAGCT AATTATTAC TTGTTTCAAT TGTGCTGGTA	960
GCTACTATCA GTTTGACTAA GAAAATCTTA GAATCTTTT TAGCTCAAGA AGCAGAAAAA	1020
ATGATTGCAA AGGAAGCTTA ACACAGAGCT TTCTTTTTTG CTCTTAGAGA GTTTTTACAA	1080
GCAGCTTATA AAATAAGAAAT TTCTGAATAG ACAAACCTCAA AAAATGGCTG GGAAATTTAG	1140
GAAAAAGCA AGCACGATTA AATTTTTTGT GTTATAATAT TTTGTGAATA GCTATGCCTA	1200
TGTTTAGCTA TGGAATAATA CGAAGTGCAG AACTTGGAAG ATAGAGAGGA AGCGATGTAA	1260
TGGCTAGAGA AGGCTTTTTT ACAGGTCTAG ATATTGGAAC AAGCTCTGTC AAGGTGCTTG	1320
TGCGCGAGCA GAGAAATGGT GAATTAAATG TAATTGGCGT GAGTAATGCC AAAAGTAAAG	1380
GTGTAAAGGA TGGAATTATT GTTGATATTG ATGCAGCAGC AACTGCTATC AAGTCAGCCA	1440
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GTAATCTTTT GCAGGTAGAA CCAACTCAGG GGATGATTCC ACTAACATCT GATACTAAGG	1560
AAATTACGGA TCAAGATGTT GAAAATGTTG TCAAATCAGC TTTGACAAAG AGTATGACAC	1620
CTGACCGTGA AGTCATTACC TTTATTCCTG AAGAATTTAT TGTGGATGGT TTCCAAGGGA	1680
TTGCTGACCC ACGTGGCATG ATGGGGGTTT GCCTTGAAAT GCGTGGTTTG CTTTATACAG	1740
GACCTCGTAC TATCTGTCAC AATTTGCGTA AGACGGTTGA GCGTGCAGGT GTTCAGGTTG	1800
AAAATGTTAT CATTTACCA CTAGCAATGG TTCAGTCTGT TTTGAACGAA GGGGAACGTG	1860
AATTTGGTGC TACAGTGATT GATATGGGGG CAGGTCAAAC GACTGTCGCT ACAATCCGTA	1920
ATCAAGAACT CCAGTTCACA CATATTCTCC AAGAAGGTGG AGATTATGTA ACTAAAGATA	1980

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TCTCCAAGGT TTTGAAAACC TCTCGCAAAT TAGCGGAAGG CTTGAAACTG AATTACGGGG	2040
AAGCCTATCC GCCTCTTGCA AGCAAAGAAA CCTTCCAAGT AGAGGTTATT GGAGAAGTAG	2100
AAGCAGTCGA AGTGACGGAA GCCTACTTGT CAGAAATTAT TTCTGCACGA ATCAAGCACA	2160
TCCTTGAACA AATCAAGCAA GAATTAGATA GAAGGCGTCT ATTGGACCTC CCTGGTGGTA	2220
TTGTCTTAAT CGGTGGGAAT GCCATTTTAC CAGGTATGGT TGAGCTTGCT CAGGAAGTCT	2280
TTGGCGTCCG TGTCAAGCTT TATGTTCCAA ATCAAGTTGG TATCCGTAAT CCAGCCTTTG	2340
CGCATGTGAT TAGTTTATCA GAATTTGCGG GTCAATTAAC AGAAGTTAAT CTTTGGGCTC	2400
AGGGAGCGAT AAAAGGTGAG AATGACTTAA GTCATCAGCC AATTAGTTTT GGTGGGATGC	2460
TGCAAAAAAC AGCTCAGTTT GTACAATCAA CGCCTGTTCA ACCAGCTCCT GCTCCAGAAG	2520
TAGAGCCGGT GGCCTTACA GAACCAATGG CGGATTTCCA ACAAGCTTCA CAAAATAAAC	2580
CGAAATTAGC AGATCGTTTC CGTGGATTGA TCGGAAGCAT GTTTGACGAA TAAAGAGGAA	2640
AAATAAATTA TGACATTTTC ATTTGATACA GCTGCTGCTC AAGGGGCAGT GATTAAAGTA	2700
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GGCGTAGAAT TTATCGCAGC AAACACAGAT GTACAAGCAT TGAGTAGTAC AAAAGCTGAG	2820
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GTGGTTCGTA AAGCCGCTGA AGAAAGCGAA GAAACACTGA CGGAAGCTAT TAGTGGTGCC	2940
GATATGGTCT TCATCACTGC TGGTATGGGA GGAGGCTCTG GAACTGGAGC TGCTCCTGTT	3000
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GGTTTGAAG GAAGTAAGCG TGGACAAATTT GCTGTAGAAG GAATCAATCA ACTTCGTGAG	3120
CATGTAGACA CTCTATTGAT TATCTCAAAC AACAATTGTC TTGAAATTGT TGATAAGAAA	3180
ACACCGCTTT TGGAGGCTCT TAGCGAAGCG GATAACGTTT TTCGTCAAGG TGTCAAGGG	3240
ATTACCGATT TGATTACCAA TCCAGGATTG ATTAACCTTG ACTTTGCCGA TGTGAAAACG	3300
GTAATGGCAA ACAAAGGGAA TGCTCTTATG GGTATTGGTA TCGGTAGTGG AGAAGAACC'T	3360
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GAGGCTTCAC AAATTGTGAA CCAGGCAGCA GGTCAAGGAG TGAACATCTG GCTCGGTACT	3540
TCAATTGATG AAAGTATGCG TGATGAAATT CGTGTAACAG TTGTTGCAAC GGGTGTTCGT	3600
CAAGACCGCG TAGAAAAGGT TGTGGCTCCA CAAGCTAGAT CTGCTACTAA CTACCGTGAG	3660
ACAGTGAAAC CAGCTCATTC ACATGGCTTT GATCGTCATT TTGATATGGC AGAAACAGTT	3720
GAATTGCCAA AACAAAATCC ACGTCGTTTG GAACCAACTC AGGCATCTGC TTTTGGTGAT	3780

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TGGGATCTTC	GCCGTGAATC	GATTGTTTCGT	ACAACAGATT	CAGTCGTTTC	TCCAGTCGAG	3840
CGCTTTGAAG	CCCCAATTTTC	ACAAGATGAA	GATGAATTGG	ATACACCTCC	ATTTTTCAAA	3900
AATCGTTAAG	TAAATGAATG	TAAAAGAAAA	TACAGAACTT	GTTTTTCGAG	AAGTTGCAGA	3960
GGCTAGTCTG	AGTGCTCATC	GAGAGAGTGG	TTCGGTCTCT	GTCATTGCAG	TTACCAAGTA	4020
TGTAGATGTA	CCGACAGCGG	AAGCCTTGCT	TCCGCTAGGT	GTCCATCATA	TCGGTGAAAA	4080
TCGTGTAGAT	AAGTTTCTGG	AAAAATATGA	AGCTTTAAAA	GATCGAGATG	TGACTTGGCA	4140
TTTGATTGGT	ACCTTGCAAA	GACGTAAGGT	GAAAGATGTC	ATTCAATACG	TTGATTATTT	4200
CCATGCATTG	GACTCAGTAA	AGCTAGCAGG	GGAAATTCAA	AAAAGAAGTG	ACCGAGTCAT	4260
CAAGTGTTTC	CTTCAAGTAA	ATATTTCTAA	AGAAGAAAGC	AAACACGGTT	TTTCGAGAGA	4320
GGAACTGCTG	GAAATCTTGC	CAGAGTTAGC	CAGACTAGAT	AAGATTGAAT	ATGTTGGTTT	4380
AATGACGATG	GCACCTTTTG	AGGCTAGCAG	TGAGCAGTTG	AAAGAGATTT	TCAAGGCGGC	4440
CCAAGATTTA	CAAAGAGAAA	TTCAAGAGAA	ACAAATTCCA	AATATGCCTA	TGACCGAGTT	4500
AAGTATGGGA	ATGAGTCGTG	ATTATAAAGA	AGCGATTCAA	TTCGGTTCCA	CTTTGTCTCG	4560
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ATTTATAGAT	TATTTTACGG	AGGATGAGGA	TTCAAGTCTC	CCTTATGAAA	AAAGAGATGA	4680
GCCTGTGTTT	ACTTCAGTAA	ATTCTTCACA	GGAACCGGCT	CTCCCAATGA	ATCAACCTTC	4740
ACAGTCGGCT	GGCAGAAAAG	AGAACAATAT	CACCAGACTT	CATGCAAGAC	AACAGGAATT	4800
GGCAAAATCAG	AGTCAGCGTG	CAACGGATAA	GGTCATTATA	GATGTTCTGT	ATCCTAGAAA	4860
ATATGAGGAT	GCAACAGAAA	TTGTTGATTT	ATTGGCAGGA	AACGAAAGTA	TCTTGATTGA	4920
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TCATGTTTTA	GCTGGAAATT	TGAAAAAGGT	AGCTTCTACC	ATGTATTTGT	TGACACCAGT	5040
GAACGTTATT	GTAATGTTG	AAGATATCCG	TTTACCAGAT	GAAGATCAAC	AGGGTGAGTT	5100
CGGTTTTGAT	ATGAAGCGAA	ATAGAGTACG	ATAATGATTT	TTTTAATTCC	TATGATTTAT	5160
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TAGCTGTGCG CTTCTTTACC TTGTTCTGCG ATAGAGTCAG TAAAGATTTG AGCGTAGATT	19080
GGGATGTTTG TGTCTTGAGA AACAGTTTTT ATTGGACGGT CATCCACACT TGATTCTACA	19140
AAGAGTGATG GAACTTTTGT TTGGCGAAGT TTTTCAACCA AGGTCTTGAT TTGTTTCAGGA	19200
GTTCCTTCTT CTTCAGTATT GATTTCCAG ATGTAAGCAC TTGGGACACC ATAGGCTTTA	19260
GAGAAGTATT TGAATGCTCC TTCGCTGGTT ACAATGAGTT TCTTTTCAGC AGGGATCTTA	19320
TTAAATTTAT CCTTACTTTC TTTATCAAGT TTGTCTAACT TATCAGTATA TTCTTTGAGA	19380
TTTTTTTCAT AGAATTCCTT ATTGTTAGGG TCTTTGGCGC TCAATTGTTT GCGGATATTT	19440
TTAGCAAAAA TAATACCGTT TTCAAGGTTA AGCCAAGCGT GTGGGTCTTC TTTTCCTTTT	19500
TCATTTTGAC CTTCAAGGTA GATAACATCA ACGCCGTCGC TGAATGCGAA GTAGTCTTTG	19560
TTTTCAGTTT TCTTGGCATT TTCTACCAAT TTTGTAAACC AAGCATTGCC ACCTGTTTCA	19620
AGGTTGATAC CGTTATAGAA AATCAAATTA GCCTCAGAAG TTTTCTTAAC GTCTTCAGGA	19680

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AGTGGTTCGT ATTCGTGTGG GTCTTGCCCA ATCGGAACGA TACTATGAAG GTCAATTTTG	19740
TCACCAGCAA TATTTTGTAGT AATATCAGCG ATGATTGAGT TTGTAGCAAC AACTTTTAGT	19800
TTTTGACCAG AAGTTGTATC TTTTTTCCG CTAGCACATG CTACAAGAAT GATTGCAGAA	19860
AGAAAGAGAA CGAGTAATGT ACCTAATTTT TTCATTAGAT CCTCCAATTT ATTAGGGCTT	19920
TGCCCTTAT TTTAACAAAT GTTTATTTT CAGTTTCAA TATCGTTGTT TGGGAGCGAT	19980
AAAGAAGCTA ATGAGAAAGA AACTAGCAGC TGTAAGCAGC ATACTAGAAC CTGCCGCAAC	20040
ATTAAAACTA TAGCCAATAA AGAGTCCCAA AACTGAAGCA GTAGCTCCGA AGGTTGAGGA	20100
AAGGAAAATC ATACTTTTCA GACTATTAGC ATACAGATAA GCAGTTGCAG CTGGGGTAAT	20160
CAGCATGGCT ACAATCAGGA TAGTTCCGAC ACTTTGCATG GCTGTCACAG ACACGAGAGT	20220
CAGGAGTACC ATGAGAAGGT AGTGATAGAA ATTGACAGGC ATTCCTCATG CTTTAGCCAA	20280
GAGTTCATCA AAGGAAGTTA TCAAGAGTTG CTTGAAGAAA ATCCAGATTA ACAAGAGGAT	20340
AGCTGCCCCC ACACCCATAG TAATAACAT ATCCGTATCT TGGACGGCCA GGATATTACC	20400
AAAAAGGATA TGGAAAAGGT CAGTTGAACT TTTAGCGACA CCAATCAAGA TGATACCGAG	20460
GGCTAAGAAA GAAGAAAAGG TAATGCCGAT GGCGGTATCG CTTTGTGATA TCGAGTTTCC	20520
TTTGATGTAG GTAATGATGA TGGCAGCTAG CAATCCAAAG ACAATGGCTC CGATAAGAA	20580
GTCAAGGCCC AAGATGAAGG ATAGGGCTAC ACCTGGTAAG ACAGCATGTG AAATGGCATC	20640
TCCCATGAGT GACATCCCGC GTAGAATAAT GAAACATCCC ACAGCTCCAG CTACAATCCC	20700
GACGACAATA GCTGTTATCA AGGCATTTTG TAGGAAATGG AATTTTGTCA ATCCATCGAT	20760
AAATTCGTCA ATCATAGGTC ACCTCCATTG AAAAAGAGTT GATTACCGTA AGCTTCTTTT	20820
AGATTGGTTT CGGTAAAAGT TTCTTTTGTT GGACCAAAGG CAATCACTTC TCGATTGACA	20880
AGTAAGACTT GATCGAAGTA GTGGGAATC TTGCTGAGGT CGTGGTGAAC GATGAGAACC	20940
GTCTTCCAG CTTTTTCAA ATCTCTCAGC GTATTATGA TGATTTCCTC ACTGACAGAG	21000
TCAATCCCAG CAAAGGGTTC ATCCAAGAGG ATATAGTCGG CTTCCTGCAC CAAACATCTG	21060
GCAATCAAGA CCCGCTGAA TTGACCTCCA GACAGTTGAC TAATTTGACG TTCAGCGTAG	21120
TCAGCTAGGC CGACGATTC AAGGGCTCT TGCACTTTCT TCCAATGTTT AGCCTTTAAA	21180
CTTCGAAAGA GAGGAATAGA GGGAAATAGT CCTAACGAGA CGCATTCCTT GACCTTGATG	21240
GGAAAGTTGT AGTCGATATT GATTTTGTG TCGACATAGG CAATTCGGTG TAAGGATTTT	21300
TTAATTCCT TGTCATCGAG AAATGCCTGA CCTTGATGTG GGATAATTCC CAACATACCT	21360
TTTAATAGTG TTGATTTCCC AGCGCCGTTT GGACCAATGA TGCCGGTAAT TGTGGTCCA	21420
TGGAGCACTA GTGAAATATC CTTAAGTGCC AACGTTTCTT TGTAGGAGAC ACTGAGGTTT	21480



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TCGATACGTA TCATAAACTT GTATTCCTCC TGTCTCTTAA TATACATTAA AAAAAAATT	21540
AAGTCAAGTT AATTTTGTAA AAAATTAAAA TAATAACTGA AAAATAGATT CTAAAGATAA	21600
CTTTCAGGAT AAATTTCTAA ATTATAAAC GCATAGTATC AAGTGTA AAAA AACTTGGAAT	21660
TATGCGTTT ATCATGGAAA GATTTTAT AATAGCTAAA AAATAA	21706

(2) INFORMATION FOR SEQ ID NO: 37:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 6171 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 37:

GATCCCCAGG AAAAACCGAG GTTTTCCCAA TCAATCGTTA CTGTCATATT CCACTCCTTA	60
TTCTAAAAAC CTATTTCTTA TATCTACAC TATTTTCTA AAATAGCAAG TATATTTTGT	120
AATTTTCAGA AAATTTCTCC AATAAAAACC AACTCTTAGA ACTGATTCTT CATTTCACTT	180
ATTTATCTTC AGTAACTACT TCCTGAAGAT AAGCGTCAAA AACTTCTTCA TCTGAAATCG	240
TGTCAGAAAT GAAGCTTCCA TTGCTAGTGC GTTCTGACAA GTTCAAGTCT TGCAATCGGC	300
TTTCATAGAT TGTTCCTTTA TTGGATGGA CAAGCAGAGT TTGGTCGTTT ACATCCACTT	360
CCGTACTGAA GAAATCGCCA ACAAATCCTT GCTCTGCAAC TGCTCCTGCC AAGAAGACAC	420
GATGCCGTTT GTTTTCAAC TCACGCAAGA CTGTGAATCC TCGTTTGGCA CGGCTGGTTG	480
CTAGAATTTT CTCAATGGAA ACACGTTTCA AGCTTCCACG CTGGGTCAAG AGGTAGAAGG	540
ACGAAGTATT ACAGATAAAG CCAGATTGGA GGACATCATC TTCTTTCAAA TTCATAGCCT	600
TGACACCTGC TGCTTAGCA CCGACAACCG GAACCTCTT GATATTGAAA CGCAGGGCAT	660
AACCATTTTG ACTAACAAG ACAACATCAT CTAGTTTAAT CGGAGCCACT GCTACAATCT	720
GATCTGTATC GTCTTTGAGC TTAGCATACT TGACAGACTT AGATCTATAG GTCCGCCATG	780
GAGTGAATTC TTTTCGCTCT ACCCGTTTGA TTGACCAAG GCGAGTCACT GCAAAGTAGG	840
TTGTCGCATC GTCAAACTGA TCCAGTACTT CCACATAAAG GATTTCTTCA TTCGTTTCAA	900
AGTTTGTGAT GGTTTGGCTC AGATGCTCTC CGATGTCCTT CCAACGAATA TCTGCCAACT	960
CATGGATTGG TCTGTAGATG ACATTTCOA GACTTGTGAA CATCAAGAGG TGCTGGGTTG	1020
TCTTGCCAGA TTGAACAAAA ATCAAACGGT CATCATCAG CTTGCCAAT TCTTCCAAGG	1080
TGGAAGCCGC AAAGGAACGT GGAAGGTAC GCTTGATGTA ACCTGCCTTG GTCACGCTGA	1140

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CGTAGGTATC TTCCTCAGCG ATAAGACTAG CTGTATCAAT CTCAATTGCT TTCGCAGTGT	1200
CTTCTAAAGA ACTCAAACGA GGAGTTGCAA ATTTCTTCTT GACCTCACGA AGTTCTTTCT	1260
TCATGAGATT GTACATAGTC CTTTCATCAC CGATAATAGC CGCCAGCATA GCAATCTTCT	1320
CACGAAGCTC TGCTTCTTCT TCCTGCAAGA CAACCACATC GGTATTGGTC AAACGGTACA	1380
GTTGCAAAGT TACGATAGCC TCAGCCTGTT CTTCCGTAAT ATCATAGCTA ACTTTGAGGT	1440
TTTCCTTGGC GTCCGCCTTA TTCTCAGAAG CACGGATAAG AGCAATGACT TCATCCAAAA	1500
TCGAAATCAC ACGAATCAAA CCTTCGACGA TATGGAGACG TTTCTCAGCC TTTTCTTTGT	1560
CAAAGCGTGA ACGCGCCAAA ATCACTTCTC GACGGTGAGC GATATAGCTA GACAGGATTG	1620
GAACAATCCC AACCTGACGA GGTGTGAAAT TGTCAATCGC CACCATATTA AAGTTGTAGT	1680
TGATTTGTAG GTCGGTGATC TTAAATAAGT AGTTGAGAAC AAGCTCAGTA TTAGCGTCTT	1740
TCTTAAGTTC GATAGCGATA CGAAGACCAT CACGGTCAGA CTCATCACGA ACCTCAGCAA	1800
TCCCAGCTAC CTTGTATTTA ACACGAACAT CATCGATTTT CTTGACTAGA TTGGCCTTAT	1860
TGATTTTATA AGGAATCTCA ATAATAACGA TTTGTTCTT ACCACCTTTT AGCTTTTCAA	1920
TTTCAGTCTT GGAACGAACA ACCACGCGCC CTTTCCCAGT CTCATAAGCT TTCTTGATTT	1980
CATCAGCACC CTGAATAATA GCCCCTGTAG GGAAGTCTGG TCCAGGCAAG AATTCCATGA	2040
GTTTATCAAT CTTTGAGTT GGGTGGTCAA TCATGTAAAC TGCAGCATCT ATGACCTCAG	2100
CTAAATTATG GGGAGGAATG TCTGTGGCAT AACCAGCCGA AATCCCAGTC GAACCATTGA	2160
CCAAGAGGTT TGGAAAGGCT GCTGGCAAGA CCGTTGGTTC TTTCTCCGTA TCGTCAAAGT	2220
TCCATGCAAA AGGAACTGTC TTTTCTCGA TATCCTGAAG AAGGTAGCCT GCAATTTTCA	2280
ACAAACGTGC CTCAGTATAA CGCATAGCCG CAGGAGGATC TCCGTCCATA GAACCGTTAT	2340
TACCGTGCAT TTCAACTAGA ATCTCAGGAT TTTTCCAGTT CTGTGACATA CGAACCATGG	2400
CATCATAGAT AGAAGAATCC CCGTGTGGGT GGAAATTCCC CATGATGTTT CCGACTGACT	2460
TGGCCGACTT ACGGTAGCTC TTGTCAAAG TATTGCTATC CTTATTCATA GAATAAGAA	2520
TACGGCGCTG AACCGGCTTC AACCCATCAC GAATATCTGG CAAAGCCCGG TCTTGAATAA	2580
TGTACTTGGA GTAGCGACCA AAGCGCTCTC CCATGATGTC CTCCAGGGAC ATGTTTGA	2640
TGTTAGACAT AAGATACAAA GCCCATAAAA TACCAAGTGA AAATAGAAAA TTCTTGAAGT	2700
AAGCAAACCT ACAAGAGAAT TTATCTTTT CACACAGTAT CTAGGGCGTG TTCAACTCCT	2760
TTCAAAGAAT GTAGAGTAGG TTTTATGCA GTAAAAGATA TTTTACGGGA ATTCCTCCCG	2820
TGTTCAAGTA CGATAAGTAA CCAAATATC CTGTTTGTAT TTTTCAATAT GAAAATCTGG	2880
TTTTCCAAAA TTAGTCTTAG TTTGTGCTT AGCCGCTCCC TTAAGCGCCT CTTTGAGATA	2940

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AGCACTCATA GCAGATTCTT CATTAATAAT CCTGCAATTT TTTCAAACCA AGATTTTCAA	3000
ACTGCTTTTT CACATAGTCA TTCACATCCG ACTCTAATTT CCAGTTTACT AACATATTAT	3060
TTTCTTTCAT TAAACACTG TCGTTTCTTC TAGCGTAAAC TTGACATTAT CTTCAATCCA	3120
TTTAGGGCGT GGTTCACCT TATCTCCCAT GAGAACATTG ACGGGCGCTT CGGCGCGCGC	3180
TAAATCTTCA ATTGTGACAC GGATGAGGGT ACGTGTCTT GGGTTCATGG TTGTTTCCCA	3240
GAGCTGGTCC GCATTCTCT CACCAAGTCC TTTGTATCGT TGGAGGGTAG CGCCTTTACC	3300
GAATGTTTA CGGAGTCTT CTAGTTCTCC GTCCGTCCAA GCGTAGGCCA CTTCTTCTTT	3360
CTTGCCTTTA CTTTGGACA TCTTGTAAG AGGTGGGAGG GCAATATAGA CATGACCTGC	3420
CTCGACTAGC GGACGCATGT AACGGTAGAA AAATGTCAAG AGCAAGGTCT GGATATGGGC	3480
ACCGTCGGTA TCCGCATCGG TCATGATAAT GATCTTATCA TAGTTGGCAT CTTCAATAGA	3540
GAAGTCTGCT CCAACACCCG CACCAATGGT ATAAATCATG GTATTGATCT CTTCATTTTT	3600
GAGGATATCC GCCATCTGG CCTTGGCTGT ATTGACAACC TTACCACGAA GAGGTAGAAT	3660
AGCCTGGAAC TTGCGGTCAC GACCTTGTTC GGCAGAACCA CCGGCAGAGT CCCCTCAAC	3720
TAGATAGAGT TCATTCTTAG CAGGATTCTT AGATTGGGCT GGGGTCAATT TCCCAGACAA	3780
CAAGCCCTTA TCTTCTTGT TTTCTTCCC ATTTCCGGCTC TCATCAGCGC CTTACGTGC	3840
TGCTTCACGA GCATCACGGG CCTTGATAGC CTTGCGGATG AGGTAGAAG CTAATCCCC	3900
ATTTTCCATA AGGAAAAAGG TCAACTTATC AGCCACTATT CCATCCACAA CTGGGCGAGC	3960
TAGGGGGCTT CCTAGTTTAT CCTTGGTCTG TCCTTCAAAC TGCAAGTGTT CTTCAGGAAC	4020
TAAGATAGAA AGAACGGCCG CTAGTCCCTC ACGATAGTCT GAACCTTCAA GGTTTTATC	4080
TTTTTCCTTG AGAAGACCTG TTTTACGTGC ATAGTCATTC ATGACCTTGG TAATGGCAGA	4140
CTTGAGTCCCT GTCTCGTGC TTCCACCGTC CTTGGTGCGA ACGTTATTGA CAAAAGATAG	4200
AATGTTATCT GAGAATCCGT CATTGTACTG GAGGGCTACT TCCACTTGAA AACCATTGTC	4260
TTCCCTTCA AAGTAAAGAA CTGGCGTCAA GATTTCCCTTA TCTTCGTTGA GATAAGAAAC	4320
AAAATCTTGT ACTCCATTCT CATAGTGGAA CTCAATCGCT TCATTTGTTT GCTTGTCGGT	4380
TAAAGACAAG GTCACATTTT TCAAGAGAAA GGCTGATTCA TTAAGGCGCT CTGAAATGGT	4440
ATTGTACTTG AAATCTGTCG TAGAAAAATAT AGTCGCGTCA GGCATAAAAG TAACTTTGGT	4500
GCCTGTTTTA GACTTGGGTG CTGTACCGAT TTTCTTCAA GTCGTGACAG GTTTTCCACC	4560
ATTTTCGAAA CGTTGCTTGT AACTGCGCC ATCACGGGTA ATTTCAACTT CTAACCAGCT	4620
AGAAAGGGCG TTAACAACGG AAGAACCAC TCCGTGAAGT CCACCTGATG TCTTATAGCC	4680

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ACCTTGACCG AATTTCCCTC CGGCATGAAG AATGGTAAAG ATAACCTCAA CAGTTGGAAT	4740
TCCCATAGCG TGCATACcTG TCGGCATCCC ACGTCCATGG TCTTGAACCG TTAGACTACC	4800
GTCTTTATTG ATAGTTACAT CAATACGATC ACCAAACCCA GACAAGGCTT CATCGACTGC	4860
ATTATCAACG ATTTCCCAAA CTAGGTGATG AAGACCAGCG CCATCGGTCG ATCCAATATA	4920
CATCCCTGGA CGTTTTCGGA CCGCATCCAA CCCTTCTAGC ACCTGAATAG CATCATCATT	4980
ATAATTGTTA ATATTGATTT CTTTTTTTGA CACAAGGAAC CTCCTATTCTG TTCATCTTTA	5040
CTATTCTACA GGTTTCCAA GGATTTTGCA AAATTTTCT TTTCTCGATG TGACAATTTC	5100
AGCAGAGATT CTCTGCTTTT CTTTCCCAAT TCATGATATA ATAGGAGTAT GATTACAATA	5160
GTTTTATTAA TCCTAGCCTA TCTGCTGGT TCGATTCCAT CTGGTCTCTG GATTGGACAA	5220
GTATTCTTTC AAATCAATCT ACGCGAGCAT GGTTCCTGGTA ACACCTGGAAC GACCAACACC	5280
TTCCGCATTT TAGGTAAGAA AGCTGGTATG GCAACCTTTG TGATTGACTT TTTCAAAGGA	5340
ACCCTAGCAA CGCTGCTTCC GATTATTTT CATCTACAAG GCGTTTCTCC TCTCATCTTT	5400
GGACTTTTGG CTGTTATCGG CCATACCTTC CCTATCTTTG CAGGATTTAA AGGTGGTAAG	5460
GCTGTGCGAA CCAGTGCTGG AGTGATTTTC GGATTGCGC CTATCTTCTG TCTCTACCTT	5520
GCGATTATCT TCTTGGAGC TCTCTATCTT GGCAGTATGA TTCACTGTC TAGTGTACA	5580
GCATCGATTG CGGCTGTTAT CGGGGTCTG CTCTTCCAC TTTTGGTTT TATCCTGAGT	5640
AACTATGACT CTCTCTCAT CGCTATTATC TTAGCACTTG CTAGTTTGAT TATCATTCGT	5700
CATAAGGACA ATATAGCTCG TATCAAAAAT AAAACTGAAA ATTTGGTCCC TTGGGGATTG	5760
AACCTAACCC ATCAAGATCC TAAAAAATAA AATGCCAGTT CTGTACTGCC CCCAAACAGT	5820
TAGACAAATA ATTTATCCAA AGGATTTAGT TCTGTACTGC ACAGGACTAA GTCCTTTTAG	5880
TTTTACCTTA ATTCGTTTGT TGTTGTAGTA ATCAATATAG TCTATAATGG CTTGTTCCAA	5940
TTGATTAAAGT GATTTAAATG TTTTCTCATA GCCATAAAAC ATTTCCGATT TTAATAATGCC	6000
AAAGAAAGAT TCCATCCTAC CGTTGTCTTG GCTGTTGCCC TTACGTGACA TGGATGCTTG	6060
AATTCCTTA CTCTCTAGGA ACCGATGATA AGAATCGTGT TGGTATTGCC AGCCTTGGTC	6120
ACTATGGAGA ATCGTATTCT CGTAGTGCTT CTCTGTGAAT GCCTGTTCCA A	6171

(2) INFORMATION FOR SEQ ID NO: 38:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 18475 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 38:

TATTACAAAT AAAAAACGG AGGAGTGCTT TATGAAAGCC TATACTTATG TTAAACCAGG	60
ACTTGCTTCT TTTGTTGATG TAGACAAACC AGTTATTCCG AAGCCAACAG ACGCTATTGT	120
GCGTATTGTA AAAACCACTA TTTGTGGAAC AGACCTCCAT ATTATCAAAG GGGATGTTCC	180
TACTTGCCAA AGTGGTACCA TTCTTGCCCA CGAAGGGATT GGGATTGTTG AAGAAGTTGG	240
GGAAGGAGTT TCCAACCTCA AAAAAGGTGA CAAGGTCTTG ATTTCTTGCG TCTGTGCCTG	300
TGGTAAATGC TACTACTGTA AAAAAGGAAT TTATGCTCAC TGTGAAGACG AAGGGGGCTG	360
GATTTTCGGT CACTTGATTG ATGGTATGCA GGCTGAATAT CTACGTGTCC CTCATGCAGA	420
TAATACTCTT TACCATACTC CAGAAGACTT GTCAGATGAA GCTTTGGTTA TGCTGTCAGA	480
CATTCTGCCT ACTGGATATG AAATTGGTGT CTTAAAAGGG AAAGTAGAAC CTGGTTGCAG	540
CGTAGCCATT ATTTGGTTCAG GTCCAGTTGG ATTGGCTGCT CTTTAAACAG CCCAATTCTA	600
TTCACCAGCT AAATTGATTA TGGTAGACCT AGACGATAAC CGCTTGGAAG CTGCCCTATC	660
ATTCCGTGCG ACTCATAAGG TTAATTCCTC AGACCCTGAA AAAGCCATTA AAGAAATTTA	720
TGATTTGACA GATGGTCGTG GTGTGGATGT CGCTATCGAA GCTGTTGGTA TTCCTGCAAC	780
ATTTGATTTT TGTCAAAGA TTATCGGTGT AGACGGAACG GTTGCCAACT GTGGTGTGCA	840
TGGTAAACCA GTTGAATTCG ATTTAGATAA ACTTTGGATT CGCAACATCA ATGTAACAAC	900
TGGTTTGTA TCTACAAATA CGACTCCACA ATTGTTGAAA GCACTTGAAA GTCATAAGAT	960
TGAACCGGAA AAATTGGTAA CTCACTATTT CAAACTCAGT GAAATTGAAA AAGCCTACGA	1020
AGTCTTCAGT AAGGCAGCAG ACCACCATGC CATTAAGGTC ATTATCGAAA ACGATATCTC	1080
AGAAGCCTAA GTAGTAAAAA TATTTTGTGA CATAAGTAAA TAGAAATTCA GTCATCCATC	1140
AGATGGCTGG ATTTTTTATC AAAAAATTAA GAAATGAGCA TATTTCTTTC CTTGTCTGGC	1200
GGAATTGGTT ATAATATACG GTACAAAGGA ATGAATGAAT ATGTATCGTG TTATAGAAAT	1260
GTACGGAGAT TTTGAACCGT GGTGGTCTT AGAAGGTTGG GAAGAAGATA TTGTAGCAAG	1320
TAGAAAATTT GACCAGTATT ATGATGCTCT CAAATACTAC AAAACTTGCT GGTTTAGATT	1380
GGAACAAGAA TCGCCTCTTT ATAAAAGTAG AAGCGACTTG ATGACCATTT TTTGGGACCC	1440
GGAAGACCAA CGCTGGTGTG ATGAATGTGA TGAGTATTTA CAACAATACC ATTCTTTGGC	1500
TCTTTTGCA GATGAGCAGG TTATCCCAGA CGAAAACTA CGCTCAGGCT ATGAAAAACA	1560
AACCACTCAG GAAAGGAATC GTTCTTGCCG TATGAAATTA AAATAGAGAA AAGTAACTTT	1620
TTTGGAGTTG CTTTTTTTAT TTTTCTAACT CTTTGCGAAT AGTATAGGTG AGGAGGTAAG	1680

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TATGGTTCAA GAAATTGCAC AAGAAATCAT TCGTTCAGCT CGGAAAAAAG GGACGCAGGA	1740
TATCTATTTT GTCCCTAAGT TAGACGCCTA TGAGCTTCAT ATGAGGGTAG GAGACGAGCG	1800
CTGTAAAAAT GGTAGCTATG ATTTTGAAAA GTTTGCAGCC GTTATCAGTC ACTTTAAGTT	1860
TGTGGCGGGT ATGAATGTGG GAGAAAAAAG ACGTAGTCAA CTGGGTTCCCT GTGATTATGC	1920
CTATGACCAT AAGATAGCGT CTCTACGTTT ATCTACTGTA GGCGATTATC GGGGGCATGA	1980
GAGTTTGTTT ATCCGTTTGT TGCACGATGA GGAGCAGGAC CTGCATTTT GGTTCAGGA	2040
TATTGAAGAA TTAGGCAAGC AGTACAGGCA ACGGGGACTC TATCTTTTGT CTGGTCCGGT	2100
TGGGAGTGGT AAGACGACCT TGATGCATGA ATTGTCCAAG TCACTCTTTA AAGGACAGCA	2160
AGTTATGTCC ATCGAAGATC CTGTCGAAAT CAAGCAGGAC GACATGCTTC AGTTGCAGTT	2220
GAACGAAGCA ATCGGCCTAA CCTATGAAAA TCTAATCAAA CTTTCCTTGC GTCATCGACC	2280
AGATCTCTTG ATTATCGGAG AAATTCGTGA CAGCGAGACG GCGCGTGCAG TGGTCAGAGC	2340
TAGTTTGACA GGTGCGACAG TCTTTTCAAC CATTCACGCC AAGAGTATCC GAGGTGTTTA	2400
TGAGCGTCTG CTGGAGTTGG GTGTGAGTGA AGAAGAATTG GCAGTTGTTT TGCAAGGAGT	2460
CTGCTACCAG AGATTAATCG GGGGAGGAGG AATCGTTGAC TTTGCAAGCA GAGATTATCA	2520
AGAACACCAA GCAGCCAAGT GGAATGAGCA AATTGACCAG CTTCTTAAAG ATGGACATAT	2580
CACAAGTCTT CAGGCTGAGA CGGAAAAAAT TAGCTACAGC TAAGCAAAAA AATATCATCA	2640
CCCTATTTAA CAATCTCTTT TCTAGCGGTT TTCATCTGGT GGAGACTATC TCCTTTTGTG	2700
ATAGGAGTGC TTTGTTGGAC AAGCAGTGTG TGACCCAGAT GCGTGTGGGC TTGTCTCAGG	2760
GGAAATCATT CTCAGAAATG ATGGAAGTT TGGGATGTTT AAGTGCTATT GTCACTCAGT	2820
TATCCCTAGC TGAAGTTCAT GGCAATCTCC ACCTGAGTTT GGGAAAGATA GAAGAATATC	2880
TGGACAATCT GGCTAAGGTC AAGAAAAAAT TGATTGAAGT AGCGACCTAT CCCTTGATTT	2940
TGCTGGGTTT TCTTCTCTTA ATTATGCTGG GGCTACGGAA TTACCTGCTC CCACAACG	3000
ATAGTAGCAA TATTGCCACC CAAATTATCG GTAATCTGCC CCAAATTTT CTAGGCATGG	3060
TAGGGCTTGT TTCCGTGCTT GCCCTTTTAG CACTCACTTT TTATAAAGA AGTTCTAAGA	3120
TGAGTGTCTT TTCTATCTTA GCACGCCCTC CTTTATTGG AATCTTTGTG CAGACCTACT	3180
TGACAGCCTA TTATGCACGT GAATGGGGGA ATATGATTTT ACAGGGAATG GAGTTGACGC	3240
AGATTTTCA AATGATGCAG GAACAAGGT CCCAGCTCTT TAAAGAAGTC GGTCAAGATC	3300
TGGCTCAAAC CCTGAAAAAT GGCCGTGAAT TTTCTCAGAC GATAGGAACC TATCCTTTCT	3360
TTAGGAAGGA ATTGAGTCTC ATCATAGAGT ATGGGGAAGT TAAGTCCAAG CTGGGTAGTG	3420
AGTTGGAAAT CTATGCTGAA AAAACTTGGG AAGCCTTTT TACCCGAGTC AACCGCACCA	3480

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TGAATTTGGT GCAGCCACTG GTTTTATCT TTGTGGCACT GATTATCGTT TTTCTTTATG	3540
CGGCAATGCT CATGCCCATG TATCAAAATA TGGAGGTAAA TTTTAAAAAT GAAAAAATG	3600
ATGACATTCT TGAAAAAGC TAAGGTAAA GCTTTTACAT TGGTGGAGAT GTTGGTGGTC	3660
TTGCTGATTA TCAGCGTGCT TTTCTTGCTC TTTGTACCTA ATCTGACCAA GCAAAAAGAA	3720
GCAGTCAATG ACAAAGGAAA AGCAGCTGTT GTTAAGGTGG TGGAAAGCCA GGCAGAACTT	3780
TATAGCTTAG AAAAGAATGA AGATGCTAGC CTAAGAAAGT TACAAGCAGA TGGACGCATC	3840
ACGGAAGAAC AGGCTAAAGC TTATAAGAA TACAATGATA AAAATGGAGG AGCAATCGT	3900
AAAGTCAATG ATTAAGGCCT TTACCATGCT GGAAAGTCTC TTGGTTTGG GACTTGTGAG	3960
TATCCTTGCC TTGGGCTGT CCGGCTCTGT CCAGTCCACT TTTTCAGCGG TAGAGGAACA	4020
GATTTTCTTT ATGGAGTTTG AAGAACTCTA TCGGGAAC CAAAAACGCA GTGTAGCCAG	4080
TCAGCAAAAG ACTAGTCTGA ACTTAGATGG GCAGACGCTT AGCAATGGCA GTCAAAAGTT	4140
GCCAGTCCCT AAAGGAATTC AGGCCCCATC AGGCCAAAGT ATTACATTG ACCGAGCTGG	4200
GGGCAATTCG TCCCTGGCTA AGGTTGAATT TCAGACCAAGT AAAGGAGCGA TTCGCTATCA	4260
ATTATATCTA GGAAATGGAA AAATTAACG CATTAAGGAA ACAAAAAATT AGGGCAGTGA	4320
TTTACTGGA AGCAGTAGTC GCTCTAGCTA TCTTTGCCAG CATTGCGACC CTCCTTTGG	4380
GACAAATCA AAAAAATAG CAAGAGGAAG CAAAAATCTT GCAAAAGGAA GAAGTCTTGA	4440
GGGTAGCTAA GATGGCCCTG CAGACGGGGC AAAATCAGGT AAGCATCAAC GGAGTTGAGA	4500
TTCAGGTATT TTCTAGTGAA AAAGGATTGG AGGTCTACCA TGGTTCAGAA CAGTTGTTGG	4560
CAATCAAAGA GCCATAAGGT CAAGGCTTTT ACCTTGTTAG AATCCCTGCT TGCCCTCATT	4620
GTCATCAGTG GGGGATTACT CTTTTTCAA GCTATGAGTC AGCTCCTCAT TTCAGAAGTT	4680
CGCTACCAGC ACAAAGCGA GCAAAAGGAG TGGCTCTGT TTGTGGACCA ACTTGAGGTA	4740
GAATTAGACC GTTCGCAGTT CGAAAAAGTA GAAGGCAATC GCCTATACAT GAAGCAAGAT	4800
GGCAAGGACA TCGCCATCGG TAAGTCAAAG TCAGATGATT TCCGTAAAC GAATGCTCGT	4860
GGTCGAGGTT ATCAGCCTAT GGTTTATGGA CTCAAATCTG TACGGATTAC AGAGGACAAT	4920
CAACTGGTTC GCTTTCATT CCAGTTCCAA AAAGGCTTAG AAAGGGAGTT CATCTATCGT	4980
GTGAAAAAG AAAAAAGTTA AGGCAGGTGT TCTCCTCTAC GCAGTCACCA TAGCAGCCAT	5040
CTTAGTCTT TTGTTGCAAT TTTATTGAA CCGACAAGTC GCCCACTATC AAGACTATGC	5100
TTTGAATAAA GAAAAATGG TTGCTTTGTC TATGGCTAAA CGAACCAAAG ATAAGGTTGA	5160
GCAAGAAAGT GGGGAACAGT TTTTAAATCT AGGTCAGGTA AGCTATCAAA ACAAGAAAAC	5220

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TGGCTTAGTG ACGAGGGTTC GTACGGATAA GAGCCAATAT GAGTTTCTGT TTCCTTCAGT	5280
CAAAATCAAA GAAGAGAAAA GAGATAAAAA GGAAGAGGTA GCGACCGATT CAAGCGAAAA	5340
AGTGGAGAAG AAAAAATCAG AAGAGAAGCC TGAAAAGAAA GAGAATTCAT AGTCAATTCA	5400
ACTATAATGC GTTGAATCCA GAATAGTCCA CTGTAGTTTC TAGAAAATTG CTGGAAATGG	5460
ATGTTAAGCT CCAATTCATT TGTTTATATC TTATTTTCAGT TTAATACTACT TTGTGCTAAA	5520
TTAAAGATAT GAAACATGAT TTTAACCACA AAGCAGAAAC TTTGATTCC CCTAAAAATA	5580
TCTTCCTCGC AAACCTGGTA TGTCAAGCAG CCGAGAAACA GATTGATCTT CTATCAGACA	5640
AAGAAATTTT AGATTTTCGGT GGTGGCACGG GTCTATTAGC CTTGCCCTTA ACCCCTAGCC	5700
AAGCAGGCTA AGTCAGTCAC TCTGTAGAC ATTTCTGAGA AAATGTTGGA GCAAGCTCGT	5760
TTGAAAGTGG AGCAGCAAGC AATCAAGAAT ATCCAGTTT TGGAGCAAGA TTTACCGAAA	5820
AATCCCTTGG AGAAAGAGTT TGATTGCCTT GCTGTTAGTC GGGTTCTTCA TCATATGCCT	5880
GATTTGGATG CGGCTCTCTC ACTGTTTCAT CAACATTGA AGGAAGATGG GAAACTCATC	5940
ATTGCTGATT TTACCAAGAC AGAAGCTAAT CATCATGGAT TTGATTTAGC TGAAGTGGAA	6000
AACAAGCTAA TTGAGCATGG TTTTTCATCT GTGCATAGTC AGATTCTCTA TAGTGCTGAA	6060
GACCTGTTTC AAGGAAATCA CTCAGAATTC TTTTAAATAG TAGCCCAAAA ATCACTCGCC	6120
TAGTCAGGGA GTGATTTTTC TATAAGGATG GAAAAAGAA GGGAAATTG GTAAGATAGG	6180
AATATGGATT TTGAAAAAT TGAACAAGCT TATACCTATT TACTAGAGAA TGTCCAAGTC	6240
ATCCAAAGTG ATTTGGCGAC CAACTTTTAT GACGCCTTGG TGGAGCAAAA TAGCATCTAT	6300
CTGGATGGTG AAACCTGAGCT AAACCAGGTC AAGGAGAACA ATCAAACCTT TAAGCGTTTA	6360
GCACTACGCA AAGAAGATG GCTCAAGACC TACCAGTTTC TCTTGATGAA GGCTGGGCAA	6420
ACAGAACCCT TGCAGGCCAA TCACCAGTTT ACACCGGATG CTATTGCTTT GCTTTTGGTG	6480
TTTATTGTGG AAGAGTTGTT TAAAGAGGAG GAAATTACTA TCCTCGAAAT GGGTTCTGGG	6540
ATGGGAATTC TAGGCGCTAT TTTCTTGACC TCGCTTACTA AAAAGGTGGA TTACTTGGGA	6600
ATGGAAGTGG ATGATTTGCT GATTGATCTG GCAGCTAGCA TGGCAGATGT AATGGTTTG	6660
CAGGCTGGCT TTGTCCAAGG AGATGCCGTT CGCCACAAA TGCTCAAAGA AAGCGATGTG	6720
GTATCATGTG ACTTGCCTGT CGGCTATTAT CCTGATGATG CCGTTGCGTC GCGCCATCAA	6780
GTTGCTTCTA GCCAAGAACA TACTTACGCC CATCACTTGC TCATGGAACA AGGCCTTAAG	6840
TACCTCAAGT CAGACGGATA CGCTATTTTT CTAGCTCCGA GTGATTTGTT GACCAGTCTT	6900
CAAAGTGATT TGTAAAAAGA ATGGCTGAAA GAAGAGGCGA GTCTGGTTGC TATGATTAGT	6960
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AGATTTTGTT ATAATAGTTG AAAACGCTTA AAAAGGGGTA TCATGTTATG ACAAAAACAA	7200
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AAGTATTGGC GAAAGGTTG ATTGAACGTA TCGGTTTGAA AGATTCAATT TCAACTGTAA	7320
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AAATTTTATT GGATGACTTG ATTCGTTTCG ATATTATCAA GGCTTATGAC GAGATTACAG	7440
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CAGGGATTTT GTGGTTTGGT TGTGATGTTG ATGATGAAAA GAATGTCTTT GCGTTACAG	8280
GAGACATCTC AACAGAGGCA GCTAAAAATCC GTGTCTTGGT TATCCAACA GATGAAGAAT	8340
TAGTCATTGC CCGTGACGTT GAACGCTTGA AAAAATAAGT GAACTAAAA AAATATTCAA	8400
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TGAGTTTGA AGAAAACTT TCGTGTAATA AGAGAGAAAG ATTTTAAGGC GATTTTCAAG	8580
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ATTAAGCGAC GGATTGCGCA TATTATCCAG AATGCAAAAG GGAGTCTGGT AGAAGATGTC	8760

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GTTCGTATCT	GAGTTGACAA	ACGCCTTCCA	AGGTATTTC	AACAAATTGT	TGCCAGGTTT	12480
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AGGATTTACC	TTTGGTTTGA	TTGGTCAATT	GATTACAATT	GTTTGTCTCA	TCGTCTTTAA	12600
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GGTCTACGCT	GATAAACGCG	GCGGATGGAA	AGCGGCTGTT	ATCCTTTCCT	TTATATCAGG	12720
TGTCCTTCAA	GTGCTCTAG	GAGCTCTTTG	TGTGGCCCTT	CTCGATTGG	CATCTTATGG	12780
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TACAGTAAAA	GGTTGGAGGG	GGCTGGACAG	AACTGAGAG	TTATCGTTTC	TGTCCTTCTC	13320
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ATCCGACTAG	GTTTAGAGGC	TAACAATTGG	AAAGAAGCAG	TCAAGGTAGC	AGTAGATCCC	13440
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CAGGCTTGCC	AGACTAAAGA	AGATGTCTTG	GCTATGATTG	AAGAATCTAA	GGATAGCCCT	13800
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AAGTGAAGTG	GCTGAAGTCT	TGCGTAGCCT	TTCCAGAT	AAGATTATTG	TGGCAGACAC	14040
AAAATGTGCT	GATGCTGGTG	GAACAGTTGC	TAAAAATAAT	GCGGTTGCTG	GAGCAGACTG	14100

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ATAAACCATC ATGAAATAAC TTTTATGTTG CAGGTTCTAC CTTATTTGCT GTTAAGCTGT	16980
CATAATGTTG AACAGTATCA AGAAAGACAT CAGGATATAG AGAAAGAATT TTCTTTGATA	17040
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CCATACACAG CTGCAGCAAT TCTCAATAAT CCTAAGTTAG AGCATGTTAA GTTGG	18475

(2) INFORMATION FOR SEQ ID NO: 39:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 7186 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 39:

CCAGGATTTG GTACCGTTGC AAGTGGTGTG CCTTTCCTCC TAAAGGAAAA TGGAGGAAAA	60
ATCAATCAAT CAGCACATTC AGATATCAAA GTTGCTAAGG TATTGGTCAA GGATGAAGAT	120
GAAAAAATC GCTTGCTTGC AGCAGGGAAT GACTTTAACT TTGTAACCAA TGTGGATGAT	180
ATTTTATCAG ACCAGGATAT TACTATCGTA GTGGAATTGA TGGGGCGTAT TGAGCCTGCT	240
AAAACCTTTA TCACTCGTGC CTTGGAAGCT GGAAAACACG TTGTTACTGC TAACAAGGAC	300
CTTTTAGCTG TCCATGGCGC AGAATTGCTA GAAATCGCTC AAGCTAACAA GGTAGCACTT	360
TACTACGAAG CAGCAGTTGC TGGTGGGATT CCAATTCCTC GTACTTTAGC AAATTCCTTG	420
GCTTCTGATA AAATPACGCG CGTGCTTGGA GTAGTCAACG GAACTTCCAA CTTTCATGGT	480
ACCAAGATGG TGGAAAGAAG CTGGTCTTAC GATGATGCTC TTGCGGAAGC ACAACGTCTA	540

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GGATTTCAG AAAGCGATCC GACGAATGAC GTAGATGGGA TTGATGCAGC CTACAAGATG	600
GTTATTTTGA GCCAATTTGC CTTTGGCATG AAGATTGCCT TTGATGATGT AGCCCCAAG	660
GGAATCCGCA ATATCACACC AGAAGACGTA GCTGTAGCTC AAGAGCTTGG TTACGTAGTG	720
AAATTGGTTG GTTCTATTGA GGAACTTCT TCAGGTATTG CTGCAGAACT GACTCCAACC	780
TTCTTACCTA AAGCGCACC ACTTGCTAGT GTGAATGGCG TAATGAACGC TGTCCTTGTA	840
GAATCTATCG GTATTGGTGA GTCTATGTAC TACGGACCAG GTGCGGGTCA AAAACCAACT	900
GCAACAAGTG TTGTAGCTGA TATTGTCCGT ATCGTTCGTC GTTTGAATGA TGGTACTATT	960
GGCAAAGACT TCAACGAATA TAGCCGTGAC TTGGTCTTGG CAAATCCTGA AGATGTCAAA	1020
GCAAACTACT ATTTCTCAAT CTTGGCTCTA GACTCAAAAG GTCAGGTCTT GAAGTTGGCT	1080
GAAATCTTCA ATGCTCAAGA TATTTCCTTT AAGCAAATCC TTCAAGATGG CAAAGAGGGT	1140
GACAAGGCGC GTGTCGTTAT CATCACACAC AAGATTAATA AAGCCAGCT TGAAAATGTC	1200
TCAGCTGAAT TGAAGAAGT TTCAGAATTC GACCTCTTGA ATACCTTCAA GGTGCTAGGA	1260
GAATAAGATG AAGATTATTG TACCTGCAAC CAGTGCCAAT ATCGGGCCAG GTTTTGAATC	1320
GGTCGGTGTA GCTGTAACCA AGTATCTTCA AATTGAGGTC TGCGAAGAAC GAGATGAGTG	1380
GCTGATTGAA CACCAGATTG GCAAATGGAT TCCACATGAC GAGCGTAATC TCTTGCTCAA	1440
AATCGCTTTG CAAATTGTAC CAGACTTGCA ACCAAGACGC TTGAAAATGA CCAGTGATGT	1500
CCCTTTGGCG CGCGGTTTGG GTTCTTCCAG CTCGGTTATC GTTGCTGGGA TTGAACTAGC	1560
CAACCAACTG GGTCAACTCA ACTTATCAGA CCATGAAAA TTGCAGTTAG CGACCAAGAT	1620
TGAAGGGCAT CCTGACAATG TGGCTCCAGC CATTTATGGT AATCTCGTTA TTGCAAGTTC	1680
TGTTGAAGGG CAAGTCTCTG CTATCGTAGC AGACTTTCCA GAGTGTGATT TTCTAGCTTA	1740
CATTCCAAAC TATGAATTAC GTACTCGCGA CAGCCGTAAGT GTCTTGCCTA AAAAATTGTC	1800
TTATAAGGAA GCTGTTGCTG CAAGTTCTAT CGCCAATGTA GCGGTTGCTG CCTTGTGGC	1860
AGGAGACATG GTGACCGCTG GGCAAGCAAT CGAGGGAGAC CTCTTCCATG AGCGCTATCG	1920
TCAGGACTTG GTAAGAGAAT TTGCGATGAT TAAGCAAGTG ACCAAAGAAA ATGGGGCCTA	1980
TGCAACCTAC CTTTCTGGTG CTGGGCCGAC AGTTATGGTT CTGGCTTCTC ATGACAAGAT	2040
GCCAACAATT AAGGCAGAAT TGGAAAAGCA ACCTTTCAAA GGAAAAGTGC ATGACTTGAG	2100
AGTTGATACC CAAGGTGTCC GTGTAGAAGC AAAATAAAGA ATAGAAGATA GGATGGGGAA	2160
ACTCTTGACC AGAGGGGTTT ATATCCTTTT TGTGAAAAGA AGTTTATACT CAATGAAAAT	2220
CAAAGAGCAA ACTAGGAAGC TAGCCGAGG CTGCTCAAAA CAGTGTTTTG AGGTTGCAGA	2280
TAGAAGTAC GAAGTCAGCT CAAGACACTG TTTTGAGGTT GCAGATAGAA CTGACGAAGT	2340



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CAGTAACCAT ACTACGGTAA GGTGACGCTG ACGTGGTTTG AAGAGATTTT CGAAGAGTAT	2400
TAGTTAAAAA CGTGATAAAG GAGAAATAAA GATGGCAGAA ATTTATCTAG CAGGTGGTTG	2460
TTTTTGGGGC CTAGAGGAAT ATTTTTCACG CATTTCCTGA GTGCTAGAAA CCAGTGTGG	2520
CTACGCTAAT GGTCAAGTCG AAACGACCAA TTACCAGTTG CTCAAGGAAA CAGACCATGC	2580
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TTATTTCCGA GTTATCGATC CTCTATCTAT CAATCAACAA GGAATGACC GTGGTCGCCA	2700
ATATCGAACT GGGATTATTT ATCAGGATGA AGCAGATTTG CCAGCTATCT ACACAGTGGT	2760
GCAGGAGCAG GAACGCATGC TGGGTCGAAA GATTGCAGTA GAAGTGGAGC AATTACGCCA	2820
CTACATTCTG GCTGAAGACT ACCACCAAGA CTATCTCAGG AAGAATCCTT CAGGTTACTG	2880
TCATATCGAT GTGACCGATG CTGATAAGCC ATTGATTGAT GCAGCAAACT ATGAAAAGCC	2940
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TGCTACAGAG GCTCCATTTA CCAATGCCTA TGACCAAACC TTTGAAGAGG GGATTTATGT	3060
AGATATTACG ACAGGTGAGC CACTCTTTT TGCCAAGGAT AAGTTTGCTT CAGGTTGTGG	3120
TTGGCCAAGT TTTAGCCGTC CGATTTCCTA AGAGTTGATT CATTATTACA AGGATCTGAG	3180
CCATGGAATG GAGCGAATG AAGTTCGTTT TCGTTCAGGC AGTGCTCACT TGGGTCATGT	3240
TTTCACAGAT GGACCGCGGG AGTTAGGCGG CCTCCGTTAC TGTATCAATT CTGCTTCTTT	3300
ACGCTTTGTG GCCAAGGATG AGATGGAAAA AGCAGGATAT GGCTATCTAT TGCCCTTACTT	3360
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GGGATTTATG AAACACCTAT TATCTTACTT CAAACCCTAC ATCAAGGAAT CAATTTTAGC	3480
CCCCTTGTTC AAGCTGTTAG AAGCTGTTTT TGAGCTCTTG GTTCCCATGG TGATTGCTGG	3540
GATTGTTGAC CAATCTTTAC CTCAGGGAGA TCAAGGTCAT CTCTGGATGC AGATTGGCCT	3600
GCTCCTTATC TTTGCAGTAA TTGGCGTTTT AGTGGCCTTG ATAGCTCAAT TTTACTCAGC	3660
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CTTGCCCAAG GACAGCAGAG ACCGTCTGAC AACTTCTAGT TTGGTCACTC GCTTGACTTC	3780
GGATACCTAC CAGATTCAGA CTGGTATCAA TCAATTCTTG CGTCTCTTTT TACGAGCGCC	3840
CATTATCGTT TTTGGTGCCA TTTTATGGC TTATCGAATC TCAGCTGAGT TGACTTTCTG	3900
GTCTTTAGTC TTGGTTGCCA TTTTGACCAT TGTCATTGTA GGGTTATCTC GATTGGTCAA	3960
TCCTTTCTAC AGTAGTCTCA GAAAGAAAAC GGACCAACTG GTTCAGGAAA CGCGCCAGCA	4020
ATTGCAAGGG ATGCGGGTTA TTCGTGCTTT TGGTCAAGAA AAACGAGAGT TACAGATTTT	4080

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TCAAACCCTT AACCAAGTTT ATGCTAGATT ACAAGAAAAG ACAGGTTTCT GGTCTAGTTT	4140
ATTAACACCT CTGACCTATC TGATTGTCAA TGGAACTCTT CTCGTTATTA TCTGGCAAGG	4200
CTATATTTC AATTCAAGGAG GAGTGCTCAG TCAAGGTGCT CTCATTGCTC TTATCAATTA	4260
CCTCTTACAG ATTTTGGTGG AATTGGTCAA GCTAGCCATG TTGATCAATT CCCTCAACCA	4320
GTCTTATATC TCAGTCAAGC GAATCGAGGA AGTCTTTGTT GAGGCTCCAG AGGATATCCA	4380
TTCAGAGTTA GAACAAAAGC AAGCTACCAG AGATAAGGTT TTACAAGTCC AAGAATTGAC	4440
CTTTACCTAT CCTGATGCGG CCCAGCCTTC TCTGAGATAC ATTTCTTTG ATATGACTCA	4500
AGGACAAATT CTAGGTATCA TCGGGGGAAC TGGTTCTGGT AAATCAAGCT TGGTGCAACT	4560
CTTACTTGG AATTATCCAG TAGACAAGGG GAACATTGAC CTTTATCAAA ATGGACGTAG	4620
TCCTCTTAAT TTGGAGCAGT GCGGCTCTTG GATTGCCTAT GTACCTCAA AGGTGCAACT	4680
CTTTAAAGGA ACCATTTCGT CCAACTTGAC TCTAGGTTTC AATCAAGAAG TATCTGACCA	4740
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ATTGTCTATC GCCCAGCAG TCTTGCGCCA GGCTCCGTTT CTCATCCTAG ATGATGCAAC	4920
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AAACACGAGC TTAATTTTGA TCTCTCAACG AACCTCAACT TTACAGATGG CGGACCAGAT	5040
TCTCCTCTTG GAAAAAGGTG AGTTGCTAGC TGTGGCAAG CACGATGACT TGATGAAATC	5100
CAGCCAAATC TATTGTGAAA TCAATGCATC CCAACATGGA AAGGAGGACT AGAATGAAAC	5160
GACAAACTGT AAACCAGACG CTCAAACGTT TAGCCGTAGA TTTAGCAAGC CATCCTTTCC	5220
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TTCTGATTGG GCAGGTCATT GACCAAGTCC TAGTGGCTGG TTCATCACCA GTTTTGTGGC	5340
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ATAAGCTCCA TCGTTTACCG ATTGCCTTTG TAGATAGGCA AGGTAGTGGA GAGATGGTTA	5520
GTCGTGTAAC CACGGACATC GAACAGTTGG CAGCTGGCTT GACCATGATT TTTAACCAAT	5580
TTTTCAATTG TGTTTTGATG ATTTTGGTCA GTATTCTAGC CATGCTCCAA ATTCATCTCC	5640
TCATGACTCT CTTAGTCTTG CTGTTGACGC CACTGTCCAT GGTGATTTC ACGTTTATTG	5700
CCAAGAAATC CTATCATCTC TTCCAGAAGC AAACAGAGAC GAGGGGAATT CAGACTCAGT	5760
TGATTGAAGA ATCGCTTAGT CAGCAGACTA TAATCCAGTC CTTCAATGCT CAAACAGAAT	5820
TTATCCAAAG ATTGCGTGAG GCTCATGACA ACTACTCAGG CTATTCTCAG TCAGCCATCT	5880

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TTTATTCTTC AACGGTCAAT CCTTCGACTC GCTTTGTAAA TGCACCTATT TATGCCCTTT	5940
TAGCTGGAGT AGGAGCTTAT CGTATCATGA TGGGTTTACG CTTGACCGTC GGTGCTTTAG	6000
TGACTTTTTT GAACATATGT CAGCAATACA CCAAGCCCTT TAACGATATT TCTTCAGTGC	6060
TAGCTGAGTT GCAAAGTGCT CTGGCTTGG TAGAGCGTAT CTATGGAGTC TTAGATAGCC	6120
CTGAAGTGGC TGAAACAGGT AAGGAAGTCT TGACGACCAG TGACCAAGTT AAGGGAGCTA	6180
TTTCCTTTAA ACATGTCTCT TTTGGCTACC ATCCTGAAAA AATTTTGATT AAGGACTTGT	6240
CTATCGATAT TCCAGCTGGT AGTAAGGTAG CCATCGTTGG TCCGACAGGT GCTGGAAAAAT	6300
CAACTCTTAT CAATCTCCTT ATGCGTTTTT ATCCCATTAG CTCGGGAGAT ATCTTGCTGG	6360
ATGGGCAATC CATTTATGAT TATACACGAG TATCATTGAG ACAGCAGTTT GGTATGGTGC	6420
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GCCAAGCTCA GCTCTTGACC ATAGCCCGAG TCTTTCTGGC TATTCCAAG ATTCTTATCT	6660
TAGACGAGGC AACTTCTTCC ATTGATACAC GGACAGAAGT GCTGGTACAG GATGCCTTTG	6720
CAAACTCAT GAAGGGCCGC ACAAGTTTCA TCATTGCTCA CCGTTTGTCA ACCATTTCAGG	6780
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AACTCATGGA TAGAAAGGGT AAGTATTACC AAATGCAAAA AGCTGCGGCT TTTAGTTCTG	6900
AATAAGCCAT TCTCTTTTGA AAGTTTATGG ACGAAAAAAG TTGCCTTCGA GTGACTTTTTT	6960
TGTTACAATA GCTAGAAAAA TTGTTCACTG TAATACTCAA TGAAAATCAA AGAGCAAAC	7020
AGGAAGCTAG CCGTAGTTG CTCAAAGCAC AGCTTTGAGG TTGTAGATAA GACTGACGAA	7080
GTGAGTTCAA AACACTGTTT TGAGGTTGCA GATAGAACTG ACGAAGTCAG CTCAAAACAC	7140
TGTTTTGAGG TTGCAGATAG AACTGACGAA GTCAGCTCAA AACAGG	7186

(2) INFORMATION FOR SEQ ID NO: 40:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 14273 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 40:

CTGAAAATTC TAAAAAATTT ATAAGTAAGG AATTAATTAG TTATTTTGT GATAAAGTTT	60
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ATGATGAAAT ATTTGTTGAA GAGGTAGTTC CGCACGTTTT TCTGCCATAT GAATCTGACT	120
TACTTCTTAT TTTACCAGCT ACGGCAAATG TGATTGGCAA AATTGCTAAT GGTATTGCTG	180
ATGATTTAGT TACAGCAACT GTTTTAAACT TTAATAAAAA AATAATTTTT TGTCCCAATA	240
TGAACTCTAC TATGTGGGAC AATCACATAG TTCAAAGAAA TGTATCAATT CTAAGGAGT	300
TGGGACATAT ATTTTTATTT GAGTCTAAAA AAACATATGA GGTAGGATTG CGTAAAGCAA	360
TAGATTCAAC ATGTTCAATG TTACAACCAC AGTCGTTAGT AAAAGAAGCTT ATCAAATTAG	420
AAAATATTGT CCTGAAGAG GGACATTAAA AACTACTGAG AATATTAATG AGGGGAAAAA	480
ATGGAAAATT CATCAATCGA TGTAGATATG CTGTTGGAAG AATTGACACA AGAAGCAATG	540
GTGTTGTTG CTGTTGATAA GGAAGTTTAA TTTAAACTTA TGGCAATATA TGAAAGGTTA	600
CTGGATGTTT TAAATTATGC AGGCAGTAGC CTTTATTAT ATACAAATGG ATAAAGTAAG	660
GATAATACAA TGATTAATAA AAAAATACAA CAAGTTGTTT TGAATCATT ACAGAATTTT	720
TTGAATGGGA ACTTCATTTC GCCTGTGTA GTCTATGATT TTGGCTTGCT GGAACTGTA	780
CTTGATGAAT TTAATAATCA AATTCCTGTA ACATTCAATT ACCAACTTTT TTATGCCGTT	840
AAAGCAAATT CAAATGAGAA GATACTTGAA TTCTTAGTAG ATAAATTTGA TGGAGTTGAT	900
GTGGCGTCAT TATCTGAATT AGATGTGGCT AAAAAATTTT TCCCACCAAC TCAAATTTCT	960
GTTAATGGTG CCGCATTTC TTATGAACT TTATATAATC TGATTAATAA ACAATATAAA	1020
GTTGATATTA ACTTTTTGGA ACATCTTCAA CAATTTTCCC CAAAAGAATC TGTGGAATA	1080
AGAGTAACGG AGCCAGATGA ACTTAATAAT CGTATGAGTC GATTGGAAT AAATATTGTC	1140
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ATGGAAAATC GTTTGAAAGA ATTTTTTCTA TCACTTATGG AAATCTATAA AAAGTACGAT	1380
ATTGATAGTA CTGTGACTAC AATAATAGAA CCAGGTAGTG CAATTACTTC ATTTTCTGCC	1440
TATATGATTA CTAGCCAGT TAATGTTAGT GAGGTGAATG AGCAGCAGGT TATCACGTTA	1500
GACACATCAA TATACACAA TACATTATGG TTTGTTCCGC ATATTATTAC AACGTTAAAT	1560
TCAAGTAGTA AAGAGCGTTA TAGTACTATT CTCTATGGTA ATACCTGTTA TGAACATGAC	1620
AAGTATAAAA TGAAAGTTTC GCTTCCAAGG TTAAGTCAAA ATAGCAGTAT AGTGTTTTTT	1680
CCTGTAGGAG CTTATATAAA AAGCAATCAT TCAAATTTAC ATCGTAATGA TTTTATGCCG	1740
GAGGTATATT TGTGGACAAA AACTTGACA TATTAGATAA AGTTAAGGAA TATTTAGGAA	1800
ATAAACTAC TCAAATTTCTG GATAATCAAT ATAAAGAATT TTTGAACTT AATGATATAA	1860

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GGCGAGCGTT TGGTATTCA GAAAAAGTAT TAAACAATTC TTTTAATTTT ACGAGTAAAG	1920
AATTTAATGA TTTAATTAAT AACGAAAATT ATTTATTCTGA ATATGCATGT AGAATTAGAG	1980
AGGAATGGAG AAAAAAATGC TTTAATCATT CTTATCGTTT TCTATGCTCA CCTATAATTA	2040
CAGATGATTT TCTTAACACG AAGACATTGA GAAGTAGCCA AATTGAATAT AAATATGAGC	2100
GATATTTATC GAAAAGTTCG ATAGGCGATA GAGCGGTTGA TGGCTTTGTT TCCTTCAATA	2160
CTTTAACAGC TAATGGTATG TCTGCTATTA AACTATGTCT TGAGATATTA AACTCTATTT	2220
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TAAATAATCT TGCTAAATCA GGTATTAGTT GCTATGAGGT AAGTAATGT GAATGGATA	2340
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AAACTGATTT CAAGATAGTA GAATATTTTG TTAAGTATAA AAATAATCA ATAAAAGTCG	2460
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GATTAGAATT GACAAATGGG GGAATAATAG AAGTGTTTAT TCCTAATCAT TTGAGAAAGT	2640
TGAAAAATTT TATTGAAGAG GAATTCATAA AATTTAGAAA TTCTCACGGA GCTAATCTAA	2700
GCCTCTATGA ATACTGTTTG CTTGATAATT CTTTAACTTT AAAAAATGAT TGGAATATT	2760
CTGATTTAGT TATGAAATTT ACGAGTAATT TTTATGCTGA TATAAAGAC TTGTTTCATGG	2820
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TATTTCTGAT AAAGTATTAG ATTCTATTTT TAATTCATTC GCATCATTTT TACAGGTGGC	3600

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AGTAGGATTT ATTTTATTGG TTAAGATAGA TATAGGCATA TTTTACTTG CTCTATTTAT	3660
ATTGTTGTTG TTAATAATTA GAACTAGCAA TGCGAATATA GAAACTTCT CTTTCAAATA	3720
TTACAAGAGA GAAGTGTGTC AAGGTACAAA GTTTATTTTA AATAATAAAT TATTATTTAA	3780
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TTTCTATCAA GAAATACCGA GCAGAGCTGG CTATCATGAT GTCTTGCAAG CGATCTATCA	7020
AGGCCAATCA TCGTATTGAT GATCATTCAG CTAGACAACT CCTCTATCAG CTTTCTCAAT	7080
GTGACAATCC CTATAACTGT CCTCACGGAC GTCCTGTTTT GGTGCATTTT ACCAAGTCGG	7140

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ATATGAAAA GATGTTCCGA CGTATTCAGG AAAATCACAC CAGTCTCCGT GAGTTGGGGA	7200
AATATTAAAA GTATAAAAA GTCTGGGAAA AATTTTCAAA ATCAAAAAA CGCATAAAAT	7260
CAGGTGTTC AAAAACTGA TTTTATGCGT TTTATCATGG AAATAGTTAC TTCATTTTTT	7320
CCTAATTCCT TTCGAACTC TTTTAAACG ACGTCAGTTT TATCAGTAAT CTCAAAACAG	7380
TGTTTGTAGC TAATTTTGCC AGTTTGTCT GTAACATCGA AGTTGTGTTT TACCACTCTG	7440
CGACTGGTTT CCTAGTTTGC TCTATGATTT TCACAGAGCA TTAAATGCG ATTTTGCCAA	7500
GTTCCTTTAT TCGTCTAAAA GTAGAGTCTG TTCTATGCGT CTAATGTACG AATCAGGTTG	7560
ACCATTTCAA TAGCTCCTTG TGCACACTCA GAACCCCTAT TTCCTGCTTT AGTACCAGCT	7620
CGTCTATGG CTGTGTCAT TGTATCTGTC GTTAGCACAC CAAACATAAC AGGAATTCG	7680
CTATTTAAAC TGATTTGGGC GATTCCTTA GATACCTCGC TACATACATA ATCATAATGA	7740
CTGTATTCC CTCTAATGAC AGCTCCCAAG CAGATAATTG CATCATATTT TTTACTTTTT	7800
GCCATTTTTG ATGCAATCAG TGGTATTTCA AAAGCTCTG GAACCCAGGC TACCTCTATA	7860
TCTTCTCGT TTACATCTC TCTTTTGAGA TTATCTAGTG CTCCAGATAA TAATTTTGAA	7920
GTATAAATT CATTAAATCT CGCTACAACA ATACCTATTT TAATATTGTT TGCTACTAAA	7980
TTACCTTCAT AAGTGTCAT TTATTTTCC TCCATATTTA AAATGTGACC CATTCGATTT	8040
TTCTTTGTTT CTAAATAAAA ACTATCGTAA GGATTGGCTT CTATTTGAT TGATATTCTA	8100
CTGGAAATGG TAATCCATA TTTTCTAAC TGTTCAACCT TGTCAGGATT ATTTGTCAGT	8160
AAATGAAGTG ACTGAAGTCC CAGATCTTTA AGCATTTTTG CTCCAATATG ATATTCTCTT	8220
AAATCACCTT CAAAGCCTAA TGCAAGATTG GCATCAAGCG TATCCATGCC TTGATCTTGT	8280
AAATGATAGG CTTTAAATTT ATTGATAAGT CCAATTCCTC GTCCCTCCTG TCGCAAGTAA	8340
AGTAAGACAC CCGAACCATT CTCAACAATC ATTTTCATAG CCTTATCGAA TTGCTGTCCA	8400
CAATCGCAAC GTAAAGAGCC TAAAACATCT CCTGTTAAAC ATTCGGAGTG GACCCGACAT	8460
AATACATTGG CTTTCCTCTC TATATTTCCC ATAATAAGAG CAAGATGATG TTCCCCATTT	8520
AGTTTATCTA TATAGCTAAT TGCTTTGAAA TTACCGTATC TAGTAGGCAT ATTGACAGTT	8580
GAAACTCGTT CTACCAGCTG ATCATATACT TTCTATATT CTTGTAATTC TTTGATGGTA	8640
ATTAGTGGA TGTGTGTTT TTTGAGAAC TGAATTAAAT CATCTGTTCT CATCATTTTG	8700
CCATCATGAT TCATTATTTT ACAACATAGG CCACACTCTT TTAGTCCAGC TAATTTAAT	8760
AAATCAACAG TTGCTTCTGT GTGTCCATT TTTCTAGGA CACCACCTTT TTTGCAATT	8820
AAAGGAAACA TGTGTCCTGG CCTGCGAAAA TCAGAGGGTG TTATATCTTC AGCTACACAC	8880
ATACGTGCGG TCAGTCCTCT TTCCTCGGCA GAAATACCTG TGCTCGTTTC TTTATAATCA	8940



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ATTGAACTG TAAAAGCAGT CTTATGATTA TCTGTATTGT TTTCAACCAT AGGTGAAAGC	9000
ATTAATTGAT TAGCTAAACT TTCGCTCATA GGCATACAAA TTAATCCTTT GGCATAAGTA	9060
GCCATAAAAT TAACATTTTC TGTGTAGCT GCTTGTGCAG AACAAATTAA GTCTCCTTCA	9120
TTTTCTCTAT CCTGTGCGTC TATAACAAGA ACAAGTCGTC CCTTCTGCAA TGCTTCTAAT	9180
GCTTCTTGTA TTTTTCGATA TTCCATTGAC TGATTATCCT TTCTGCTAAA ATCCATTTTG	9240
ATATAATAGT TCCTTAGATA TTTCTGATTT TGGAGAGTTA TCCATCAGTT TTTGCACATA	9300
TTTACCTAAG ATATCATTTT CAAGATTAC TGTACTCCCG ACTTGTTTAC TCTTAAGAAT	9360
GGTTTGTTC AAGGTATGAG GGATAACAGA TACTGAAAAG TTTACTTTGG AGACTTTAGC	9420
GACAGTCAGA CTAATGCCGT CAATTGTAAT AGATCCTTTT TCAACTATTA AATCTAAAAT	9480
TTCTTTTGT GTGTGATTT GATACCATAC AGCATTATCA TCTTTTTTTA TTGACGAGAT	9540
TTTTCTGTGA CCATCAATGT GTCTGTAAAC GACGTGACCC CCAAGTCGAC CGTTGACAGA	9600
TAAGGCTCTT TCTAGATTCA CCTCACTTCC ATGTTTTAAT AGAGTAAGAG CTGTTGCACT	9660
CCATGTTTCA TTCATTACAT CAACTGTAAA GGATTGATGA TTGAAATGAG TAACTGTAAG	9720
ACAGATACCA TTTACTGCTA TACTATCGCC TAAATGGATA TCCGTTAATA TTTTGTAGGC	9780
TTTAATTGAT AGTTTACAAT TACGAGAGTC TTTCTGTATT CTTTCAACTT TTCCGATTTT	9840
TTCAATTATT CCTGTGAACA TGGATAAATC ACTTCACTTT CTATGAGATA GTCATTTTCT	9900
ATTTGAGAAA ATGCATAAGG TTTCAATCTA ATAGCGTCAT TTGGCAAAGA AATACCTTCA	9960
CCTCCGACAG GAAACTTGGC ACTACCTCCA AAAACTTTTG GTGCAATATA TATTTTCAGC	10020
TCATCAACAA TTTGTTGTTT CAAAGCACTC CAATTCATTA GACTGCCCCC TTCTAGAACT	10080
AGGCTATCAA TCTGCATGTT TCCTAGATGT TGCATTAAAC TCGATAAGTC TATATGATTG	10140
CCTTTTTTCT TTATGGAAAG TATTTACAG CCATGATTTT GATATAGCTT CATTTTATTT	10200
TTGTCTTCAG AGGAAGTGGC AATGTAAGTT TTAATATCAT TTGCTGTTTT TACGATTTTA	10260
GAGTAAGAG GAGTTCGTAA ATGTGTATCG CATATGATAC GGATAGGATT TTTCCCTTCC	10320
TCCAATCTAC ATGTCAGCAA AGGATCGTCT TGAATAACAG TATTGACTCC CACCATAATT	10380
GCACTAACAT GGTGTCGTAA CTGATGCACA TGCTTTCTTG CTTCTTCTTC AGTAATCCAT	10440
TTGGATTGAT TTGTTTTAGT GGCTATTTTT CCATCCATTG ACATTGCATA TTTCATAAAA	10500
ACATAGGGTA CATGCTGGGT AATATACTTT CTAAACTTTT TTATTAAGTT AAGACTCTCA	10560
TTTTCTAAAA TTCCAACAGT AACTTGAAGA TTATTTTCCT CAAGTATCTT TACTCCTTTT	10620
CCAGATACAA TAGGATTACA GTCTAGGCTT CCAATGACTA CTCTTGTAAT ACCACTATCG	10680

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ATTATAGCAT CTATACAGGG AGGTGTTTTC CCGAAGTGAC AACAGGGTTC AAGTGTTACA	10740
TAAAGCGTCG CTCCGACAGG GGATTCTCTA CAGTTTTTAA GAGCATTCTCT CTCAGCATGT	10800
GGGCCACCAA AAAACTCATG ATAACCTTGT CCGATAATGT GATTATCTTT TACAATAACT	10860
GCGCCGACCA TAGGATTGGG ATTGACGTAA CCAGCCCCTT TTTGTGCCAG TTTTATTGCT	10920
AATTTTCATAT ATTTTGAATC GCTCATCTCG CTACCTCCAA AAAAATATAC CTTGAATAGG	10980
GGACTACTCA AGGCATACAA AAGAAAACCT ATGCGATTAA CAAAATGCT CTGAAATGAC	11040
AAGTAATCAT TTCAGAGCAC GCAAAAAGCA CAAATATACT TTTATCTTCT TTCATCCAGA	11100
CTATACTGTC GGCTTTGGAA TTTACACCAA TCATGCCTTT CGGCTCGTGG GCTATACCAC	11160
CGGTAGGGAA TTTACCCCTG CCCTGAAGAT AGTTATTCAA TTACAGATGA TTATAGTACT	11220
TAATTTTGAA TATGTCAACA GATAAATACC GATTGTTTTT GATATACTGT ATTTGTGATA	11280
ATCGATTCTC GCTCCTCGGA TAAAGAAAAT ATGATATACT AGATAACGA AATAAGAGAG	11340
AAGGAATACT ATGTACGCAT ATTTAAAGG AATCATTACC AAAATTACTG CCAAATACAT	11400
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CTCTGGGATT GGTCTGTAT CAGCTCTGCG TATTATCGCT GCTGATGACA ATGCTGGCTT	11640
GGTTCAAGCC ATTGAACCA AGAACATCAC CTAATTGACC AAGTTCCCTA AAATTGGCAA	11700
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CCTTCTGCC AAGGTCGCAG TGCAAGCAAG TGCTGAAAAC CAAGAATTGG AAGAAGCTAT	11820
GGAAGCCATG TTGGCTCTGG GCTACAAGGC AACAGAGCTC AAGAAAATCA AGAAATTCCT	11880
TGAAGGAACG ACAGATACAG CTGAGAACTA TATCAAGTCG GCCCTTAAAA TGTGCTCAA	11940
ATAGGAGCAG AGAATGACAA AACGTTGTTT GTGGGTCAAG ATGACCAACC CGCTCTACAT	12000
CGCCTATCAT GATGAGGAGT GGGGCCAGCC CCTCCATGAT GACCAAGTAT TGTGTTGAGT	12060
GTTGTGTATG GAAACCTATC AGGCAGGCCT GTCTTGGGAA ACGGTACTCA ACAAACGCCA	12120
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TGAATTGGAA GCCATGCTGG AGAATCCAGC TATCATTCGA AATAGAGCCA AGCTTTTTGC	12240
TACACGCGCT AACGCCCAAG CCTTTCTACA GTTACAGGCA GAGTACGGCT CTTTGTATGC	12300
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AGCGCCAGCT AAAACACCCT TATCTGAGAA ATTAGCCAAA GATCTCAAAA AACGAGGCTT	12420
CAAGTTCACA GGGCCAGTCG CCGTATTGTC TTTTCTACAG GCTGCAGGCG TAGTTGATGA	12480

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CTGATTTTGT CGATTCTCTA TACAGTCCTC TTTATGTTTG ATGGCGTTAA ATTGCTGGCT	12600
TCTTTAATGC CATCTGCCAT TGCAAATTAT CTTGTTTATG TAGTTTTAGC TCTATATGGC	12660
TCCTTCTTGT TCAAGGATAG ATTGATCCAA CAATGGAAGG AGATTAGAAA GACTAAAAGA	12720
AAATTCTTCT TTGGAGTCTT AACAGGATGG CTCCTTCTCA TTCTGATGAC TGTGTCTTT	12780
GAATTGTAT CAGAGATGTT GAAGCAGTTT GTGGGACTAG ATGGACAAGG TCTAAATCAG	12840
TCTAATATTC AAAGTACCTT TCAAGAACAA CCACTACTGA TAGCTGTTTT TGCTTGTGTC	12900
ATTGGACCTC TGGTAGAAGA ATTATTTTTC CGTCAGGTCT TATTGCATTA CTTGCAGGAA	12960
CGGTGTCTAG GTTTACTAAG CATTATTCTG GTAGGACTTG TTTTGTCTCT GACTCATATG	13020
CACAGTTTGG CTCTATCAGA GTGGATTGGT GCAGTTGGTT ACTTAGGTGG AGGCCTTGCC	13080
TTTTCTATTA TTTATGTGAA AGAAAAAGAG AATATCTACT ATCCCTACT TGTTACATG	13140
TTAAGCAACA GCCTCTCCTT AATCATTTTA GCTATCAGTA TAGTAAAATG AAATGAGAAC	13200
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TACTGTAATA TGTGATGAAA ATGCCAGTAA TGATACCGAG AAAAAAGCTG AGAAACTTTT	13320
CCCAGCTTTA TTTGTTATAG TCAAAGAGAA TGACTTGTTT CTGTGCATCT ACATGAGCAT	13380
GGACCCCAAA GGGTACAATT GCTCTTGGAG TTGCGTGGCC GACATTCAGA TTATAGACAA	13440
TCGGGATATT GCTGTCAATG ATATCCAATA GTGCCTCTTT ATAGTCGTCA TGGAAAGTTT	13500
CATCCATAGG TTTTCCGACC AAGAGTCCAT TGATGACCGC GAATATGCCA GTGTCCTTTA	13560
AAGTTAGCAA CATCTTTTGT AAGTCTTCTG GCTTAGGCTT TTCTTCGCTT GTTTCGAGCA	13620
AGAGGATTTT CCCTTCCCAG TCTGACAAGT CAGGAAAAAG TTTGTATTTT TGGCAGAGTT	13680
CCGTGCTATC TCGTATCGA GAGTTGTCAA AGATATCGTA GAGGGATTCT AGGCAACCAC	13740
CGAGGATTTT CCCCTCGAAC TGGGCACTTC CTTGCAACAA GTCAAAACCT GTATTTGTAT	13800
GACTGACACG AGGTGTTCCT AGGGCCGTGG GACTAAAATC AGTTCGTTCC TCATACCAAA	13860
CGTCACTAGG GCGGATTCTT GAAATTCCTC CCGTCTCAAT CAATTCCTTA AAGTAGTGAA	13920
GGCTATAGGC TAGCATTCTT TTGTCTAATT CACAAATGTC TGCTAAAAAG GATTGACCAT	13980
AAAAAGTCTT GATTCTAAT TTATGCAACA TGAGGTGGTT CATGGTTGTA TCCGAGAAGC	14040
CAAGAAAAAT TTTTGTCTG ATAACCTTTT GGAGTTGGTC ATTTTCAAAA AGATAAGGTA	14100
GCAAGCGATA GGTATCGTCT CCACCGATGG CACATAGGAT CATGTCGATG CTATCATCAG	14160
AAAAGGCATG AATCAAAATCC TCTGCACGAG CTTCAGGATG GTCCTTGATA AAGTCTAATC	14220

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CTTTTAACGA ATGGGGCAAA AAGATGGGAT TGGTCCCAGA TCCTTGAGAC GTT

14273

(2) INFORMATION FOR SEQ ID NO: 41:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 9828 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 41:

GTGAAGTCCG GCAAAAGGTG CAAGTGATGA GCTCAGGTTT TTTAGCTCTT GACATTGCCC	60
TTGGCTCAGG TGGTTATCCT AAGGGACGTA TCATCGAAAT CTATGGCCCCA GAGTCATCTG	120
GTAAGACAAC GGTTCGCCCTT CATGCAGTTG CACAAGCGCA AAAAGAAGGT GGGATTGCTG	180
CCTTTATCGA TCGGAACAT GCCCTTGATC CAGCTTATGC TCGGGCCCTT GGTGTCAATA	240
TTGACGAATT GCTCTTGTCT CAACCAGACT CAGGAGAGCA AGGTCTTGAG ATTGCGGGAA	300
AATTGATTGA CTCAGGTGCA GTTGATCTTG TCGTAGTCGA CTCAGTTGCT GCCCTTGTTC	360
CTCGTCCGGA AATTGATGGA GATATCGGAG ATAGCCATGT TGGTTTGAG GTCGTATGA	420
TGAGCCAGGC CATGCGTAAA CTTGGCCCTT CTATCAATAA AACCAAAACA ATTGCCATTT	480
TTATCAACCA ATTGCGTGAA AAAGTTGGAG TGATGTTTGG AAATCCAGAA ACAACACCGG	540
GCGGACGTGC TTTGAAATTC TATGCTTCAG TCCGCTTGGA TGTTCGTGGT AATACACAAA	600
TTAAGGGAAC TGGTGACCAA AAAGAAACCA ATGTCGTGTA AGAACTAAG ATTAAGGTTG	660
TAAAAAATAA GGTAGCTCCA CCGTTTAAGG AAGCCGTAGT TGAAATTATG TACGGAGAAG	720
GAATTTCTAA GACTGGTGAG CTTTGAAGA TTGCAAGCGA TTTGGATATT ATCAAAAAG	780
CAGGGGCTTG GTATTCTTAC AAAGATGAAA AAATTGGGCA AGGTTCTGAG AATGCTAAGA	840
AATACTTGCC AGAGCACCCA GAAATCTTTG ATGAAATTGA TAAGCAAGTC CGTCTAAAT	900
TTGGCTTGAT TGATGGAGAA GAAGTTTCAG AACAAGATAC TGAAAACAAA AAAGATGAGC	960
CAAAGAAAGA AGAAGCAGTG AATGAAGAAG TTCCGCTTGA CTTAGGCGAT GAACTTGAAA	1020
TCGAAATTGA AGAATAAGCT GTTAAAGCAG TGGAGAAATC CGCTACTTTT TCGATTTTGT	1080
ATTCAAGTTT TTAGATTATA TATAGTAGCT TGAAATAAGA TATGAACAAC TCTATTAGGA	1140
AAGTCAAATT AATTTCTAGA AATGTTTGTG CAGCTACAGC GTACTATTCC AAACCAACC	1200
AACTATAATA GATCGAAACT AGAATAGTAC ATATCTACTT CTAAACATT GTTAAAAATC	1260
GATTTGACTT TCCTTATTTT ATTCCGCTAT ATATAGTTTG CTGTTTCTTG TCGCTCCTCT	1320
GGAAAGCTGA TATAATAGCT TTATGAATAA AAAACGAACA GTGGACCTGA TACATGCTCC	1380

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GATTCITCCC TCGCTCTTAA GCTTCACCTT TCCAATTTTG CTATCAAATA TTTTCAACA	1440
GCTCTATAAC ACTGCTGATG TCTTGATTGT TGGACGATTT CTTGGTCAAG AATCCTTGGC	1500
TGCAGTAGGA GCGACGACAG CGATTTTGA CCTGATTGTA GGTTTTACAC TTGGTGTGG	1560
CAATGGCATG GGGATTGTCA TTGCTCGTTA TTATGGGGCT CGGAATTTCA CTAATAACAA	1620
GGAAGCAGTA GCAGCCACCT GGATTTTAGG TGCTCTTTTG AGCATTTCTAG TTATGTTGCT	1680
GGGCTTTCTT GGCTTGATC CTCTCTTGCA ATACTTAGAT ACTCCTGCAG AAATTTCTCC	1740
TCAATCTTAT CAATATATTT CTATGATTGT GACCTGTGTA GGTGTCAGCT TTGCTTATAA	1800
TCTTTTTCGA GGCTTGTTGC GGTCTATTGG TGACAGTCTA GCAGCCCTGG GATTTCTGAT	1860
TTTCTCTGCC TTGGTTAATG TGGTTCTGGA TCTCTATTTT ATTACGCAAT TGCATCTGGG	1920
AGTTCAATCC GCAGGACTTG CTACCATTAT TTCGCAAGGT TTATCAGCGG TTCTCTGCTT	1980
TTATTATATT CGTAAAAGTG TGCCAGAACT CTTGCCACAG TTAAACATT TCAAATGGGA	2040
CAAAAGCTTG TACGCGGATC TCTTGAGCA AGGTTTGGCT ATGGGCTTGA TGAGTTCAAT	2100
TGTATCTATC GGCAGTGTGA TTTTACAGTT TTCTGTTAAT ACATTTGGTG CAGTGATTAT	2160
TAGTGCCAG ACGGCAGCTC GACGCATTAT GACCTTTGCC CTTCTTCTTA TGACCGCTAT	2220
TTCTGCATCA ATGACGACCT TTGCTTCTCA GAATCTAGGA GCTAAGCGAC CTGACCGTAT	2280
TGTTCAAGGT CTTGCAATCG GCAGTCGTTT AAGTATATCC TGGGCAGTTT TTGTTGTAT	2340
TTTCTCTTTT TTGCCAGTC CAGCTTTGGT TTCCTTCTTG GCTAGTTTGA CAGATGGTTA	2400
CTTGATAGAA AATGGAAGTC TCTATCTGCA AATCAGTTCA ACCTTTTATC CCATTTTGAG	2460
CCTCTTGTG ATTTATCGCA ATTGCTTGCA GGGCTTGGG CAAAAGATCC TTCCTCTAGT	2520
TTCTAGCTTT ATTGAACTAA TCGGAAAAAT CGTTTTTGTG GTTTTGATTG TTCCTTGGGC	2580
AGGATATAAG GGTGTTATCC TTTGTGAACC TCTTATCTGG GTTGCCATGA CAGTTCAACT	2640
GTACTTCTCA TTATCCGTC ATCCCTTGAT AAAAGAAGGC AAGGCAATCT TGGCAACCAA	2700
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ACTTGTGTTT TCTTCTTTAG TTTGGTGTG AAAATAGTTT AACAGACTTT TGACTTCTTT	2820
TATATGATAT AATAAAGTAT AGTATTTATG AAAAGGACAT ATAGAGACTG TAAAAATATA	2880
CTTTTGAAAA TCTTTTGTAG CTGGGGTGTG ATTGTAGATA GAATGCAGAC CTTGTCAGTC	2940
CTATTTACAG TGTCAAAATA GTGCGTTTGT AAGTTCTATC TACAAGCCTA ATCGTGACTA	3000
AGATTGTCTT CTTTGTAAGG TAGAAATAAA GGAGTTTCTG GTTCTGGATT GTAAAAATG	3060
AGTTGTTTTA ATTGATAAGG AGTAGAATAT GGAAATTAAT GTGAGTAAAT TAAGAACAGA	3120

400

TTTGCTCAA	GTCGGCGTGC	AACCATATAG	GCAAGTACAC	GCACACTCAA	CTGGGAATCC	3180
GCATTCAACC	GTACAGAATG	AAGCGGATTA	TCACTGGCGG	AAAGACCCAG	AATTAGGTTT	3240
TTTCTCGCAC	ATTGTTGGGA	ACGGTTGCAT	CATGCAGGTA	GGACCTGTTG	ATAATGGTGC	3300
CTGGGACGTT	GGGGGCGGTT	GGAATGCTGA	GACCTATGCA	GCGGTTGAAC	TGATTGAAAG	3360
CCATTCAACC	AAAGAAGAGT	TCATGACGGA	CTACCGCCTT	TATATCGAAC	TCCTACGCAA	3420
TCTAGCAGAT	GAAGCAGGTT	TGCCGAAAAC	GCTTGATACA	GGGAGTTTAG	CTGGAATTAA	3480
AACGCACGAG	TATTGCACGA	ATAACCAACC	AAACAACCAC	TCAGACCACG	TTGACCCTTA	3540
TCCATATCTT	GCTAAATGGG	GCATTAGCCG	TGAGCAGTTT	AAGCATGATA	TTGAGAACGG	3600
CTTGACGATT	GAAACAGGCT	GGCAGAAGAA	TGACACTGGC	TACTGGTACG	TACATTGAGA	3660
CGGCTCTTAT	CCAAAAGACA	AGTTTGAGAA	AATCAATGGC	ACTTGGTACT	ACTTTGACAG	3720
TTCAGGCTAT	ATGCTTGAG	ACCGCTGGAG	GAAGCACACA	GACGGCAACT	GGTACTGGTT	3780
CGACAACTCA	GGCGAAATGG	CTACAGGCTG	GAAGAAAATC	GCTGATAAGT	GGTACTATTT	3840
CAACGAAGAA	GGTGCCATGA	AGACAGGCTG	GGTCAAGTAC	AAGGACACTT	GGTACTACTT	3900
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CTGGTACTAC	CTCAAACCAG	ACGGAACACT	GGCAGACAAG	CCAGAATTCA	CAGTAGAGCC	4020
AGATGGCTTG	ATTACAGTAA	AATAATAATG	GAATGCTTTT	CAAAATCAGAA	CAGCGCATAT	4080
TATTAGGTCT	TGAAAAAGCT	TAATAGTATG	CGTTTCTTGG	TGGAGATATT	TCCTTCAATT	4140
TTGTACTAT	ATTAAACAAA	AATCAAAAAG	CAAACTAGAA	AGTTATGCTC	AAATAAAATC	4200
TAAATTTGAC	AATGTAAACC	GAGTCGGATA	GCTTTAAGTA	CTGTTTGGAG	GTTGAAGATA	4260
CGATTTTGA	TAGGAACTCA	TCAATTTTAG	ATTTTAAAGC	AGCATCAATA	AATTGCTTCC	4320
TTGTTTGTGC	ATAATTTTTT	TATTTAAAAA	ATTATGACma	GAGTGTGCTA	TTCTTTTAT	4380
GAGAGGTGTA	TGAATATGAT	AAATGTATGT	GATAAATGTA	TGTGATGTTG	GAAAAAGAAT	4440
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GAATCAAAGC	ATGATTGCCA	AAATGGAAAA	AGGTGAAAGG	AATATCACGA	ATGGATTTAA	4560
GTAATAAAGC	TTCAATCTT	AGAAAAAAGT	TGGGAGCTGA	TGGTGAATCG	CCGATAGATA	4620
TTTTTAAATT	GGTACAAAAG	ATAGAAAATT	TGACGCTGGT	ATTTTATGGA	CTCGGAAAGA	4680
ATATTAGCGG	AGTCTGTTAT	AAAGGAACTC	AGTTCAGTCT	CATTGCAGTC	AATTCAGACA	4740
TGCCATTAGG	AAGGTAAAGA	TTTTCTTTAG	CACATGGACT	GTATCATCTT	TATTATGATG	4800
AGGTGAAGAA	GAGTTCAGTC	AGTCTTATCT	TGATTGGTGA	AGGAGATGAA	ACTGAAAGAA	4860
AAGCGGATCA	GTTTGCTTCT	TATTTTAA	TTTTCCCATC	TTCACTGTAT	AGGATGGTTG	4920

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AGGAAATCAG AGAAATGCC AATAGAACTC ATCTTGAAGT AGAAGATATT ATAAATTTGG	4980
GTCAGTTTAA TGGTATCAGT CATAAAGCTA TGTATATAG ATTGAGGAAT GATGGATACC	5040
TTGATGCAGA AGAAATTAAA AATATGGATA TTAGTGTTAT AGAGACAGCT TCAAGATTAG	5100
GCTATGATAC AAGTTTATAT CGTCCTTTGT CAGAAAGTAA AAAAGAAATG GCATTAGGAT	5160
AATATATTAA TTCAACTGAA CAACTTTTAG AAAATAACAG AATTTCCGAA GGAAGTATG	5220
AGGAACTGTT ACTAGATGCT TTCAGATATG ATATTGTATA TGGGCTAGAT GAAGAGGGGG	5280
GAGTTGTCGT TTGACTAGTC GTGTATTAT TGATGCAGAT TGTATTTTCA TATTTTATG	5340
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GGTGTATGAT GAAATCAATA TACCTACAAT TCCCCATTTA AAATCTAGGA TAGATCAGTT	5460
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ACTTTTCATA AGGAATCATT TTTATTGATT AAAGAAAAGA GAAGGGGAG TTTGAGTTCA	6300
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TCGAAGTTAT CAGACAGTGA AAAAAAGCAA TTACTTCAAG CTAGAGTTCC GTTTGTAGAC	6420
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GTCCCTAAGG AATTAAACACC TAGCGAACAA TTAACGTGGA TTGCCTTTT ATTGACAAAA	6540
GGTCAAAAAG TAGTAGATGT TGATTGCTT TCACAAGTCA CTGGACTTCC AAACCAACA	6600
ATTTATAGGT GTTTGAGGAC TTTTAAAGCT TTATATTGGT TAAACAAGCA AAATAAGCTT	6660

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TACACATATA CGGTGTCAAA GAAAGAATTA TTCTTAAAAAT CCGTGTCTATG TTTATTTAAT	6720
CCCATCAAAA AACGGATTTT ATTGCCAGAT GGCGATATAA AGCAGATAAA ATCTGTTTCT	6780
AACCTTCTAT ATGGTGGTGC TTATGCTTTG TCGCATTCAA CTTTTTTAGC TGAAACGGAT	6840
GAAAAATTA GCTATGTCAT ATGGCAGAGA AAATTCAATC AGTTATCCTT GCCACTTTCT	6900
CAGCATGTTT TAAAAAGAAA GATGCTAGAG ATATGGAAAT ATCGTCCTTT TGTATCTGAG	6960
TTTTGGAATG ATTTTAAAAA TAATCATGAT AAACAATTTG TAGATCCGAT TTCTCTTTAT	7020
TTGACCTTAA AAGATGATGA TGACCCACGT ATAGAGGAAG AGAGTGAAGC ACTAGAAAAT	7080
ATGATATTAC AGTATCTGGG AGAAGATGAT GCCAGCTAAT ACGAAAGTTA TTTTCAAGA	7140
AATGTTTGGC GATTTTCAGA ACTATTATGT TCTGATTGGG GGAAGTCTA CCTCTATCGT	7200
ATTGGATTCTG CAAGGATTTA AAAGTCGCAC AACAAAAGAT TATGATATGG TCATCATTTGA	7260
TGAAGTAAAA AATAAGGAAT TTTATACTAC CTTGAATCAT TTTTLAGAAT TGGGAGAGTA	7320
TCAAGGAAGT CAGAAAGATG AGAAAGCGCA GCTTTTTCGA TTTACAACAA CTAATCCTGA	7380
GTTTCCTTCT ATGATTGAAC TATTTAGTAT CTTACCAGAA TATCCATTAA AGAAGGACGG	7440
TCGAGAAATT CCCTTACATT TTGACCAAGA TGCTAGTTTA TCAGCCTTAT TATTGGATGA	7500
AGATTATTAT AATATATTGG TGCATGAAAA AGAAACCATT CAGGGGTATT CGGTATTGAG	7560
TAATGTGGT TTATACTCTT CGAAATCTC TTCAAACCAC GTCAGCTTCC ATCTACAACC	7620
TCAAACAGT GTTTTGAGCA GCCTGCAGCT AGCTTCCTAG TTTGCTCTTT GATTTTCATT	7680
GAGTATTAAT TATTTTAAAG GCTAAAGCTT GGCTGGATAT GAGGAGCGC TCTGCCACAG	7740
GTGCTCAAGG TTTAAGTAAG TCCATTAAAA AGCATTTGAA TGACCTTACC CGTTTGACAG	7800
CTTCCTTGCT AGGAGATGAA AAGTTATCGG CTATAACATC AAGTAGTGGG GTAAAAGCAG	7860
ACATGCACCG CTTTGTGATA GAATTAGAGC CTGTGAAGTC AACTATTCTT CAAAATAATG	7920
ACATTTTCATT GGATCAAAAT GAAATTTTGG AAATTTCTGAA AAATTTTCTC GATGGTTAAA	7980
ATAATTGTAG CGAGATGGCT ATATTGAATT CGTCTATATC TGGAACTAG AAAAACTTC	8040
AATTTACAGG AAAAAAGAG TCAATCTTCC CACAATCAAA CGTATAGTAT CAAGGTTTTT	8100
CAAGACCTGA TATTATGCGT TTTTTCCTTT TCAAAACTTT TTGCCCAGTC TTCGTTTTTA	8160
TCCTCTAGTC ACTTGATTG TTTTCAGGTG TTTTITAGTA TAGTAGAATG AAACGAGAAC	8220
AGGACAAATT GATCAGGACA GTCAAATCGA TTTCTAACAA TGTTTTAGAA GCAGAAGTGT	8280
ACTATTCTAG TTTCAATCTA CTATAGTTAA ATCTGCGGTC AAGTCTACTG GTGAATCTAT	8340
GATTGTAATA CTCTTCCAAA ATCTCATCAA CCACGTCAGT CTTGCCTTGC AGTCTGTATC	8400
TTACTGACCA AGCTAGTGAT GGATTTAGAA TAGGTGATTT GGAGCGTCCT ATTAGCTAGG	8460



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AAATGCTGCT CATAGTCCTT TGCTGAGGCT AGGGTGTTTC AACATTCAAC ACTCAACTGG	8520
TTGATCTAGT TGATAGGAAG GGAGTTACTA TAAAATACTC AGGCTTCCAT CATATTTTTT	8580
GAAACGATTG TGTAATCAAA ATGTACCAAT ATTGTAGTAT TGGTACAGAA GATGTTGTGA	8640
ATGGATAAAT ATATCATAAC TGCTATCTCA AAAAGATTTC ATATGCTGTG GCATATATAA	8700
TAGACTTCCT GCAAACTAG AATCCTAGT CATGATTGAT AATACCAGCA ATCAAATTCA	8760
TTCGTAATCC AAAGCGTTTA CGATGATTTC GATAGGTTGT TGAAAACATT TTAAACGTTT	8820
CTACTTTGGC AAAGATGTTT TCAACCTGTC TTCTCTCCTT AGATAGCGCA TGGTTATAGG	8880
CTTTATCTTC AGCTGTTAGC GGCTTGAGTT TGCTGGATT ACCTGGAGTT TGTGCTTGAG	8940
GACATATCTT CATGAGCCCT TGATAACCAC TGTCAGCCAA GATTTTACCA GCTTGTCGGA	9000
TATTTCTGCA ACTCATTTTG AACAACTCA TATCATGACA ATAGTTTACA GTGATATCCA	9060
AAGAAACAAT TCTCCCTTGA CTTGTGACAA TCGCTTGAGC CTTCATAGCG TGAAATTCT	9120
TTTTACCAGA ATCATTGCGT AATTCCTTTT TTAGGGCGAT TGATTTTAC TTCCGTCGCA	9180
TCAATCATT CCGTGTCCTC AGAACTAAGA GGAGTCTTG AAATCGTAAC ACCACTTTGA	9240
ACAAGAGTTA CTTCAACCCA TTGGCTCCGA CGGATTAAGT TGCTTTCGTG AATACCAAAA	9300
TCAGCCGCAA TTTCTTCATA AGTGCGGTAT TCTAGGCTTA ATTTAGGTTT TCGTCCACCT	9360
TTTGCGTGT TAAGTTGATA AGCTGTTTTT AATACAGCTA ACATCTCTTT AAAAGTCGTG	9420
CGCTGAACAC CAACAAGACG CTTAAATCGT GTATCAGTTA ATTGTTTACT TGCTTCATAA	9480
TTTCGCAGGG AGTCTATTGA CTCTTTGGTA GGTGTCAATG TTTTTTTCAT CTATCCCGAG	9540
AATTATTTTC CCGCCATTG TATTGCAAA TGCTGAGTAG GTTCCCAGA AAGACTCTGG	9600
AAGATTGTTT TTAGCTTTTT TGTATTCTAA ATCAACCCCT TCAAATTTTA AGTCCATATT	9660
TTTCCTTTAC ATCTGTTTTT TGTGGTTCTG GTATTTGTTT AAGTTGAGTG ATAATATAGC	9720
GAATTGAATT TCGAGAGTTT TTAATCAGTT AATTTCTTTT TTAACCCACT TTAATTGCTT	9780
TTTTAACACG GGTAAAAAA GAAATTAAAG TGGGTTAATT TTTCTTGA	9828

(2) INFORMATION FOR SEQ ID NO: 42:

- (1) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 3369 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 42:

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CCGCGAAAGA TATTTTGTAA CAAGAGTTTG GACGTGAGGT CCGTGGCTAT AATAAAGTAG	60
AAGTTGACGA GTTTTGTAGAC GATGTCATCA AGGACTATGA AACCTATGCT GCCTTGGTCA	120
AGTCACTTCG TCAGGAAATT GCGGATTTGA AGGAAGAATT AACTCGTAAA CCGAAACCTT	180
CACCAGTTCA AGCAGAACCC CTTGAAGCGG CAATTACAAG TTCTATGACG AATTTTGATA	240
TTTTGAAACG CCTGAATAGA TTGAAAAAG AAGTTTGTGG TAAACAAATT TTAGATAACT	300
CAGATTTTGA AGTAGTTATT TGAGATGTGC AATTTTGTGA TAATCGCGTG AGGAGAATTG	360
TTTCTCATGA GGAAAGTCCA TGCTAGCACA GGCTGTGATG CCTGTAGTGT TTGTGCTAGG	420
CGAAACCATA AGCCTAGGGA CGAGAAATCG TTACGGCAGT TGAAATGGCT AAGTCCTTGG	480
ATAGGCCAGA GTAGGCTTGA AAGTGCCACA GTGACGGAGT CTTTCTGGAA ACAGAGAGAG	540
TGGAACGCGG TAAACCCCTC AAGCTAGCAA CCCAAATTTT GGTGGGGCA TGGAGTACGC	600
GGAAACGAAC GTAGTATCTT GACTGCTATC AGCTAGAGCT GTTAGTGGTA GACAGATGAT	660
TATCGAAGGA AGTGGTCCTA GTCACCTCTG GAACAAAACA TGGCTTATAG AAAATTGCAT	720
ATAGGTTGGG GCTGAGAAAT TTTCTCAACC TCATTTTTTA AAGTGGACAT ATAGAAAGGT	780
CTTGCAAGAC TGTAACATGA AAAAAGAATT TAATTTAATT GCAACTGTGG CAGCAGGGCT	840
TGAGGCTGTC GTTGGTCGTG AAGTGCAGGA GTTGGGCTAC GATTGTGAGG TTGAAATGG	900
ACGTGTTGCT TTTCAAGGAG ACGTGAGAGC TATTATCGAA ACCAACCTTT GGCTTCGGGC	960
AGCAGATCGT ATCAAAATTA TCGTAGGAAC GTTCCCAGCT AAGACTTTTG AAGAGCTATT	1020
TCAGGGAGTT TTCGCTTTGG ATTGGGAAAA TTATTTACCA CTGGAGCTC GGTTCCTGAT	1080
TTCAAAAGCT AAATGTGTTA AGTCCAACT TCACAATGAG CCCAGTGTTC AGGCTATTTT	1140
TAAGAAAGCT GTTGTCAAGA AATTGCAGAA AACTATGCT CGCCAGAAAG GGTTCTCTCT	1200
GATGGAGAAT GGCCAGAGT TTAAGATTGA GGTCTCTATT CTCAAAGATG TGGCAACTGT	1260
CATGATTGAT ACGACCGGT CTAGCCTCTT TAAACGTGGT TATCGTACCG AAAAAGGTGG	1320
CGCTCCTATC AAGGAAAATA TGGCAGCAGC CATTTTACAA CTTTCTAACT GGTATCCAGA	1380
CAAGCCTTTG ATTGATCCGA CCTGTGGTTC GGGGACTTTC TGTATTGAGG CAGTTATGAT	1440
TGCTAGAAAG ATGGCGCCAG GTCTTCGTCG CTCTTTTGCA TTTGAGGAAT GGAAGTGGAT	1500
CAGCGATCGC TTGATTCAAG AAGTGCGCAC AGAAGCGGCT AAAAAAGTAG ACCGTGAGCT	1560
TGAGCTGGAT ATCATGGGCT GTGATATTGA TGCTCGCATG GTGGAAATTG CTAAGGCCAA	1620
TGCTCAGGTA GCTGGTGTG CAGGAGACAT TACTTTTAAG CAGATGCGCG TGCAGGATTT	1680
ACGTTCCGAT AAAATCAATG GAGTAATCAT TTCCAATCCG CTTATGGTG AACGTTGTG	1740
AGATGATGCA GGGGTGACCA AGCTCTATGC TGAGATGGGG CAAGTATTTG CACCGCTGAA	1800

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AACTTGGAGC AAATTTATCC TGAAGCTTTT GAAAGCAAGT ATGGTAGCCA	1860
AGCAGATAAG AAGCGTAAGT TATACAACGG AACCTTGAAA GTGGATCTAT ATCAATATTT	1920
TGGTCAGCGT GTCAAACGGC AAGAGGTAAA ATAGAAAGGG ATACTCATGA GTAAAAAAG	1980
ACGAAATCGT CATAAAAAAG AAGGTCAAGA ACCGCAATTT GATTTTGATG AAGCAAAGA	2040
GCTAACAGTT GGTCAAGCTA TTCGTAAAAA TGAAGAAGTG GAATCAGGAG TCTTGCCTGA	2100
GGATTCCATT TTGGACAAGT ATGTTAAGCA ACACAGAGAT GAAATTGAGG CGGATAAGTT	2160
TGCGACTCGT CAATACAAAA AAGAGGAGTT CGTTGAACT CAGAGTCTGG ATGATTTAAT	2220
TCAAGAGATG CGTGAGGCTG TAGAGAAGTC AGAAGCTTCT TCGAGGAAG TTCCATCTTC	2280
TGAAGACATC TTACTACCCT TGCCTCTGGA CGATGAGGAG CAAGGCTTGG ATCCTCTATT	2340
GCTAGATGAT GAAAAATCCAA CAGAAATGAC TGAAGAAGTG GAAGAGGAGC AAAACCTTTC	2400
TCGTCTGGAT CAAGAGGACT CAGAAAAGAA AAGTAAAAAA GGCTTTATTT TGACCGTTTT	2460
GGCGCTGTA TCAGTAATTA TTTGTGTCAG TGCTTATTAT GTCTACCGTC AAGTGGCTCG	2520
TTCGACTAAG GAAATTGAAA CTTCTCAATC AACTACAGCC AATCAATCGG ATGTGGATGA	2580
TTTTAATACA CTTTATGACG CCTTTTACAC AGATAGCAAT AAAACGGCTT TGAAAAATAG	2640
CCAGTTTGAT AACTGAGTC AACTCAAGAC TTTACTTGAT AAGCTGGAAG GTAGTCGTGA	2700
ACATACGCTT GCCAAATCTA AATATGATAG TCTAGCAACG CAAATCAAGG CTATTCAAGA	2760
TGTCAATGCT CAATTTGAGA AACCAGCTAT TGTGGATGGT GTGTTGGATA CCAATGCCAA	2820
AGCCAAATCG GATGCTAAAT TTACGGATAT TAAACTGGA AATACGGAGC TTGATAAAGT	2880
GCTAGATAAG GCTATCAGTC TTGGTAAGAG CCAGCAAACA AGTACTTCTA GCTCAAGTTC	2940
AAGTCAAAC TGCAGCTCAA GTTCAAGTCA AGCAAGTTCA AATACGACTA GTGAGCCAAA	3000
ACCAAGTAGT TCAAATGAGA CTAGAAGTAG TCGCAGTGAA GTCAATATGG GTCTCTCGAG	3060
TGCAGGGGTT GCTGTTCAAA GAAGTGCCAG TCGTGTGCC TATAATCAGT CTGCTATTGA	3120
TGATAGTAAT AACTCTGCCT GGGATTTTGC GGATGGTGTC TTGGAACAAA TTCTAGCGAC	3180
TTACAGTTCA CGTGGCTATA TCACTGGAGA CCAATATATC CTTGAACGTG TCAATATCGT	3240
TAACGGCAAT GGTATTACA ACCTCTACAA GCCAGATGGA ACCTATCTCT TTACCCTTAA	3300
CTGTAAGACA GGCTACTTTG TCGGAAATGG CGCTGGTCAT GCGGATGACT TAGATTACTA	3360
AGCAGTCGG	3369

(2) INFORMATION FOR SEQ ID NO: 43:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 9713 base pairs

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(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 43:

AAGTTTACAA TTTAAATGAA TTAACAATTT TCCCAACTAA AAGCACTCCA GTTACCGCAA	60
CGTTTGTA CT GAATGTACTA AATCGCATTC CATCAACTTC ATCTGTTTCG TCAACTTGAA	120
CAGATACTAA TTGAAGATTT AATACTTCTG CTGCCATAGC TAGCTCCTCC TATTTAAATT	180
TTTGGGATTA AGTACTTTAT CCACCTCAT ATACTCTCTC CACCAGTAAA ATGCAAGCAA	240
TGATACAAAA TAGATTTAAC TATTTTATAT AGCGAAAAC TACAAATTTT TAAGAAATAA	300
TTTTTGCA TTCTAAAGATA AAATAGGAAC TTTTAGTAAT AAATATTAAA ATAAATAAAA	360
TAATAGATAC TATAAAATTT GGAAGTATTA ACCCAAAAAG ATTCATATCA TCTATTAAAA	420
TATCCTCTAA AGAGTAGTAT ATTAAGCCA TAATTTTAAT GTTAAGTAAA AATGCAATTA	480
ATGAAGTAAC AAATGTCAA AATATAGCCT CACCAACTTT AATCTTAACC ATCTGGTAAT	540
TAGAAGTTCC TAAAATTTCA AATTGCTGAA TCTCAATCCT TTCTTGATGC GATGACAAAA	600
ATGCAATTGA AATAATATTT GCAAGTACTA TCAAAATTGG TGCTCCTACA TAGACAATAA	660
ATGCTACTTT TAGCTCTAAA TCACTGTCAT CTTGAAATTG AGATAGTATA TTCTGAGAAA	720
TCATTTGAAA ACTAGAAATT AGTAATATAG CTCCTGTAAT TGCAGCACTG ATAGATTTTA	780
TATAAGACTT ACAATATAGT AAATCCACT TCGAAACAAT GAACATAAAA TTATTTCTAA	840
ATATAATTAT AGAAAGTAGT TTGATAAAAC ATGACTGTAT AAAAGGAGAT AATTGATAAA	900
TAATCACAAT ATCTAAGATT ACAATATTGA ATATTATCTG GGCCTTCGCT AAAATTGTGC	960
TATCTTGCAA AATTTGTTGC AAAGAAAGCA ACCAGATAAC ACTAAAACCA GCCAATAGCA	1020
GTATTCCTTT TACTATTGAA AGAACATGCC TTATTTTAGA ACTCTTCCTA TTTCTAATCT	1080
TCTTGAACGT ATAAAAGCAA CCACTTAGAA AGGCTAAAAA TGAAATCAAC ACTACTGTAA	1140
TGATACATCC AACAGCACTC GTTTGAAATT GGATATCAGG TAATATATTT TCCCCGAAAA	1200
AGTATTGTAA AAAATAATAA TAATTTGACG TAACAAATAT AGAGCATAGA TATGCAATAA	1260
AACTAATAAT CGAGGAAATG ATAAAAATCT GTCCCCCAC AAGAAATGAT AGTTGAAGGC	1320
GACTTGCTCC CAACACCTCC AGAAGTTCGT AATCATCTCT AAAAATTTCA ACCAACATAT	1380
TTATTATGTT AGAGAGCACA AAGAATAATG TTA CTCTCTCC GAATACTATC GGAAACATAA	1440
AAATTGGTTT AGGATCTGGA AGTCCGACAA ATACTTGCGA ATTATTCTCA ACATTAATTA	1500
CCCCATTAAC AGCCAATCCC ATAACATAAC TCGAAACAAA AATTACTGGT GAAACGCCTA	1560

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ACCATGTTT CTTATTATGT AAAAAATTGAT AGTAAACTAA TCTGAGCATC TCTATTCCTC	1620
CGTAGTTGAT TGTACCTCTA AGATTTTATA CAACTCTTCC CCGCTAGGTC TATGAAGTTC	1680
TTTGAAATTT TTTCCATCTT TCAATATTAA TGCACGATCA GTTTTCGAGG CCAATTCTAT	1740
ATCGTGCGTT ACCATAATTA CACACTTACC CGCCCTACT AACTCTCTCA ATAATTCAAA	1800
AATTACTTCA CGAGAAACGC TGTCTAAAGC CCCAGTTGGC TCATCAGCAA ATATTATATC	1860
ACTATCAGCA ATAACCGCTC TAGCTATAGC AACCTTCTGT TGTTCCTCCAC CAGACAGAGT	1920
TCCAACAAAA TCGTTTAAAGC CAGCATTAAA CTTTCTCTT TTGAGTAAGT TTTCTACATT	1980
TTTAATAGTT AATTTTTTTT GTGATAATCG CAAAGGAAGT GCTATATTTT CTATTACCGG	2040
CAGGAAGGT ATTAAATTGT ATGCTTGAAA TATAAAGAT ACTTCGTTAC GTCTTATACT	2100
TGACAATTTT GCATTTCTGA TTTTATAGGG GTTGATTCCA TTTAAATTA CTTCCCACT	2160
TGTTGGTTCA AGCAAACTAG AAATACATTT TAATAAAGTT GACTTTCAG AACCACTAAT	2220
TCCTAGAATA CTTATAAATT CTCCTCTCGA AGCAGAAAGA GAAACATTTT TCAGCACTTG	2280
CAACGTTTTA TTATTTCTTA GTAAAAATG ATGATACAGC CCTTTCACCT TTAATATATA	2340
ATCTTTATCC ATATTCTTGC CTCCAATCAC TTAATTTTGA AAAGTGTCC ATTTTCCAAT	2400
TTATATATAT CAGTGATCT CTTGTCAATT AAGTCATAAT GATGTGAAAC TTCAATAAAT	2460
GAAATACCTA AATTGAACAG AATATCATGT ATGGAATTG AATTATCATT ATCTAAATTA	2520
GCTGATATTT CGTCAAATA GTACACTTTA TTATTTCTAA TCAGAGCTCT AGCTAAAGCT	2580
ATTTTTTGT TTTGACCTCC AGACAAATTA CTACCATTTT CACCACATTG ATAATTTAGT	2640
ATATCTATCT TTTCTAATTC TTCATATAGA TTTACCTTTT TTAACACCTC AATTATCTGA	2700
TCATCTGAAA AATATTCATT TTGAAATAA GTTACGTTCT CACGAATAGT AGTGTCAAAA	2760
ATATATGGTG TCTGATCAAC TGTGGTATT GAATCTGAAC TCTTTTCCC ATGTGATAAC	2820
AAATTTACAT AACCTTTTTG TGGCTTTAAA GAACCATTA TTAATTTAA ATCGTTGTT	2880
TTCCCACTAC CAGAAGTCC TGTTAATAAT ACCCTAAATG GTGACTTAAA TGAGAAGTCA	2940
ATACTTAATT TATTTCTGG TGTAAATAGAA TATACAACAT CTTTCATGTG TATCTCATCT	3000
ATTGATGAAG TATACAGTCC GTTATTATCA TGTTGAGCGT CTATAAAATT CTTCTCTCCA	3060
CTTAAGTATT TAAAAACGG TTTCTTTAAA TCTTTGGTTG TATTTATCTT ATTTAATGAA	3120
TAGGCAATTG ATTGTATCGG CCCTAAAACT TTATCGTTTG CTAAGAAAAT ACCTATCAGT	3180
TCATAAAAG AAAGGCTTTT ATGATAAATT AAAAAATAAC ATCTACAAC CAAGGGAAC	3240
AGAAAGCAAA AACCTGAAAT TAGTACTGCA ACCAATTTTG AAAGAACCTC TGATCGTTTC	3300

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AAATTAAAAG TAGAATCTTC TAGTTTATCC AACTTTTAT CCGACAACT AATTATTTCT	3360
TTAGTAACAG AATAAGATTT TAATGCTTA AAACCATTAA AAATTTCTTT TATTATGTGA	3420
GTATACTCTG CATTGCTGTT AGAGTACTCA TTAGCTGAAT TAGACAACAT CTTCTTCATA	3480
AAGACAGGTA CTATAATCGG CAATGCTGAT AATACAATAA ATATTATTGA nACTAGGAAG	3540
TTTAAATAAA GCATAAACT TAGAGAGACG ATGAACAACA ATATTGAAGA AATTATTTCA	3600
AAAATTTGTC TAAATAGTT TTCTTCGATT AATCTCAAAT CATTGACAA AACTGAAATA	3660
ATAGATGAGT AATCTTTAAC CATTTAGAA GAAAGATACT GTTCTCTAAA ATATCCTTGT	3720
TTAATTTTTA CATTTATATC TTTAGTTATT GATGCTCCG TTACTTCTAA ATAGTAATTT	3780
GATATATAGA TTGCTGACCA ACCCAGAATA CTTATAGCAC CAAATCTTAG AACGTCAGAA	3840
AATGAGGAAG TCTGATTTAA ACTACCTGCA TATACAATAA TTCCTGAGAG CAAGACACCA	3900
TTAAACGAAG ATAGAAATAT TAAATCCCC ATTAATATAA GTTTAGTCTT TTTTATAAAT	3960
TTTAAATAAT TCATAAGTTA TTCCTTCCCA CTTCTTCAAA GAAATAATTT AAAGTATCAA	4020
TCATTAAAGAG AACATCTGAT GGAGTAAAC CTCCATGACC AGCTGCTTTG TTTAAATACA	4080
ACAACTTTT AACTCCAATA GAATTTAATT TCTTTGACCA CTCTATCACT TCGTTATTAT	4140
TAATATATGG GTCTTTCTCA CCAAAATAT TAATATAAC AGTATTTGAG TCTCGTGCCT	4200
TTTCAATATT TTGCATAGGC GAATATGACT TTATATAAGC CTTTACTTCA GGGTCTCTAA	4260
TATCTCCCCA CTCTGCTATT TCGGTCTTAG AAAGAGGATC ATTTGGATTG TGAAGTGTAT	4320
CATAAGGATT TATAAATGGC GAAATAAGA GAATGCTTTG CAATAAATTT TTTTCTCGT	4380
TCAACACCGC ACCAGCAATT ATTCCACCTG CACTAGAAGT TATTAAACCT AATCGCTTAC	4440
TGTCAATTAC ATCATTTTCC CTTAAATAAT TTAATCCCTC AATAAAATCT CTGATAGAAT	4500
TCCATTTGTT TAACGCCTTT CCTGAGCGAT ACCATTCAAC ACCCAAATAG CCTCCACCTC	4560
TTACATGAAC TATAGCATAA ATAAAACCTG CATCTATTAT AGATAACATA ATTTATCTTA	4620
AATCAGAAAT ATCATTTCTTA CCATAAGCCC CATAGACACT TAGAATACAT TTTTCTCTTC	4680
TTGGGAGCTC ATCCGTATCT TCACTTTTCC AAAATAAAGA AATCGGTATG CTTACATCAT	4740
AACTGTCTTT TTTAGTCCAA ATCACCTTAG AAAAATATTT AGTATTATTC GATTTTATGA	4800
TGGGTCTTTC AAATTCAGTT TTTAATGTAT TTTCTATTAA ATCAAACTA AGTATTTTTT	4860
CGTAAAAAGT TCTCCTCTCT AAAACAGAA GAACACGATC AGAAATGAA TTTTCATAAA	4920
GTGTGTCTT TTCATCAAAT GTTATCTTAT TAACACTCAA CTCCCTCAA CTATTATTTT	4980
TAAATGTAGC AAGATAAAG ACGGAATTCG CTGCGTTTGA ACAGTCTAAA AGGATATAAC	5040
GTCTTATACA GTGAACTCTT CTAGCCCTAT CTTGATATGG TATAGTAATA GAACTCTGT	5100

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CTCCGAAGA AGTTTCCCTT AGAATTAGTT GATCTTCTT TTCTTCAGTT GAAGAGAGCC	5160
CAAGAAAGTA CTGTGCTTTT TCTGTACTAA ATAGAGCGAT ATCTCTAGGT GTTGGGGCTA	5220
CCGTTTCTGT GTAAGAGTGT CTAACAAAAC CCGTCCGGTC GAAACTGTAT AGAAAAATCC	5280
TGCCTTTCTG AAAGTCTACT GACTTTACAA AACAATTATT GCTATCAATG TGGACTATTT	5340
TTAATCGAAA AGAGCATTCG TTTTCTTCAA ACAGTTCCTC TTCTGTAAAG CTATCAAAAG	5400
ATTTATAGAA TAACCTACTT GGCTCCCGT ACTCTTTGGA GCGAGTATAC ATAACACCGA	5460
ATTTACCCAA ATAGAACGAA CTTTCTACTG AAATATCTTC AATGATAAAT AACTCTTCCA	5520
TAGTATATTT TTTTATTCCA ATTAAATTAG TCGTACGCAG TGAGGATACA ACCAAAATA	5580
TATAACTCTC ATCAGATGAA ATCCTAACAT CCTGTAAGAT ACTATCATCT GGCAAAGTAT	5640
ATTTTCCAC ATCAAAGACA ATTTTAAGTG AATTTGAATT GTCTAACTG GAAGAACTAA	5700
CCTTAGGAAT CCAGTCATTA TCTTCGACAT ACCATTCCTT TATTACACCA GTATTGGGTA	5760
TACTCCAATT ATCAAATTGG TACCAATATC GCCCTCTCCT AAATATCAAA GAATPCCATT	5820
TTTTAATTC CTGAAATGAT GAAGAGATAG ACCTCTTATA GTGTGTTTTT TCCTGTATTG	5880
TATTTAAAAA TATTCATTA CTCTGATTCA CAAGTATGAC CCCTTAATAA TGGTATCTAA	5940
ATATTATATT TGAGGAAGAA TCGTCAATTT ATTATCCATT ATTGATACCA ATCCAATTGC	6000
AACCCCGCA AATCCCGAAG CAATATCTGT TGTATCTTT AAACCATAT CTCCGCAAT	6060
AACAAATCCT TCTTCAATTA CACACAAATA TCTATAAAGT TGTTCATTA ATTTCTTTTG	6120
TCCTGAAAAG TTATCATCGA TATCACTATA TATATTATTA GCAACTTCAA GACCACAAA	6180
TCCGTAAAT AAACCTGGTA ATACACAAA AACTACATCA GTTGCCCTCT CTAAGAAGT	6240
TAAATATTTT AAGTATTTGC TTGACAAGAT TTCTTTATTT CTATTAATAA GTAAAAGCAG	6300
GCCAGCACTT CCAGTTGCTA GATATGGTAG TAATCTATGA CCTTGGCTGT ACTGCAATGA	6360
ATTATTACTA TCTACTTTAT AAGCAACTAA TTCTTTATCT ACAGCCAATT CTAGACCATT	6420
TTTATAGATA CTTTCAACCAG TTAATTTATA AGCTTCACCG AAGAGCCAAG CTACCCCTGC	6480
GTGACCATAT AGTAATCCAC CAAAATTCTC ATAAGGATCG TTAATCTGAA CATCACTAGC	6540
GCCAACTTTA CAAAAGTTT CTGGATTTTC TATATAATTT AAAGTATATT CTCTAAGCCT	6600
AATTAGTATT TCTTCTCCTA GTTTATTATC AATTCCCCCT TTAATAAGAA AATACAGTCC	6660
AACCAGTAAA ATTCCAGCCT GCCCACTATA TAAATTTTTA TTTTGTGAAT TCTCAAATAT	6720
CTCTATAAAA TGAGTTGTAA AAAGTTCAAC TGCCCGATCT ATCTCCCCAA ATTCATAAAT	6780
GAGCCAGATT GTACCAATTT TACCATCAAA AAGACCAGAA AGGGACGATT TCTTAAAATT	6840

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ATTTACTGCC TCATTAATAA CCTGTGTTTCG AATCTCATAA TAGTCATCAA ACTTGAAATT	6900
TTTTACTTTC TTAGCTAGTT GTTGATAACT CCAAAGGATA GCTAAATCTG AAAACGCAAT	6960
TCCTTGATTA AAATTCAGAC CATAATAATG AACTGGGAAG AATCTTGATT GAAATTCCTT	7020
ACGCCACTGT CCATAAGTTA GCGTAAACCC TCTCAATAAT TTTATAATAA AATCTTGTAT	7080
ATCTTGCTCA CTCTCGATAG TTCTAATCTC ATGCATGGGT TTTAAACTT TTTTCCTGGA	7140
AATATTCTCA ATCTGTGGAC ATTTAGAATC TAGATATGAC AATAAACTTT CTACATAATC	7200
TATATGTTCT CTTGTATAAC CCAAAGACTC AAATAGTTT TTTCTTCTA TCCTGGTTTG	7260
ACTTACATAG TTGTATGTCA AATCCGATGT AGTTACTAGT GGCATGTATA AATAATGAGC	7320
TATTTGTCTA ATACCATACC AATCTATCTC ACTGGGAAGT GTTCTCGCC ATGCTCTAAA	7380
ACCAGGGGCT GCAACTTTAT GTACAACCTT TTCATCATTT GAAAAGACAG CCTGTTCCCA	7440
GTCTATTATA CTAATCTCAT CTTTCATCCTT AACCAAGATA TTTCTTAAAT GTAAATCTTG	7500
ATGATATACA TTTTCAGAAT GAAACTTATT CGTTAAATCG ATGAGTTTTT CTACTATCTT	7560
TGAAACTCTC AATAGATAAT CTTTGGTCTT ATCAACAAC TCATATAAAG GAAATTATT	7620
GGTAACCCAT CTATTTAGTG GAACGCCCTT CATATGTTCA ATTCTTAAGA AGGTGTGCTC	7680
CCAGATCTTA CCGTGCCAGT ATATTTTAGG CGTCTCACTC CATTCATTTA GAATTTTAG	7740
TGCTTTGCAC TCCGAAGCTA ATTTCTCTGA AGAATAAGTA CCATCAAATC CTAGACCTGT	7800
ATACGGTCTA GCCTCTTTTA AAATTATTTT TTTCCCATCT TCTTTTAGCC TAGCATTATA	7860
TATCCCACCA CTGTTTGAAA ATCTAATTGC ATTATCTATA ATAAAGGGAA AGTCTCCCTG	7920
TTTTTTATCT TTCTTGTCAA GCCATTTATT CAAAAAGTCA GGGGGCACTA TACCTTTTGG	7980
AATTTTAAAT ACTGGTAAAC GTTCATCTTT AACAACTTCA TCGCCAACAA TTAATTCATC	8040
AATAGCAACC TTCTTTTCAT CATCCCTTGA CGGCCTAAAC ACACCATACC TCAGATATAT	8100
TGGTGCTTCA TCCCAACGTT TATCGCTTAA AATATATGGC CCATTATATT GCTTTAAGGC	8160
ACTTTCTAAC CTTTGCAAAA CCGACTCTAA TTCATTTTGA TTTGGATAAC ATGTAATAAA	8220
TTTACCAGAA AATCCTCGAC TAACCAATTT CCCGTTTCGC ATGATAAATT TGTCTTCTGT	8280
ACTAAGATGT TTAATGGAA TTGCAATTC ATGGCAAATT TTTGCTACAT CTTGTAACAA	8340
TTCATGTGAA CTGTTATACT CTGAACTAAT GTGTATTTTC CACCCTTGTC TTTCAACAAA	8400
TTTCCAATA GGTATTGAT AAACCCACTC ATCATTATTC ATTACTTCGT GCCAATTAAA	8460
AGGCAGACTT ACTTGGTACT TTATGCTAGT ATCTGTACTA TAATCATTAT TAGTGAAAAA	8520
GAAAGGATGC TCCAAATTGA AATTATAATC CATAACAAAA TCTCCAAGAA ATTTTATCAA	8580
ACTTAATATA TCTATAGCTA GACAGACTTA TTTAAATAAA AAGGGAGAAT CCTTTGGATT	8640



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CTCCCCATAT AAGCACTAAC ATTCCAACGT GCACATATTG GAACGACATC CATAACTCCA	8700
GAGAATCTCT AAAGTTTACA ATTTAAATGA ATTAACAATT TTCCCAACTA AAAGCACTCC	8760
AGTTACCGCA ACGATTTGTA CTGAATGTAC TAAATCGCAT TCCATCAACT TCATCTGTTT	8820
CGTCAACTTG AACAGATACT AATGAAGAT TTAATACTTC TTCTGCCATA GCTAGCTCCT	8880
CCTATTTAAA TTTTGGGAT TAAGTACTTT ATCCACCCTC ATTATCTCT CTCCACCAGT	8940
AAAATGCAAG CAATTATACA ATGTTGTAC ATAGAAAATA ATGTTTCCGT AACTTTTCAA	9000
AGTAACCTCC ATCTCTCTCC CAAACTGGA AGTTAGTTTT AGAAGTTACC TAAAAATCAG	9060
GTCACCTATT TTAAGAAAGC AGCAAACTAT AAACAGTAG GTTCCACACC AAATGTAGTC	9120
CCATACTGCC CCATAAGTCA GATTTATAGC GCACCATACC TAAAAACATC CCAAGTGAAA	9180
CATACAAACA CCAAGCTAGA ATGGTTCCTG TATGATGTGC TAAGGCAAAAT AAAACACTTG	9240
TCAAAGCAAC TCTGATATCT AATTTTCTGA CCAAATTCCT TAAAATTCTT CGATACAGAA	9300
ATTCTTCAAC CATACTCGCA TTGATTAAGA ACAATAAAAA TGAAAACCAA GGAATTTGAT	9360
GTTGAAGGCC AATTAAGTTT GCTTGATTCTG TGCTTCCTTG AGCATGAATC AGACTAAAAC	9420
ATAGACTTAT AATCAGTAGG CTAACAAATT CAACACCAAG CCATTTTCATC CTAGATTTC	9480
TATTGACCTT ATGCGCTTGT TTGCGTTGGC CATACTCCA TAAAAAGAA ATGAGTGACG	9540
AACCATAGAG AATCTGTAGT ATAGTTTACT CACCGATACA AAGAAATTC AATAAGTATA	9600
GAGTACCAA TAAAGCATTT ACTTGTGGA ATATATAAAC TGGAATTATT CTTTTCATAG	9660
TTACCTCCGA AATAAATCTT CATAATCTAA ATCTAATACC TGCACAATCC TTT	9713

## (2) INFORMATION FOR SEQ ID NO: 44:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 8657 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 44:

AAAGAAATTG TCAGAGAGTG GCTAGATGAA GTAGCAGAGC GGGCTAAGGA CTATCCAGAG	60
TGGGTGGATG TTTTCGAGCG TTGCTACACC GATACCTTGG ACAATACGGT TGAAATCTTA	120
GAAGATGGTT CAACTTTGT CTGACTGGG GATATTCCTG CCATGTGGCT TCGAGATTCTG	180
ACAGCCCAAC TCAGACCCTA CCTTCATGTA GCTAAAAGAG ATGCCCTCCT GCGTCAGACC	240
ATTGCAGGTT TGGTCAAACG TCAGATGACC TTGGTACTCA AGGATCCCTA TGCTAACTCC	300

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TTCAACATTG AGGAGAAGTG GAAAGGGCAC CACGAGACTG ACCACACAGA CCTTAACGGC	360
TGGATCTGGG AGCGCAAGTA TGAGGTGGAT TCGCTTTGCT ATCCTTTGCA GTTGGCTTAT	420
CTCCTCTGGA AAGAGACTGG CGAGACTAGT CAGTTTGATG AGATTTTGTG CGCAGCGACT	480
AAGGAAATTC TCCATCTGTG GACGGTGGAA CAAGACCACA AGAACTCTCC TTATCGTTTT	540
GTCCGAGATA CGGACCGTAA GGAAGACACC TTGGTAAATG ATGGCTTTGG ACCTGACTTT	600
GCAGTGACAG GTATGACTTG GTCAGCTTTT CGTCCGAGTG ATGACTGTTG CCAGTATAGT	660
TACTTGATTC CGTCAAATAT GTTTGCTGTA GTAGTCTTGG GTTATGTGCA AGAAATCTTC	720
GCAGCATTAAC ACCTAGCTGA TAGCCAGAGT GTTATTGCTG ATGCCAAGCG TCTTCAGGAT	780
GAAATCCAAG AAGGAATCAA AAATACGCT TACACCACCA ACAGCAAGGG CGAAAAGATT	840
TACGCTTTTG AAGTGGATGG CCTAGGAAAT GCCAGCATCA TGGATGATCC AAATGTACCA	900
AGTCTACTAG CTGCGCCCTA TCTGGGCTAC TGTTCCGGTCG ATGATGAAGT GTATCAAGCT	960
ACTCGTCGTA CCATTTTGAG CTCTGAAAAT CCATACTTCT ACCAAGGAGA ATACGCAAGC	1020
GGTCTCGGCA GTTCTCATAC CTTCTATCGC TATATCTGGC CAATCGCCCT TTCTATCCAA	1080
GGCTTGACAA CAAGAGATAA GGCAGAGAAA AAATCTTGC TGGATCAGCT GGTGCTGTC	1140
GATGGTGGTA CAGGTGTCAT GCACGAAAGC TTTATGTAG ATGATCCGAC CCTCTACTCT	1200
CGTGAATGGT TCTCCTGGGC TAACATGATG TTCTGTGAGT TGGTCTTGA TTACTTGGAT	1260
ATTCGCTAAG GGGCTCGCTT TAGCTCAACC GATTCTTATC AGAATCACA GTTTACATTT	1320
AAAACGTAA AATTAAATTT TAGAATGAGG TTTTACTTCA TGGAAAATGT TGTGTACAT	1380
ATTATCTCAC ATAGTCACTG GGATCGTGAG TGGTACTTGC CTTTGAAG CCATCGTATG	1440
CAGTTGGTGG AATTGTTTGA CAATCTCTTT GATCTCTTTG AAAATGACCC TGAGTTCAAG	1500
AGTTTCCACT TGGATGGACA AACTATTGTC CTTGATGACT ACTTACAAAT TCGCCCTGAA	1560
AATCGCGACA AGGTCCAACG CTACATTGAC GAGGGCAAAC TTAAAATTGG TCCCTTTTAC	1620
ATCTTGCAAG ATGACTACTT GATCTCCAGT GAAGCCAATG TCCGCAATAC CTTGATTGGT	1680
CAACAAGAAG CTGCCAAATG GGTAAATCA ACCCAGATTG GCTACTTTCC AGATACCTTT	1740
GGAAATATGG GACAAGCGCC TCAAATCTT CAAAAATCAG GCATTCACGT GGCAGCCTTT	1800
GGTCGTGGTG TGAAGCCGAT TGGATTTGAC AACCAAGTCC TTGAAGATGA GCAGTTTACG	1860
TCTCAGTTTT CAGAAATGTA CTGGCAGGGT GTGGATGGTA GTCGTGTTTT AGGTATTCTC	1920
TTTGCCAACT GGTACAGTAA CGGGAATGAA ATTCCAGTTG ACAAAGATGA GGCTTGACC	1980
TTCTGGAAC AAAAATTGTC AGATGTGCGT GCCTACGCTT CGACCAACCA ATGGTTGATG	2040
ATGAACGGCT GTGACCACCA GCCTGTACAG AAAAATCTGA GCGAAGCCAT TCGTGTGGCA	2100

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AATGAACTCT TCCCGGATGT AATCTTTGTT CATAGTTCCTT TTGATGAATA TGTTC AAGCT	2160
GTAGAAGGTG CGCTTCCTGA AACTTTATCA ACTGTTACAG GCGAGTTGAC CAGTCAGGAA	2220
ACAGATGGCT GGTACACACT TGCCAACACT TCTTCATCCC GCATTTACCT AAAACAAGCC	2280
TTCCAAGAAA ATAGCAACCT CCTAGAGCAA GTGGTAGAAC CCTTGACTAT TATCACTGGT	2340
GGACACAACC ACAAGGACCA GTTGACCTAT GCTTGGAAAA CACTTTTGCA GAATGCGCCA	2400
CATGATAGTA TCTGTGGCTG TAGCGTGGAC GAAGTTCACC GCGAGATGGA AACGCGTTTT	2460
GCCAAGGTCA ACCAAGTAGG AAACCTTTGTT AAAAGTAACT TGCTCAACGA GTGGAAGGGT	2520
AAAATTGCTA CGGATAAGGC TCAAAGTGAC TATCTCTTTA CTGTCATTAA CACAGGCTTG	2580
CATGATAAGG TCGATACTGT CAGCACAGTG ATTGATGTGG CGACTTGTGA TTTCAAGGAA	2640
TTGCACCCAA CAGAAGGCTA CAAAAGATG GCTGCTCTTA TCTTGCCAAG TTACCGTGTG	2700
GAGGACTTGG ATGGTCGTCC TGTAGAGGCT ACAATCGAAG ACCTCGGAGC TAATTTTGAG	2760
TATAATTTAC CAAAAGACAA GTTCCGCCAA GCTCGTATTG CTCGTCAAGT GCGCGTGACC	2820
ATTCCAGTTC ACCTAGCGCC GCTTTCTTGG ACAACCTTCC AATTGCTGGA AGGAAAACAA	2880
GAACACCGTG AGGGTATTTA CAAAACCGA GTGATTGATA CACCATTCTG AACGGTGAGT	2940
GTGGATGACA ACATCACAGT CTATGACAAG ACAACTCACG AAGCCTATGA AGACTTTATC	3000
CGCTTTGAAG ACCGTGGGA CATCGGAAAC GAGTATATCT ATTTCCAACC AAAAGGAACA	3060
GAGCCAATCT TTGCAGAGCT TAAGGGCCAC GAGGTCTTGG AAAACACAGC TTGCTATGCT	3120
AAAATCTTGC TCAAACATGA ATTGACCGTG CCTGTCAGTG CGGATGAAAA GCTAGAAGAA	3180
GAGCAACAAG GTATCATCGA GTTTATGAAG CGTGAGGCTG GACGGTCAGA AGAATTGACA	3240
AACATTCCTC TGGAAACTGA GTTGACTGTC TTCGTTGACA ATCCACAAAT CCGCTTCAAG	3300
ACTCGCTTTA CTAACACTGC CAAGGATCAC CGTATCCGTC TCTTGGTCAA GACTCATAAC	3360
ACGCGTCCAA GCAATGATTG TGAAAGTATC TATGAGGTGG TGACACGACC AAACAAACCA	3420
GCTGCTTCAT GGGAAAACCC TGAAATCCT CAACACCAAC AAGCTTTTGT CAGTCTGTAT	3480
GACGATGAAA AAGGGGTGAC TGTATCCAAC AAGGGATTGA ATGAATACGA AATCCTTGGG	3540
GATAACACCA TTGCCGTGAC CATTTTGCCT GCATCAGGTG AGCTAGGTGA CTGGGGCTAC	3600
TTCCCAACGC CAGAAGCACA ATGCTTGCGG GAGTTTGAAG TCGAGTTTGC ACTTGAATGC	3660
CACCAAGCCC AAGAACGCTT CTCAGCCTAT CGTCGTGCCA AAGCCTTGCA GACACCGTTT	3720
ACCAGCCTTC AGCTTGCTAG ACAGGAAGGA AGCGTGGTTG CGACTGGTAG CCTCTTGAGC	3780
CATTCTGTTT TCAGCATACC GCAAGTTTGT CCAACAGCCT TTAAGGTAGC TGAAAATGAA	3840

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GAAGGCTATG TGCTTCGTTA CTACAATATG TGTAGTGAAA ATGTACGTGT GCCAGAAAGT	3900
CAACATCTCT TCCTTGACCT ACTTGAACGA CCATACCCAG TTCATTTCAGG ACTATTGGCT	3960
CCACAAGAGA TTCGTACAGA ATTCATCAAA AAAGAAGAAA TTTAATTTCA AAAAGTAAAC	4020
ATCAAAAGAA AGGAGGGGCG AAAAAGTAAG AACTAACTGC TGATTGCGCC CTTTATGGT	4080
AAAAACAATG ACCATTGCAA CGATTGATAT CGGAGGGACT GGGATTAAAG TTGCCAGTCT	4140
GACTCCTGAT GGGAAAATAC TGGATAAGAC AAGTATTTCA ACGCCTGAAA ACTTGGAGGA	4200
TTTACTAGCG TGGCTAGATC AACGCTTGTC AGAACAGGAT TACAGTGGGA TTGCTATGAG	4260
CGTTCCAGGT GCAGTCAATC AAGAGACAGG TGTGATTGAT GGCTTCAGTG CGGTGCCCTA	4320
CATCCATGGC TTTTCTTGGT ATGAGGCGCT TAGCTCTTAT CAGCTACCTG TCCATTTAGA	4380
AAATGATGCC AACTGCGTTG GACTCAGTGA ACTACTAGCT CATCCAGAGC TTGAAAATGC	4440
AGCCTGTGTC GTGATTGGGA CAGGGATTGG CGGAGCCATG ATTATCAATG GTAGACTTCA	4500
TCGAGGTCGC CACGGTCTGG GTGGAGAATT TGGCTACATG ACAACCCTTG CCCCTGCTGA	4560
AAAACCTAAT AACTGGTCGC AACTAGCATC AACTGGGAAT ATGGTACGAT ACGTGATTGA	4620
AAAATCTGGT CATACTGATT GGGACGGTCG CAAGATTTAC CAAGAGGCCG CAGCTGGTAA	4680
TATCCTTTGT CAAGAAGCCA TTGAGCGCAT GAACCGCAAT CTGGCGCAAG GCTTGCTCAA	4740
TATCCAGTAT CTGATCGATC CAGGTGTCAT CAGTCTGGGT GGCTCTATCA GTCAAAATCC	4800
AGATTTTATC CAAGGTGTCA AGAAGGCTGT TGAAGACTTT GTCGATGCCT ACGAAGAATA	4860
CACGGTCGCA CCAGTTATCC AGGCCTGCAC CTATCACGCA GATGCCAATC TCTACGGTGC	4920
TCTTGCTAAC TGGCTACAGG AGGAAAAGCA ATGGTAAGAT TTACAGGACT TAGTCTCAA	4980
CAAACGCAAG CTATTGAGGT TTTAAAAGGT CACATTTCTC TACCAGATGT GGAAGTGGCT	5040
GTCACTCAGT CTGACCAAGC ATCTATCTCT ATCGAGGGTG AGGAAGGTCA CTATCAATTG	5100
ACCTACCGCA AACCTCACCA ACTTTATCGT GCCTTGTCCT TGTGGTAAAC AGTTCTAGCA	5160
GAAGCTGATA AAGTAGAGAT TGAGGAACAA GCAGCTTACG AAGATTGGC TTACATGGTT	5220
GACTGTTCTC GAAATGCGGT GCTGAATGTG GCTTCTGCCA AGCAGATGAT TGAGATATTG	5280
GCTCTCATGG GCTACTCAAC CTTTGAGCTT TACATGGAAG ACACTTACCA GATTGAAGGG	5340
CAGCCTTACT TTGGCTATTT CCGTGGAGCT TATTCAGCAG AGGAGTTGCA GGAAATCGAA	5400
GCCTATGCCC AACAGTTTGA CGTGACCTTT GTACCATGCA TCCAGACCTT GGCCCACTTG	5460
TCGGCCTTTG TCAAATGGGG TGTCAAGGAA GTGCAGGAGC TCCGTGATGT AGAGGACATT	5520
CTTCTCATTG GCGAAGAAAA GGTTTATGAC TTGATTGATG GCATGTTTGC CACGTTGTCT	5580
AAACTGAAGA CTCGAAGGT CAATATCGGG ATGGACGAAG CCCACTTGGT TGTTTGGGA	5640

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CGCTACCTGA TTCTGAACGG TGTGTGGAT CGTAGTCTCC TCATGTGCCA AACTTGGAG	5700
CGCGTGCTGG ATATTGCTGA CAAATATGGT TTCCACTGCC AGATGTGGAG TGATATGTTT	5760
TTCAAACCTCA TGTCAGCGGA TGGCCAGTAC GACCGTGATG TGGAAATTCC AGAGGAAACT	5820
CGTGTCTACC TAGACCGTCT CAAAGACCGT GTGACTCTGG TTTACTGGGA TTATTATCAG	5880
GATAGCGAGG AAAAATACAA CCGTAATTTT CGCAATCATC ACAAGATTAG CCATGACCTT	5940
GCATTTGCAG GGGGAGCTTG GAAGTGGATT GGCTTTACAC CTCACAACCA TTTTAGCCGT	6000
CTAGTGGCTA TCGAGGCTAA TAAAGCCTGC CGTGCCAATC AGATTAAAGA AGTCATCGTA	6060
ACGGGTTGGG GAGACAATGG TGGTGAAACT GCCCAGTCT CTATCCTACC AAGCTTGCAA	6120
ATCTGGGCAG AACTCAGCTA TCGCAATGAC CTAGATGGTT TGTCTGCGCA CTTCAAGACC	6180
AATACTGGTC TAACGGTTGA GGATTTTATG CAGATTGACC TTGCCAACCT CTTACCAGAC	6240
CTACCAGGCA ATCTCAGCGG TATCAATCCC AACCGCTATG TTTTTTATCA GGATATTCTT	6300
TGTCCGATTC TTGATCAACA CATGACACCT GAACAGGACA AACCGCACTT CGCTCAGGCT	6360
GCTGAGACGC TTGTAACAT TAAAGAAAAA GCTGGAACT ATGCCTATCT CTTTGAAACT	6420
CAGGCCAGT TGAATGCTAT TTTAAGTAGC AAAGTAGATG TGGGACGACG CATTCGTCAG	6480
GCCTACCAAG CGGATGATAA AGAAAGTTTA CAACAAATCG CCAGACAAGA ATTACCAGAA	6540
CTTAGAAGCC AAATTGAAGA CTTCCATGCC CTCITTAGCC ACCAATGGCT GAAAGAAAAA	6600
AAGTCTTTG GTTTGGATAC AGTTGACATC CGTATGGGCG GACTCTTGCA ACGCATCAAA	6660
CGAGCAGAAA GCCGTATCGA GGTTTATCTG GCTGGTCAGC TTGACCGCAT CGACGAGCTG	6720
GAAGTTGAAA TCCTACCATT TACTGACTTC TACGACGACA AGGATTTCGC AGCAACTACA	6780
GCCAACCAGT GGCATACCAT TGGACAGCG TCGACGATTT ATACGACTTA ATATTCTTCG	6840
AAAATCTCTT CAAACCAGT CAGCTTCCAT CTGCAACCTC AAAACAGTGT TTTGAGCAAC	6900
CTGCAGCTAG CTTCTAGTT TGCTCTTTGA TTTTCATGTA GTATAAAAC AAGAACACCT	6960
TGCTTGGCGC AGGGTGTTTC GCGTGAAACA GAAGAATTAT CTGGTTTCAA ATGCTACAGT	7020
TAGACAACT TATGATAAAA TAGCAGAAAG TGAATGTTT CTAAGAGCAA TTGGAGGTAT	7080
TATGCTACAC TTAATAATTAG TAAACAAGA AATAGAAGCT GAAAAGCCAG CATCTGTAGA	7140
AGCTTGGATC ATTTCCGTCA AATTTAAAAA AGGTTGCTAC CGACATATAT AGATTCCAAA	7200
AACAAAAACG TTAGCGGAAC TAGCAGATGT GATTTTATGG AGTTTGTATT TTGCAATGA	7260
TCATGCTCAC GCATTTTCA TGGATAATGT TGAGTGGAGT CATGCAGATT CTTACTTTCG	7320
TAGCTTTGTT AGTGACGATG TTGAAGAACG TTACACAGAA AATGTCTATC TGGATAGCCT	7380

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AAGTGTCAAA CAAAAATTTA AGTTTATTTT CGACTTCGGT GATGAATGGC GTTTTGAATG	7440
CCAAGTGCCTG AGAGAAATCG AGACAGAGGA CGAAGAAGCT TATCTCGTAC GTTCGGTTGG	7500
AACGTCGCCA GAACAATATC CAGATTATGA TGGTTTGTAC TATGAAGAAT GGTAATAATTG	7560
AAATCAGTCT GTGTAGGCTT AGTATTTCAA TAGACTTCCT GCAAACTAG AATCCTAGTT	7620
CATGATTGAT AATACCAGCA ATCAAATTCA TTCGTAATCC GAAGCGTTTA CGATGATTTT	7680
GATAGGTTGT TGAACACATT TTAAACGTTT TTACTTTGGC AAAGATGTTT TCAACCTTGC	7740
TTCTCTCCTT AGATAGCGCA TGGTTATAGG CTTTATCTTC AGCTGTTAGT GGCTTGAGTT	7800
TGCTGGATTT ACGTGAAGTT TGTGCTTGAG GACATATCTT CATGAGCCCT TGATAACCAC	7860
TGTCAGCCAA GATTTTACCA GCTTGTCGA TATTTCTGCA ACTCATTTTG AACAACTTCA	7920
TATCATGACA ATAGTTCACA GTGATATCCA AAGAAACAAT TCTCCCTTGA CTTGTGACAA	7980
TCGCTTGAGC CTTCATAGCG TGAAATTTCT TTTTACCAGA ATCATTCGCT AATCTTTTTT	8040
TTAGGGCGAT TGATTTTTAC TTCCGTCGCA TCAATCATTA CCGTGTCTC AGAACTAAGA	8100
GGAGTCTCTG AAATCGTAAC ACCACTTTGA ACAAGAGTTA CTTCAACCCA TTGGCTCCGA	8160
CGGATTAAGT TGCTTTCGTG AATACCAAAA TCAGCCGCAA TTTCTTCATA AGTGCGGTAT	8220
TCTAGGCTTA ATTTAGGTTT TCGTCCACCT TTTGCGTGT TAAGTTGATA AGCTGTTTTT	8280
AATACAGCTA ACATCTCTTT AAAAGTCGTG CGCTGAACAC CAACAAGACG CTTAAATCGT	8340
GTATCAGTTA ATTGTTTACT TGCTTCATAA TTTCGCAGGG AGTCTATTGA CTCTTGGTA	8400
GGTGTCATG TTTTMTTCAT CTATCCGAG AATTATTTTC CCGCCATTG TATTTGCAAA	8460
TGCTGAGTAG GTTTCCGAGA AAGACTCTGG AAGATTGTTT TTAGCTTTTT TGTATTCTAA	8520
ATCAACCCCT TCAAATTTTA AGTCCATATT TTTCTTTTAC ATCTGTTTTT TGTGGTTCTG	8580
GTATTTGTTT AAGTTGAGTG ATAATATAGC GAATTGAATT TCGAGAGTTT TTAATCAGTT	8640
AATTTCTTTT TTAACCC	8657

(2) INFORMATION FOR SEQ ID NO: 45:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 11384 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 45:

TCTATTTTGG GTATAGACTT ACCTATAAAG AAAAATATCT ATACACTGCC TTACTAGCTA	60
TACTGAACGA GTCAACAAA ACGATATATA TTGATGATAT AAATACAGCA AGATTTTTTA	120

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ACTTCTTTGG CAATGATATT CCTAATTCGT CTTTAAAAA AATTGACTAT ATCGCACCTT	180
CAGAAATTGT TTCATTTAGT ACGTACGTTT GACAACGTTT TAAAGTAATT CCTAAAAATT	240
TGGAACATAT ATTTAAATCA AGTTTTTTAT TAGAGAATAT AGATGTTTCT GGTTACACTG	300
TAAATATTTT AGAAGATCAA TTAACAAAAC ATAGAACAAT CAAAATTAGT AAAAATAAC	360
TGGTTGATCT CATGTATAAA TACCTAACAA AACCACGCGC CTTGCCTGCT GATGGAAAGA	420
AAGGTACAAA TACATGAATA TCAAAGAAAA AATCAAAAAG AATGGCCAAA GAGTTTATTA	480
TGCTAGTGTT TATCTAGGCG TTGACCAACT AACGGGCAAA AAAGCCCGTA CAACTGTTAC	540
AGCAACCACT AAAAAGGGCG TTAAAGTAAA AGCGCGTGAT GCGATCAATA CTTTGTCTGC	600
TAATGGCTAT ACAGTTAAAG ACAAGCCGAC AATTACAACA TATAATGAGC TTGTAAAAGT	660
TTGGTGGGAT AGTTACAAGA ATACAGTTAA GCCAAATACT CGCCAATCCA TGGAGGGATT	720
GGTTAGAGTG CATTTATTGC CTGTATTTGG CGATTACAAG CTATCTAAAC TTAATACGCC	780
TATTTCTCAA CAGCAAGTAA ACAAATGGGC TGACAAGGCA AATAAAGGCG AAAAAGGGGC	840
ATTTGCTAAC TACTCTTTGC TCCATAACAT GAATAAGCGT ATTTTGAAAT ATGGCGTAGC	900
TATCCAGGTA ATACAATACA ACCCAGCTAA TGATGTCATC GTTCCACGCA AACAGCAAAA	960
AGAAAAGGCT GCTGTCAAAT ACTTAGACAA CAAAGAATTA AAACAGTTTC TTGATTATTT	1020
AGATGCTCTG GATCAATCAA ATTATGAGAA CTTATTTGAT GTTGTCTGT ATAAGACTTT	1080
ATTGGCCACT GGTGTCCGTA TTAGTGAGGC TCTGGCTCTT GAATGGTCTG ATATTGACCT	1140
AGAAAGCGGT GTTATCAGCA TCAATAAGAC ACTAAACCGC TATCAGGAAA TAACTCACC	1200
TAAATCAAGC GCTGGTTATC GTGATATACC AATAGACAAA GCCACATTAC TTTTACTGAA	1260
ACAATACAAA AACCGTCAAC AAATTCAGTC TTGGAAATTA GGCCGATCTG AAACAGTTGT	1320
ATTCTCTGTA TTTACGGAGA AATATGCTTA TGCTTGTAAC TTACGCAAAC GCCTAAATAA	1380
GCATTTTGAT GCTGCTGGAG TAACTAACGT ATCATTTTAT GGTTTCCGCC ATACACATAC	1440
TACTATGATG CTCTATGCTC AGGTTAGCCC GAAAGATGTT CAGTATAGAT TAGGCCACTC	1500
TAATTTAATG ATCACTGAAA ATACTTACTG GCATACTAAC CAAGAGAAATG CAAAAAAGC	1560
CGTCTCAAAT TATGAAACAG CTATCAACAA TTTATAAAAA ATAAGGGTGA CCCATTTCCG	1620
GGCTACCCCT TTAATATACC AAAAATTAGT AGGGGTAGTA AAAAGGGTAT TAAATTATAA	1680
AAAGCACTAA GGGAAAGCGC CCCAAAGTGC TTATTTCAA GGCTTTATAG CCTATAATCA	1740
CATAAAGAGA TTATTTTTTA AGGTTGTAGA ATGATTTCAA TCCACGATAT TCAGCTACTT	1800
CACCAAGTTG GTCTTCGATA CGAAGCAATT GGTGTATTT AGCGATGCGG TCTGTACGTG	1860

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AAAGTGAACC AGTCTTGATT TGTCCTGCGT TAGTTGCAAC TGCAATATCA GCGATTGTTG	1920
AATCTTCAGT TTCACCTGAA CGGTGTGATA CAACAGCAGT GTAACCAGCT TCTTTAGCCA	1980
TTTCGATAGC TTCAAAAGTT TCAGTAAGAG TACCGATTTG GTTAACCTTG ATAAGGATTG	2040
AGTTAGCAGC ACCTTCTTGG ATACCACGTG CAAGGTAGTC AGTGTTTGTT ACGAAGAAGT	2100
CGTCACCAAC AAGTTGTA CTCTTACCAA GACGTTCACT AAGAGCTTTC CAACCATCCC	2160
AGTCGTTTTT ATCCATACCA TCTTCAATAG TGATGATTGG GTATTTGTTA ACCAATTCTT	2220
CAAGGTAGTC GATTTGTTCT GCAGATGTAC GAACAGCAGC ACCTTCACCT TCAAATTTAG	2280
TGTAGTCGTA AACTTTACGT TCTTTATCGT AGAATTCTGA TGAAGCACAG TCAAATCCGA	2340
TAAATACGTC TTTACCTGGT ACATATCCAG CAGCTTCAAT CGCAGCAAGG ATAGTTTCAA	2400
CACCATCTTC AGTTCCTTCG AAACGAGGAG CGAATCCACC TTCGTCACCT ACGGCAGTTT	2460
CCAAACCACG TGATTTAAGG ATTTTCTTAA GAGCGTGGA GATTTCAGCA CCGTAACGAA	2520
GGGCTTCTTT AAATGTTGGC GCACCAACTG GCAAGATCAT GAACTCTTGG AAAGCGATTG	2580
GAGCGTCAGA GTGAGAACCA CCGTGTATGA TGTTTCATCAT TGGAGTTGGA AGAACTTTAG	2640
TGTTGAATCC ACCAAGATAG CTGTAAAGTG GGATTTCAG GTAGTCAGCA GCAGCAGGAG	2700
CTACAGCGAT AGACACACCG AGGATTGCAT TCGCACCCAA TTTACCTTTG TTAGGAGTAC	2760
CGTCAAGTGC GATCATAGCA CGGTCAATAG CTTGTTGATC ACGTACATCG TAGCCAATGA	2820
TAGCTTCAGC AATGATGTTG TTTACGTTGT CAACAGCTTT TTGTGTACCA AGACCACCGT	2880
AACGAGATTT GTCACCGTCG CGAAGTTCAA CTGCTTCGTG TTCACCAGTA GAAGCTCCTG	2940
ATGGAACCAT ACCACGTCCG AAAGCACCTG ATTCAGTGTA AACTTCTACT TCAAGTGTG	3000
GGTTACCGCG TGAGTCTAGG ACTTCGCGAG CGTAAACATC AGTAATAATT GACATTTTTT	3060
ACTCTCCTTA TGAGTTAAAT TTTTACACC TCTATAATAC CTTAAAACCC CTCCTTTTTT	3120
AAGAAAAAAC GTTATCTTTG TGCAACTTTT CCTTAACCTT ATAAAGTAAT CGCTTTCTTT	3180
TGCTCTTTTT ATTCTAACTT TTATGATATA CTGTTTTCAT GACAGATTTA TCAAAACAAT	3240
TACTTGAAAA AGCTCATGGT GGGTTAAAA TAAATCCGA TGAGCAAAGA CGCTATCTTG	3300
GTACTTTTGA GGAAAGAGTT CTTGGATATG TAGATATTGA CACAGCAAAT AGCCCTCAGT	3360
TAGAAAAAGG CTTTTTATTT ATTTTAGAAA ACCTTCAGGA AAAAGCAGAG CCACTATTTG	3420
TGAAGATTTT ACCAACTATC GAATTTGATA AGCAAGTTTT TACTTAAAA GAAGCAAAAG	3480
AAACTGATAG TCAAGCCACC ATAGTATCTG AAGAGCATAT TACTTCTCCT TTTGGCCTGG	3540
TTATTCATAG CAATGCACCA GTTCAAGTAG AAGAAAAAGA CCTTCGACTT GCTTTTCCAA	3600
AACTTTGGGA AGTTAAAAAG GAAGAACCAG CCAAAACATC CTTATGGAAG AAATGGTTTA	3660



GCTAAATCTT GCACATATTT AATAAGTGCC CAATATTGGC AGCCGTGCGC TCCAGATAGA	3720
AACTGGCATT TTTCAAATA TCTTCTAAAG GTTCACCTTT CTCCAAAATA GAAAAGACAG	3780
CTTGATATTT TTCAAATGGT AGGGGAGGTA AATCTTCAGC AAGACTACCG CAAATAGCAA	3840
TAACAGGAAC TCCAACAGGG GTTCTTTTGT CAACACCTAT AGGCGCTTTC CCAGCAAAGC	3900
TTTGACTATC AAGTCTTCCT TCTCCAACAA CAACCAAGTC AGCATCTGAA ACTTTCTTAT	3960
CAAAGTTGAT TAAGTCCAAG CAGGTATCAA TTCCAGACAC GATACTTGCC TGAGCAAAGG	4020
CACACAAACC ACCAGCAAGG CCTCCACCTG CTCCTGCTCC TTTAATTTCT AATGTTGCAG	4080
GTGAGAATTT TTCATAAAAA TCTTGGATCG CCTGATCTAC GACTGCAAAC ATAGTCGGAT	4140
GTAGACCTTT TTGATTGCCA AAAGTGTAAG TCGCACCTTG ATGACCACAT AAGGGACTCA	4200
CGACATCTGC TAAATATGA ATTTGAACAC CTTCAGGAAT TTTATAGCAA TTTTCTGTTG	4260
AAACAGAAGC TAAGTTTAAT AAGGATTGAC CGGAAGCAGG CAAGACATTT CCATCCCTAT	4320
CATAAAATG ATAACCTAAA CCAGCAGCAA TCCCCAGTCC TCCATCATTA CTGGCCGTGC	4380
CACCAACACC GATATAAATA TCTTTAATCC CTTTAGAGAT GAGATGAAGA ATCAACTCTC	4440
CAATACCACA AGTTTGGATT TGAAGTGGAT TTCGTTTCTC TAGCGGAATT TTTCCAAGAC	4500
CAACCAAGTC AGCTACTTCA AATAGTGCCA GTTCCCCTTT TTGAAAATAG CGCATGGCTT	4560
CTTTTGTGCC AAAAGGGTCT GTCACTTGGA TCCATTTTTC TTTTAGGTCA AGAGAATGTC	4620
GGATAGCATC TACAGTACCT TCTCCCCCAT CACCAACAGG GCAGAGGAGA CATCTACAT	4680
CTGCTATCGA TTGTTGGAAG CCTCTTTTTA TTGCTTCAGC TACCTGTTGA GCTGTCAAGC	4740
TTTCCTTAAA CGAATCCGGT GCAATTACAA TCTTCATATT TTCCCTCATT CTAAACAGTC	4800
AATCAAAGGG AGAACTTCTA AAAAATCCCT CTTGTCAACA TGATGTGGTA TTTCTTTTTT	4860
GAGCACTTCT TTGGCACAAA AGGCGATTCC TAACCTCGCC GACTTCAACA TTAATAGATT	4920
ATTAACCCCA TCACCGATTG CCACCGTTCT TTCTTTAGAA AGTTTATGTT TCTTCTCCA	4980
TTTTTCCAGA GTCTCTTTTT TGACCTGGGG ACTTATAATT TGTCCTAATA ATTTTCTGT	5040
TAAAAGACCT TCTTTGACTT CAAGCTAGTT GGCAGTGAAA TAGGCAATAC CAAGGGATTT	5100
TGCTAATCTC TCCAACATTT GGTGTAAATC CACCAGACAC CAGACCAACT AGGATGCCAT	5160
TCTTTTGGAG AATAGAGATG AACTCTGGGA CATTTAGCGA TAGATGAATT GAGTTGAAGA	5220
CGTTATCAAA GACCAAAATA GGAAGACCTT CCAACAAGGA CACTCTTTTT CTTAAACTGC	5280
TTTCAAAGAC CAACTCTCCT CGCATGTGTC GACTTGTAAT CTGCGAAATT TCCGCCTCAT	5340
GACCTGCCTC TCTCCCTAAA AGATCAATCA CTTCTTCTAG GATTAAGGTT CCATCTACAT	5400

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CCAAAACACA CAAGCCTTTT ACTTGAGACA TCAGTTCTCC TCTCTAAACA GCCTAAAAAT	5460
CGTATGAAGT CATCATACGA TTTTATCTAT TAATTAACATA AACTATGGTA CAAGTCAAGG	5520
TATGACTTGC AGGCTGTATC CCATGAGAAG TCACTCTCCA TAGCTTGTTT TTGTAGGTTT	5580
CTCCAAATGT CTGGATGGTT TCTATACAAG TCCAATGCTG TTGGAAAGT CCAATTTAAC	5640
CAATAAGGAG ATAGATTGTC AAAGCTAAAG CCAGTACCGC TTCCTTCGAT TGGATTGAAA	5700
GCGCGAAGT TATCTCGCAA GCCTCCAAT TCATGGACCA ATGGCAAGT TCCATAACGC	5760
ATAGCCATCA TTTGAGACAA GCCACACGGT TCAAAACGAC TTGGCATGAG GAAGAGGTCA	5820
CAAGCAGCGT AGATTTCCTG AGCAAGTTTG ACATCAAAAG TGATATTGTG TGATAGCTTG	5880
TCTGGGTAAA TCTGAGCAA CCATGAGAAA GCTCCTTCAA AGGCTGGATC GCCAGTCCCC	5940
AAAAGAACA TCTGAACATC TTCTTGCAAG ATATGGTGAA GACTTTCGAC CACCACATCA	6000
AAACCTTTTT GACGTGTCAA ACGAGAAACA ATTCCCACCA GTGGAACGTC TGCTCTAACA	6060
GGCAAGCCAA CTCTTCTTG CAATTTTGCC TTATTTTGG CTTTCCAGA CAAATCTTCC	6120
TGATTGAAAT GATAGCTAA AAGAGCATCC GTCTGAGGAT TATAAAGATC AGCATCAATC	6180
CCATTCACGA TACCAGATAC TTTACCAGAC TCCATTTTAA GAATCTGATC CAAATTACAT	6240
CCAACTGAC TAGTCATAAT TTCATGAGCA TAGCTAGGTG AAACGGTGA AACACGGTTC	6300
GCATAGAGAA TACCTGCCTT CATCCAGTTC AGACAGTTGT TCCATCGAAG GGTGCCATCA	6360
GCGTAACGTT CAAAGCCAAC TCCAAACAAA TCACCAACA TTCCTTCTGA AAATTGTCCT	6420
TGGAATTCTA AATTATGAAT GGTAAAACT GTTCAATGT CCTCATAGGC TTGAATCCAA	6480
CGGTATTTTT CCTTCAACAA GAAAGGAATC ATAGCTGTAT GGTAGTCATG AACATGGAGA	6540
AGATCAGGAA TAAAGTCAAT CCTTCCATA GCCTCAATGG CAGCCAGTTG GAAAAGGCA	6600
AAGCGTTCTC CGTCATCAAA ATCACCCTAA ACATGACCAC GGAAGAAATA ATATTGATTG	6660
TCAATAAAGT AGAAGGTTAC ACCATTTAAT ACTGTTTCT TAATTCACA ATACTGTCTG	6720
CGCCAACCAA CGCTCACCTC AAAATGAAGC ACATCTTCAA TCTGATTTC AAATTTAGCC	6780
TCTACCATAT CATAGTAGGG TAAATCACT GCAACTTCGT GCCCAGCTT TACCAGTGAT	6840
TTTGAAGAG CGCCAATGAC GTCTCCCAA CCACCTGTTT TTGAAAAGG TGCACCTCT	6900
GCTGCTACAA ATAAAATTT CATGAATGAA TATCCTCTGT TACTTTAGCA CCTTCTTAA	6960
CCACAACGAG ATGTTCTGCA GTTCTCGAA TCACAACACC ATGCTCAACT TCAACCCCT	7020
TGTCCAAGAT AGCATATTCG ACCTGAGCCC CTTCTCCAAT AACAAACGA GGAAGAGCA	7080
GGCTATCTTT AACCAAGCTA TCCTTATGGA CATGAATATT ACGTGATAGA ACAGAATTAG	7140
CTACTTGACC TTCAATAATA CTACCAGAGG CAAACTGAGA AGTGCTTACC TTAGATGTAT	7200

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TAGCATAGTA AGTTGGCTCT TCGTTTTTGA CCTTTGTATA AATCTTTTGG TTGGTGAGA	7260
AAAGAGAATA GAATTTTTGT GATTCAAGCA TATCGATATT CGCTTGATAA TAAGATTAA	7320
CAGAGTGAAT ATTGGCTAGA TAGCCCGTGT ACTCGTAGGC GAAAGCTCCC TCTTTTACAG	7380
CCAAATCCCG TAAAACATAG CGCAATTTCT CTGGATGTTT TTTTTAGCT TCTTCTCCA	7440
AGTGTTCAT CAACCAAGGT GTATCAACGA CAAAGATATC TGTAGACATA TTGAACGTTT	7500
CAGCTGTTGA CTTGCTATCA AAGAGTTTAT GAGAAAGAAC ATGGTCTGTT TCATCTACAT	7560
CCAAGATTGC ATTTACTTCT GAAATATCTT TCTTAGCTAG TTTTTATAA ACTACAGTGA	7620
TAGGCTCTTT TGTGTACTA TGTAGGTGGA AAAGTTGGTT CAAATCAATG TTAATAAGAA	7680
CATCGCAGTT GAGGGCAACC GTTTGGTTTG AGCCAGAACG TTTCAAATAA GTAAGAAGCT	7740
GTGGTAGTA TTTTCTTCCA ACTGTACTAC TTTCTACACG GGTATTGTAA ATTCCTAGAT	7800
AGTAATGGCT AAGAAGGTT GATAAGCCCC ACTCGCGTCC TGAACGAATA TGGTCAAATA	7860
CTGAGCTGAT ATTATCCTGC TGGAAAATAC CAAAGACACT ACGAACACCT GCATTAGCAA	7920
GGCTTGAAAG TGGGAAGTCA ATCAAACGAT ATTTCCACC AAATGGCAAA CTGCTACTG	7980
GACGGTGGTC CGTCAATGTC GACATATTGT GAAAACCAAC TGTATTTCCT AAAATGGCAG	8040
AATATTTATC AATCTTCATC TGTGCTACC CCCACTACTT CATTATATCC TACAACTTGT	8100
ACTTCATCTG TTCCATCAAT TTCGACACCG TCAGAAATAA TCGCACCTTC ACCAATAATG	8160
GCACGTTTAA TCTTAGCTCC TTGACCAATG ATAGCTCCAC TCATGATAAC TGAATCAAGG	8220
ACTTCGCTC CTTCGCGAAC TTGCGCGCCT GTTGAAAGGA TAGAATGTTT AACAGTTCCA	8280
TCAACGAAAC ATCCGTCTAC AACTAATGAG TCTTCCACAT GAGCATTGTC CCCGAGGAAG	8340
TTTGGTGGTG AAATCAAGTT TCTTGAGTAA ATCTTCCATT GACGGTTACG ACTATCCAAG	8400
GCATTTTCTG GAGAAATATA CTCCATGTTT GCTTCCCAA GTGACTCAAT AGTACCAACA	8460
TCTTTCCAAT AACCACTAAA TTCGTAAGCA TAAACACTTT CACCTGACTC AAGGTAATTT	8520
GGAATGACAT TTTTACCAA GTCTGACATG CCAACCTTGC TCTTTTCAGC AGCGACTAAC	8580
ATATTACGAA GCGTTGCCA ATCAAAAATG TAGATTCCCA TAGAAGCTTT TGTAGATTTA	8640
GGTTGAGCTG GTTTTTCTTC AAATTCAACA ATACGATTGT TAGCATCTGT GTTCATGATA	8700
CCAAAACGGC TTGCTTCTTT AAGAGGGACG TCTAAAACG CTACTGTCAA GCTGGCATTA	8760
TTATCCTTAT GAGACTGGAG CATATCATCA TAGTCCATT TGTAGATGTG ATCCCCAGAC	8820
AAAATCAAGA CATACTCAGG ATTGACACTG TCGATATAGT CGATATTTTG GTAAATAGCG	8880
TGACTAGTCC CCTCAAACCA ACGATTTCCT TCACTGACG AATAAGGTTG AAGAATAGAG	8940

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ACACCTGAAT TAATACCGTC TAGTCCCCAG CTTGAACCAT TCCCAATATG GTTGTGAGA	9000
GCAAGTGGTT GATACTGTGT AACGACCCCA ACATTGTGAA TCCCTGAGTT GGCACAGTTT	9060
GATAGGGCAA AGTCAATGAT ACGGTAGCGC CCACCAAAAT GCACAGCTGG TTTTGCATG	9120
CTTTGAGTGA GTTTACCGAG ACGAGTTCCT TGCCCACCAG CAAGAATCAA AGCTAACATT	9180
TCATTTTCA TTTTCTACTC CTTTPTGGTT TTTATTGTG ACGGTTTTAG TAGATTTCAA	9240
GCGACGTTTG ATTTCCATA CACTTGCTCC CATAGCCGGT AGGGTAAAGG TTAAGTCTG	9300
CTCATAATCT TTCCATAGTC CTTCTTGCCT TTGAACAGTT TGATTATGTT CTTTCCAAAC	9360
GCCTCCCCAC TCTTCCAAC CAGTATTCCA TACTTCTTCG TAAATTCCTG CAACGGGTAG	9420
TCCGATTGTA AATCTTTCC GCTCAACAGG TACCATATTA AAGATACAGA CTAACATTTT	9480
TCCCTTTTTA CCCTTACGAA TAAAGGAAAG AACACTCTGG TCTCGATTAT CCGCATCAAT	9540
GATTTCAATA CCATCATAGC TGGTATCAAT TTCCCACAGA CAGCGATGAT CTTTGTAATA	9600
CTGGTTTATG TGAGAAGCGA AATACTTCAT CTTAGCATTC ATTGGGTCTT CTAGGTTAGA	9660
CCATTCCAAC TGTTCTTCAG ATTTCCATTC TAGGAATTGA CCGTATTTCG TACCCATGAA	9720
GAGCAATTTT TTACCAGGGT GACAAATTTG GTACGTATAG AGATTGCGCA AGCCTGCGAA	9780
TTGATTGTAA CGATCTCCCC ACATCTTATG CATCATACTC TTCTTGCCAT GAACCACTTC	9840
ATCGTGCGAG AATGGCAAGA GATAATTCTC CTTGAAAACA TACATAAAGC TGAAAGTCAC	9900
CAGGTAAAG TCATATTTAC GATAGATCGG ATCTTCTTCG TAGAAACGGA GGATATCATT	9960
CATCCAGCCC ATGTTCATT TGTAGTCAA TCCTAGACCA CCAATCTCTT TCATTCCCGT	10020
AATCTTGATC GCAGACGAAC TTTCTTCTGC AATCATCATC ACATCTGGAT ATTCTAACTT	10080
AATAACCTCA TTCAAGCGCT GAAGGAAATA ATAACCTTCA TAGTTGAGAT TTCCGCCATC	10140
TTTATTAGGT GTCCATGGAG CATCATCATA GTCCAAATAG AGCATGTTGC TAACAGCATC	10200
CACACGAATA CCATCCAAAT GATAGACATC AATCCAATGC TTAATGCAAG AAATTAAGAA	10260
GGACTGGACT TCATTTTTTC CAAGGTCAAA ATTAAGGGCA CCCCAACCAT GGTATGAGC	10320
CTTATTATGG TCTTGGTATT CAAAAGTCGG TGTCCCATCA TAATAGGCTA AGGCATCATC	10380
GTTGATGGTA AAGTGACTGG TACCCAGTCC ACAATAACCC CAATATTATG GGTATGACAC	10440
TCCTCGACAA AATCTTGAAA CTCTCTGGT CGGCCATAAG CATGCTCTAA AGCGAAGTAA	10500
CCCATAAGCT GATACCCCA ACTCAAGCCC AAAGGATGGG ACATCAAGGG CATAAACTCA	10560
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CTATAAGGAC TGCCATCAGA ATTTCTTTTC CATGATCCAG CGTGAAC TTC ATAAATATTG	10680
ACAGGACGCT CTTCAAAGCC CCAACGTTTT CTTCGTGCCA GCCAAAGTCC ATCTTCCAT	10740

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TTCTTCTCAG GAAGCTCTGT TACGATTGCC CCGTTCCCTG GACGAGCCTC ATACCTGACA	10800
GCAAAAGGGT CAATCTTCAT CAGTTGATGA CCATTTTGAC GTGTGACATG ATATTTGTAA	10860
ATATGCCCTT CTTGAGCCAT ATTGGTAAAG ACTTCCCAGA CCCCCAAATC ATTTCTTACC	10920
ATTGGAATCT GATTTTCAAT CCAGTTGGTA AAATCACCAA CCAAGTGAAC AGCCTGAGCA	10980
TTAGGTGCCC AAACACGGAA GGTATAGCCA TGCTCTCCAT TTAGTTCTTC CCTATGTGCT	11040
CCTAGATAAT GTTGGAGATA AAAATTTTCA CCCGTCATAA AGGTTTTTTAA TGCTTCTCTA	11100
TTATCCATAT ACTCCCTTC TCCTGTAAGC GTTTTCTATG TTTTATTAT ACTACCTTTT	11160
TAGAGAAGAT TCAAGTAAAT TACTATACTT CTTTAATTAT TTTGAAAATC TACAACAAGT	11220
TCACTTACTC GTTCAATTGT AAATCAATAT TTTTCAAAA AATTGCGAAA ACGCCTTTCT	11280
TTTTCTACTA TAGTGAATG AAATAAAACA TGCGCAAATC GATTAAAGAA TTTAATCTAA	11340
TTTCTAACAA TGTCTTAGAA ATCAAAGTGT ACTATTTTAA CTCC	11384

(2) INFORMATION FOR SEQ ID NO: 46:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 7577 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 46:

TGTTGATTTG TTAGTAGACG TTGACCAACG TCCTTCGGCT GGAAAAGGAA TTCTCCTTAG	60
TTTCCAACAC GTTTTCGCCA TGTGTGGTGC GACCATCTTG GTACCATTGA TTTTGGGAAT	120
GCCTGTATCT GTTGCCTTTT TTGCTTCAAG TGTGGAACA CTCATCTACA TGATTGCTAC	180
TGGTTTTAAA GTTCCAGTTT ATCTAGGTTT TTCATTTGCC TTTATCACAG CTATGTCACT	240
GGCTATGAAA GAAATGGGGG GGGATGTATC TGCTGCCCAA ACAGGGGTTA TCTTGACTGG	300
TTTGGTCTAT GTCCTTGTG CTACCAGCAT CCGATTTGTA GGAACAAAAT GGATTGATAA	360
ACTCTTGCCA CCAATCATTA TCGGTCCTAT GATCATCGTT ATCGGTCTTG GACTTGCAGG	420
TTCAGCTGTT ACCAATGCAG GTCTTGTAGC AGACGGAAAT TGGAAAAATG CTCTGGTAGC	480
CGTTGTTACT TTCCTAATTG CTGCCCTTAT CAATACAAAA GGAAAAGGCT TCCTACGAAT	540
CATTCCATTC CTCTTTGCCA TTATCGGTGG TTACCTTTTC GCACTAACTC TTGGCTTGGT	600
TGACTTTACA CCAGTTCTTA AAGCCAACTG GTTCGAAAT CCTGGTTTCT ACTTGCCATT	660
TAGCACAGGT GGTGCCTTTA AAGAGTACAA TCTTTACTTT GGTCCAGAAG CCATCGCTAT	720

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CTTGCCAATC GCTATCGTAA CAATTTCTGA ACATATCGGA GACCATACTG TTTTGGGTCA	780
AATCTGTGGT CGTCAATPCT TAAAAGAACC AGGTCTTCAC CGTACTCTTC TTGGTGACGG	840
TATCGCAACT TCTGTTTCTG CCTTCCTTGG TGGACCAGCC AATACAACCTT ACGGAGAAAA	900
TACAGGGGTT ATCGGTATGA CTCGTATCGC TTCTGTCTCA GTTATCCGTA ACGCTGCCTT	960
CATCGCGATT GCCCTCAGCT TCCTTGGTAA ATTCACTGCC TTGATTTCAA CTATTCCAAA	1020
CGCTGTACTT GGTGGTATGT CAATCCTTCT CTATGGGGTT ATCGCCAGCA ATGGTTTGAA	1080
AGTCTTGATT AAAGAACGTG TTGATTTTCG TCAAATGCGA AACCTCATCA TCGCAAGTGC	1140
TATGTTGGTT CTTGGACTTG GAGGAGCTAT CCTTAAACTT GGTCCAGTTA CACTTTCAGG	1200
TACTGCCCTT TCAGCCATGA CAGGAATCAT CTTGAACCTG ATCTTGCCAT ACGAAAATAA	1260
AGACTAAGAG TCTAAATACA CCTAATCCAC TCAGACAGCT GAGTGGATTT TTCGTATACC	1320
ATAATAAAG TGTCTTAACA AAATTATTAA AATCAAAAAA CGTATAATAT CAGATATTCT	1380
AAAACCTTGA TACTGTACGT TTTATCATAG AAATTTTAC TTTATTTTCT CATCAAATGA	1440
GATTTGCATC AATCTCTGT CTTACTTGGC TTTCTTCTTC GCTTTCTTCA TTTGTTAGC	1500
CATACGTTTC ATGGACTGTT TCATGGCAAA TTCACCAATT TTACCTTTCA AACCGCCACC	1560
AAACATCTGG CTCATATCTG GCATTCCTGC TCCTCCGAGA GCTGATAAGT CAGGCATACC	1620
GCCTTGTCCT ATCATTCCTT CAAGGGCAGA CATATCCATT CCTCCCATAT TTGGCATATT	1680
TTTAGGAAGG TTATTTGGAT TAATCCCAT TTGCTTCATC ATTTTATTCA TATCCCCAGA	1740
CATAACACCC TGCATGAGCT GTTAGCCTG GTTAAAGTCC TTGATGAATT TATTGACTTC	1800
GACGAATGTA TTTCCAGAAC CAGCAGCAAT ACGACGCCGA CGGCTTGGAT TTAACAAATC	1860
TGGGTTTTCG CGCTCTTCAG GTGTCATCGA AGACACAATG GCACGTTTAC GAGCAATCTG	1920
GCGTTCATCC ACCTTCATGT TTTGAAGGGC TGGATTGTTG GCCATACCTG GAATCATCTT	1980
GAGCAAGTCT TCCATCGGCC CCATATTTTG CACCTGATCT AATTGATCGA TGAAATCATT	2040
AAAATCAAAG GTGTTTTCGC GCATCTTCTC AGCCATTTC AAGGCTTTTT GTTCATCGTA	2100
TTCTTGAGAA GCTTTCTCAA TCAAAGTGAG CATATCCCC ATACCAAGGA TACGGCTAGA	2160
CATGCGGTCT GGGTGAAGG TTTCAATGTC CGTAATCTTT TCACCTGTAC CAGTGAACCT	2220
GATTGGTTTT CCAGTAATGT GACGAACAGA CAGAGCAGCA CCACCACGAG TATCGCCATC	2280
AATCTTGGTA AGGATGACCC CAGTCACTTC CAACTGAGCA TTAAACTCAC GCGCAACATT	2340
GGCTGCTTCC TGACCAATCA TAGCATCAAC GACAAGCAAG ATTTCAATTG GTTGAGCCAA	2400
TGCTTTCACA TCACGAAGCT CATTATGAG GAGCTCATCA ATCTGCAAC GACCCGCAGT	2460
ATCAATCAAG ACATAGTCGT TATGATTAGT TTGGGCTTGC TCCAAACCTT GACGTACAAT	2520

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CTCAACAGCT GGTACTTCTG TTCCAAGTGC AAAGACAGGC ACATCAATCT GTTGTCCTCAA	2580
GGTCTTAAGC TGGTCAATGG CAGCTGGACG ATAAATATCC GCCGCAATCA TCAAAGGACG	2640
AGCATTTTCT TCTTTCTTGA GTTTGTTGGC CAATTTACCA GCAAAGGTTG TTTTACCAGC	2700
CCCTTGTAAG CCAACCATCA TGATGATGGT TGAATCTTA GGTGACTTGA TAATTTCTGC	2760
CGTATCAGAA CCTAAAACGG CTGTCAATTC CTCATCAACG ATTTTAATAA TCTGTTGCGC	2820
AGGATTAAGT GTATCAATGA CCTCATGCCC GACTGCACGC TCACGAACTT TCTTGATAAA	2880
GTCTTTTACA ACAGGCAAGG CAACGTCGGC CTCGAGCAAG GCCAAGCGAA TTTCTTTGGT	2940
TGCCTCTTGG ACATCAGATT CAGAGATTTT TCCTTTTMTA CGTAGATTTT TAAAGACGTT	3000
CTGCAACGTT TCTGTTAAAC TTTCAAATGC CATTTTCTT CCTCTTATTC TCTATTATCA	3060
ATGCTTGTAA AAATTTCTAT CTGCTCCTGC AGAAAGTCAT CCTTGGGATA GCGCTCCAAA	3120
ATCTGATCAA AAATCTGACT GCGGACAATA TAGTCCGAGT ACATGTGCAA TTTCATCTCA	3180
TAATCTTCCA GAATCTTTTC TGTTGCGTTG ATATGTGCAT AGACAGCCTG ACGACTGACA	3240
CCGAACCTCT CGGCAATTC AGCAAGGCTG TAATCATCAG CGTAGTAGAG CTCGATATAA	3300
TTTCTTTGCT TATCTGTCAA AAGCGCCGCA TAAATTCAA AGAGCGCATT CATACGATTG	3360
GTCTTTTTCGA TTTCATAAC TTTTATTATA CCAAAAATTA GCCTAATCTA CCACACTAGG	3420
AAGCGGATCC AAGAAGATAG ATAGCTAAAT TTGAAAAAGA CATGAGCCTA GCCCAAGTA	3480
ATTTCCAATT GATAGCTGGC AAAGGGATGT CCCTCTTGAT TTTGTAGTTG ATAATCTAGT	3540
TCAATCTTTT GCCTATCAAC TTGATAATGG CTCGTTTGA TGATAAACTC CTGCATGCCC	3600
ATAGGTGTAG GAATATAGGC TAACTATCG CTATCTTTA GAAAGCGCAT AATGGTCTTG	3660
GGATTAGAAA ATCGGCTCAT CACAAGTTCT TGACCATGAA ATTTAATCAC TACTTTTCC	3720
TTTCTCTCAT TATAGAAAAG CAGGTAGCTA TAATCTCCTT TTTTCATGCAC TTCCACATCA	3780
TAAAGCTGGT CAATCACTTC CAACTGCTCA TCAAACTGAA TCGTATTTG CATCCGAATC	3840
TTACATCAG GCCCTCTTC TTGTCTCTG TCCTACTATT TTACCAAAAA GAGCAGGATT	3900
TTGCTATAAT GGTATATGA ACGAAAAAGT ATTCCGTGAC CCTGTTTACA ACTACATCCA	3960
TGTCAATAAT CAAATCATCT ATGACTTGAT TAATACAAA GAATTTGAGC GTTTGCGCCG	4020
GATCAAAACA CTGGGAACCT CCAGTTATAC CTCCACGGT GGAGAACACA GTCGCTTCTC	4080
TCAGTGTCTA GGAGTCTATG AAATTGCACG ACGCATCACA GAGATTTTCG AAGAAAAATA	4140
TCCTGAGGAA TGGAATCCTG CCGAGTCTCT CTTGACCATG ACCGCTGCTC TCCTACACGA	4200
CCTTGGGCAT GGTGCCTACT CCCATACTTT TGAACATCTC TTTGATACAG ACCATGAAGC	4260

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CATTACTCAG GAGATTATTC AAAATCCTGA GACAGAGATT CACCAAGTCC TGCTACAAGT	4320
GGCACCTGAT TTCCCAGAAA AGGTGGCCAG TGTCATTGAC CATACCTATC CTAATAAGCA	4380
GGTCGTGCAG CTCATTTCCTA GTCAGATTGA CGCAGATCGC ATGGACTATC TCTTGCGCGA	4440
CTCCTATTTT ACAGGAGCAT CCTATGGGGA ATTTGACCTG ACTCGAATCC TCCGAGTCAT	4500
TCGTCCTATC GAAAAATGGTA TCGCCTTTCA GCGCAATGGC ATGCACGCCA TCGAAGACTA	4560
CGTCCTCAGT CGCTACCAGA TGTACATGCA GGTTTATTTT CACCCCGCAA CACGCGCCAT	4620
GGAAGTTCTC CTACAGAATC TTCTCAAACG CGCCAAGGAA CTCTATCCTG AGGACAAGGA	4680
TTTCTTTGCC CGAACTTCTC CACACCTCCT GCCTTTCTTC GAAAAAATG TGACCTTGAC	4740
TGACTATCTG GCTCTGGATG ATGGCGTGAT GAATACCTAC TTCCAGCTTT GGATGACCAG	4800
TCCTGACAAG ATTCTTGCA GATTATCGCA TCGCTTTGTC AACCGCAAGG TCTTTAAATC	4860
CATTACCTTT TCACAAGAGG ACCAAGATCA ACTTACTAGC ATGAGAAAAT TGGTTGAGGA	4920
TATCGGCTTT GATCCCGACT ACTACACTGC CATTACATAAG AACTTTGACC TCCCTTATGA	4980
TATCTATCGT CCCGAATCTG AAAACCCACG GACACAGATT GAGATTTTAC AAAAAAATGG	5040
AGAAGTGGCC GAACTCTCTA GCCTGTCTCC TATCGTCCAA TCCCTTGCTG GCAGTCGCCA	5100
CGGAGATAAT CGCTTTTATT TTCCAAAAGA AATGTTGGAC CAAAACAGCA TCTTTGCAAG	5160
CATTACCCAG CAATTTTAC ACTTGATTGA GAACGATCAT TTTACCCCAA ATAAAACTA	5220
GAAGAGGAAA TTTATGAGTA TTAACTAAT TGCCGTTGAT ATCGACGGAA CCCTTGTCOA	5280
CAGCCAAAAG GAAATCACTC CTGAAGTTTT TTCTGCCATC CAAGATGCCA AAGAAGCTGG	5340
TGTCAAAGTC GTGATTGCAA CTGGCCGCC TATCGCAGGC GTTGCCAAAC TTCTAGACGA	5400
CTTGCACTG AGAGACGAGG GGGACTATGT GGTAACCTTC AACGGTGCCC TTGTCCAAGA	5460
AACTGCTACA GGACATGAGA TTATCAGCGA ATCCTTGACT TATGAGGATT ATCTAGATAT	5520
GGAATTCCTC AGTCGCAAGC TCGGTGTCCA CATGCATGCC ATTACCAAGG ACGGTATCTA	5580
TACTGCAAAAT CGCAATATCG GAAAATACAC TGTACACGAA TCAACCTCG TCAGCATGCC	5640
TATCTTCTAC CGTACCCCTG AAGAAATGGC TGGCAAAGAA ATTGTTAAAT GTATGTTTAT	5700
CGATGAACCA GAAATTCTCG ATGCTGCGAT TGAAAAAATT CCAGCAGAAT TTTACGAGCG	5760
CTACTCCATC AACAAATCTG CTCCTTTCTA CCTCGAACTC CTTAAAAAGA ATGTAGACAA	5820
GGGTTACGCC ATTACTCACT TGGCTGAAAA ACTCGGATTG ACCAAAGATG AAACCATGGC	5880
AATCGGTGAT GAAGAAAATG ACCGTGCCAT GCTGGAAGTC GTTGGAACCC CCGTTGTCAT	5940
GGAAAATGGA AATCCAGAAA TCAAAAAAAT CGCCAAATAC ATCACCAGAA CAAATGACGA	6000
ATCCGGCGTT GCCCATGCCA TCCGAACATG GGTACTGTAA AAGTATCATT TTTCAATAAG	6060



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AATTGATTAG CAATAAAATC CAATGAATTT TTTTAGCAAA CTATTTAATT TAAAACAAAA	6120
TAATCATAAT AGAGACACAA ATTCTGATTG TAACAATTTT TACCTAAACG AATTAGAATG	6180
TGGCCTTACT CCTGGGCAAC TCATACTCAT AGATTGGACT CAAAAAACAG GGAGAAATTA	6240
TAATTTCCCA AGATATTTTA AATACTCTCT TCAAATTGAC CCTGAATCTA CACACAATCA	6300
ATTATACAAA TTAGGATACT TCACTAAAAA TAAGACTTTA TCATATCTTA CAGTAGTAGA	6360
ATTAAAAACT ATATTATCTA AACATAATTT AGCTACTTCT GGAAAAAAG CAGAATTAAT	6420
TACAAGAATA ATTAATAATG TTAACATTGA CAATTTAGAT ATTCCGTTTCG AATTTAAACT	6480
AACAAAAGAA GCACAAAATC TTATTATCGA ACATAGTGAC TATATCAAAG CATACTATGA	6540
TAAAGACATA ACTATGGAAG ATTATTGTAA AGAAAAAAC AATATCTCTT TTAAAGCAAC	6600
TTTTGGTGAT ATAAATGGA GTCTCTTAAA TAAACAAGCT CATAGGAATA CTGTATCAGG	6660
AGATTTTGGA TGCTTATCTA ACACACGAAA GGCTCAGGGA AGACATTTGG AACAGAAGG	6720
TAATATTAAA CATGCTTTAA TATATTACAT AGAATCTTTG ATAATTACTA TTTCAGGATT	6780
AGAAAACAA TTTTCAGCCA CTGATTATCC AGTATATTAT CCCGATTCTGA TACCTGACTA	6840
CTCACTAAAA CATATTCAA CATTAAATGGA ATCATTATCT GATGACGATT ATGATTTTGC	6900
TTTGATGAA GCATTATTTT GCTTCTCAAT TTTGAATGCA AATCATTTTT TATCTAAGGA	6960
AGATATTGAC TATTTAAGAG TTAATTTACC TCGTTCCACT GCTGAAGAAA TAAACAATTA	7020
CTTAAAGAAA TATGAATGTT ATAGTCCTTT AAATAATTTA GAACTTGACG ATTTTGAATA	7080
AATTGACTAT ACAAACATTT ATATACTCGA TATAGTCTCA ATTTTATCTG ATGATTGCCC	7140
AAATTTTTCATAATAAAAC GCATAATATT ATGGAGACAA TCCCCTATAT TATGCGTTCT	7200
TTTAATATCA AAGACTTTTT GACAACTTC TTTGATATCT AATTACATGC CCCCTGCAGG	7260
AATCGAACCT GCAACTACTC CTTAGGAGGG AGTTGTTATA TCCATTGAAC TAAGGGAGCT	7320
AGATAAAAC TCTGCTAAAT GAGCAGAGTT TTTTAGTCGA ATTAACGACG GATTTCTTTG	7380
ATACGAGCTG CTTTACCTTG AAGAGCACGC AAGTAGTACA ATTTGCGACG ACGTACTTTA	7440
CCGTAACGAA CAACTTCGAT TTTTCAACA CGTGGAGTGT GGATTGGGAA GATACGCTCA	7500
ACACCTACAC CGTTAGAGAT TTTACGAACT GTGTAGTTTT CTGAGATTCC AGCACCTTTA	7560
CGTGCGATAA CAACACG	7577

(2) INFORMATION FOR SEQ ID NO: 47:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 4945 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

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(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 47:

CCTCGCTGAT GATGGTGCT GTTTTATTG CTGGTCCAGC CTTGGCTGAA GAAACTGCAG	60
TTCTTGAAAA TAGCGGAnCT AATACAGAGC TTGTTTCAGG AGAGAGTGAG CATTCGACCA	120
ATGAAGCTGA TAAGCAGAAT GAAGGGGAAC ATGCTAGAGA AAACAAGCTA GAAAAGGCAG	180
AAGGAGTAGC GATAGCATCT GAAACTGCTT CGCCAGCAAG CAATGAAGCT GCAACTACTG	240
AAACTGCAGA AGCAGCTAGC GCAGCTAAAC CAGAGGAAAA AGCAAGTGAG GTGGTTGCAG	300
AAACACCATC TGCAGAAGCA AAACCTAAGT CTGACAAGGA AACAGAAGCA AAGCCCGAAG	360
CAACTAACCA AGGGGATGAG TCTAAACCAG CAGCAGAAGC TAATAAGACT GAAAAAGAAG	420
TCCAGCCAGA TGTCCTAAA AATACAGAAA AAACATTAAA ACCAAAGGAA ATCAAATTTA	480
ATTCTTGGA AGAATTGTTA AAATGGGAAC CAGGTGCTCG TGAAGATGAT GCTATTAACC	540
GCGGATCTGT TGTCCTCGCT TCACGTCGGA CAGGTCATTT AGTCAATGAA AAAGCTAGCA	600
AGGAAGCAAA AGTTCAAGCC TTATCAAACA CCAATTCTAA AGCAAAAGAC CATGCTTCTG	660
TTGGTGGAGA AGAGTTCAAG GCCTATGCTT TTGACTATTG GCAATATCTA GATTCAATGG	720
TCTTCTGGA AGGTCTCGTA CCAACTCCTG ACGTTATTGA TGCAGGTCAC CGTAACGGGG	780
TTCTGTATA CGGTACACTC TTCTTCAACT GGTCTAATAG TATTGCAGAT CAAGAAAGAT	840
TTGCTGAAGC TTTGAAGCAA GACGCAGATG GTAGCTTCCC AATTGCCCGT AAATTGGTAG	900
ACATGGCCAA GTATTATGGC TATGATGGCT ATTTTCATCA CCAAGAAACA ACTGGAGATT	960
TGGTTAAACC TCTTGAGAA AAGATGCGCC AGTTTATGCT CTATAGCAAG GAATATGCTG	1020
CTAAGGTAAG CCATCCAATC AAGTATTCTT GGTACGATGC CATGACCTAT AACTATGGAC	1080
GTTATCATCA AGATGGTTTG GGAGAATACA ACTACCAATT CATGCAACCA GAAGGAGATA	1140
AGGTCCGGC AGATAACTTC TTTGCTAACT TTAAGTGGGA TAAGGCTAAA AATGATTACA	1200
CTATTGCAAC TGCCAACTGG ATTGGTCGTA ATCCITTATGA TGTATTTGCA GGTTTGGAAT	1260
TGCAACAGGG TGGTTCTTAC AAGACAAAGG TTAAGTGGAA TGACATTTTA GACGAAAATG	1320
GGAAATTGCG CCTTCTCTT GGTTTATTTG CCCAGATAC CATTACAAGT TTAGGAAAAA	1380
CTGGTGAAGA TTATCATAAA AATGAAGATA TCTTCTTTAC AGGTTATCAA GGAGACCCTA	1440
CTGGCCAAAA ACCAGGTGAC AAAGATTGGT ATGGTATTGC TAACCTAGTT GCGGACCGTA	1500
CGCCAGCGGT AGGTAATACT TTTACTACTT CTTTAAATAC AGGTCATGGT AAAAAATGGT	1560
TCGTAGATGG TAAGGTTTCT AAGGATTCTG AGTGGAATTA TCGTTCAGTA TCAGGTGTTT	1620

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TTCCAACATG GCGCTGGTGG CAGACTTCAA CAGGGGAAAA ACTTCGTGCA GAATATGATT	1680
TTACAGATGC CTATAATGGC GGAAATTCCT TTAATTTCTC TGGTGATGTA GCCGGTAAGA	1740
CAGATCAGGA TGTGAGACTT TATTCTACTA AGTTAGAAGT AACTGAGAAG ACCAAACTTC	1800
GTGTTGCCCA CAAGGGAGGA AAAGGTTCTA AAGTTTATAT GGCATTCTCT ACAACTCCAG	1860
ACTACAAATT CGATGATGCA GATGCATGGA AAGAGCTAAC CCTTTCTGAC AACTGGACAA	1920
ATGAAGAATT TGATCTTAGC TCACTAGCGG GTAAAACCAT CTATGCAGTC AACTATTTT	1980
TCGAGCATGA AGGTGCTGTA AAAGATTATC AGTTTAACCT AGGACAATTA ACTATCTCGG	2040
ACAATCACCA AGAGCCACAA TCGCCGACAA GCTTTCTGT AGTGAAACAA TCTCTTAAAA	2100
ATGCCCAAGA AGCGGAAGCA GTTGTGCAAT TTAAAGGCAA CAAGGATGCA GATTTCTATG	2160
AAGTTTATGA AAAAGATGGA GACAGCTGGA AATTACTAAC TGGCTCATCT TCTACAACTA	2220
TTTATCTACC AAAAGTTAGC CGCTCAGCAA GTGCTCAGGG TACAACTCAA GAACTGAAGG	2280
TTGTAGCAGT CGGTAAAAAT GGAGTTCGTT CAGAAGCTGC AACCACAACC TTTGATTGGG	2340
GTATGACTGT AAAAGATACC AGCCTACCAA AACCCTAGC TGAATAATC GTTCCAGGTG	2400
CAACAGTTAT TGATAGTACT TTCCCTAAGA CTGAAGGTGG AGAAGGTATT GAAGGTATGT	2460
TGAACGGTAC CATTACTAGC TTGTCAGATA AATGGTCTTC AGCTCAGTTG AGTGGTAGTG	2520
TGGATATTCG TTTGACCAAG CCACGTACCG TTGTTAGATG GGTGATGGAT CATGCAGGAG	2580
CTGGTGGTGA GTCTGTTAAC GATGGCTTGA TGAACACTAA AGACTTTGAC CTTTATTATA	2640
AAGATGCAGA TGGTGAGTGG AAGCTAGCTA AGGAAGTCCG TGGTAACAAA GCACACGTGA	2700
CAGATATCAC TCTTGATAAA CCAATCACTG CTCAAGACTG GCGCTTGAAT GTTGTCACTT	2760
CTGACAATGG AACTCCATGG AAGGCTATTC GTATCTATAA CTGGAAAATG TATGAAAAGC	2820
TTGATACTGA GAGTGTCAAT ATTCCGATGG CCAAGGCTGC AGCCCGTTCT CTAGGCAATA	2880
ACAAGGTACA AGTTGGCTTT GCAGATGTAC CGGCTGGAGC AACTATTACC GTTTATGATA	2940
ATCCAAATTC TCAAACTCCG CTCGCAACCT TGAAGAGCGA AGTTGGAGGA GACCTAGCAA	3000
GTGCACCAAT GGATTGACA AATCAATCTG GTCTTCTTTA TTATCGTACC CAGTTGCCAG	3060
GCAAGGAAAT TAGTAATGTC CTAGCAGTTT CCGTTCCAAA AGATGACAGA AGAATCAAGT	3120
CAGTCAGCCT AGAAACAGGA CCTAAGAAAA CAAGCTACGC CGAAGGGGAG GATTTGGACC	3180
TTAGAGGTGG TGTCTTCGA GTTCAGTATG AAGGAGGAAC TGAGGACGAA CTCATTGCCC	3240
TAATCAGCAG AGGTGTATCA GTATCAGGTT TTGATACGCA TCATAAGGGA GAACAGAATC	3300
TTACTCTCCA ATATTTGGGA CAACCGGTAA ATGCTAATTT GTCAGTGACT GTCAGTGACC	3360

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AAGACGAAGC AAGTCCGAAA ACTATTTTGG GAATTGAAGT AAGTCAGGAA CCGAAAAAAG	3420
ATTACCTAGT TGGTGATAGC TTAGACTTGT CTGAAGGACG CTTTGCAGTG GCTTATAGCA	3480
ATGACACCAT GGAAGAACAT TCCTTTACTG ATGAGGGAGT TGAAATTTCT GGTACGATG	3540
CTCAAAAGAC TGGTCGTCAA ACCTTGACGC TTCATTACCA AGGCCATGAA GTTAGCTTTG	3600
ATGTTTGGT ATCTCCAAA GCAGCATGA ACGATGAGTA CCTCAAACAA AAATTAGCAG	3660
AAGTTGAAGC TGCTAAGAAC AAGGTGGTCT ATAACCTTGC TTCATCAGAA GTAAAAGAAG	3720
CCTTCTTGAA AGCAATTGAA GCGGCCGAAC AAGTGTGAA AGACCATGAA ACTAGCACCC	3780
AAGATCAAGT CAATGACCGA CTTAATAAAT TGACAGAAGC TCATAAAGCT CTGAATGGTC	3840
AAGAGAAAT TACGGAAGAA AAGACAGAGC TTGATCGCTT AACAGGTGAG GTTCAAGAAC	3900
TCTTGGCTGC CAAACCAAC CATCCTTCAG GTTCTGCCCT AGCTCCGCTT CTTGAGAAAA	3960
ACAAGGCCTT GGTGAAAAA GTAGATTGA GTCCAGAAGA GCTTACAACA GCGAAACAGA	4020
GTCTAAAGA TCTGGTTGCT TTATTGAAAG AAGACAAGCC AGCAGTCTTT TCTGATAGTA	4080
AAACAGGTGT TGAAGTACAC TTCTCAAATA AAGAGAAGAC TGTCATCAAG GGTTTGAAAG	4140
TAGAGCGTGT TCAAGCAAGT GCTGAAGAGA AGAAATACTT TGCTGGAGAA GATGCTCATG	4200
TCTTTGAAAT AGAAGGTTTG GATGAAAAAG GTCAAGATGT TGATCTCTCT TATGCTTCTA	4260
TTGTGAAAAA CCCAATTGAA AAAGATAAGA AAGTTAAGAA AGTATTTTTC TTACCTGAAG	4320
GCAAAGAGGC AGTAGAATTG GCTTTTGAAC AAACGGATAG TCATGTTATC TTTACAGCAC	4380
CTCACTTTAC TCATTATGCC TTTGTTTATG AATCTGCTGA AAAACCACAA CCTGCTAAAC	4440
CAGCACCACA AAACACAGTC CTTCCAAAAC CTACTTATCA ACCGACTTCT GATCAACAAA	4500
AGGCTCCTAA ATTGGAAGTT CAAGAGGAAA AGGTTGCCTT TCATCGTCAA GAGCATGAAA	4560
ATACTGAGAT GCTAGTTGGG GAACAACGAG TCATCATACA GGGACGAGAT GGAAGTTTAA	4620
GACATGTCTT TGAAGTTGAT GAAAACGGTC AGCGTCGTCT TCGTTCAACA GAAGTCATCC	4680
AAGAAGCGAT TCCAGAAATT GTTGAAATTG GAACAAAAGT AAAACAGTA CCAGCAGTAG	4740
TAGCTACACA GGAAAAACCA GCTCAAAATA CAGCAGTTAA ATCAGAAGAA GCAAGCAAAC	4800
AATTGCCAAA TACAGGAACA GCTGATGCTA ATGAAGCCCT AATAGCAGGC TTAGCCAGCC	4860
TTGGTCTTGC TAGTTTAGCC TTGACCTTGA GACGGAAAAG AGAAGATAAA GATTAAATAT	4920
CGAAAAATCT TGTGAAATCT TTCCG	4945

(2) INFORMATION FOR SEQ ID NO: 48:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 25002 base pairs
  - (B) TYPE: nucleic acid

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(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 48:

GACAACTCAA GTAGCTTTT CTTATTTTGA AAAAGGAGAT CAGAGTTTAA CTATGTCAGA	60
AAAATCACAA TGGGGGTCGA AACTTGGTTT TATTCTAGCA TCTGCTGGCT GGCCATCGGG	120
CTTGGTTCCG TTTGGAAGTT TCCCTACATG ACTGCTGCTA ATGGCGGTGG AGGCTTTTAA	180
CTAATCTTTC TCATTTCCAC TATTTTAATC GGTTCCTC TCCTGCTGGC TGAGTTTGCC	240
CTTGGCCGTA GTGCTGGCGT TTCCGCTATC AAAACCTTTG GAAACTGGG CAAGAATAAC	300
AAGTACAACT TTATCGGTTG GATTGGCGCC TTTGCCCTCT TTATCCTCTT ATCTTTTAC	360
AGTGTATCG GAGGATGGAT TCTAGTCTAT CTAGGTATTG AGTTTGGGAA ATTGTTCCAA	420
CTTGGTGGA GCGGTGATTA TGCTCAGTTA TTTACTTCAA TCATTTCAAA TCCAGCCATT	480
GCCCTAGGAG CTCAAGCGGC CTTTATCCTA TTGAATATCT TCATTGTATC ACGTGGGGTT	540
CAAAAAGGGA TTGAAAGAGC TTCGAAAGTC ATGATGCCCC TGCTCTTTAT CGTCTTTGTT	600
TTTATCATCG GTCGCTCTCT CAGTTTGCCA AATGCCATGG AAGGGGTTCT TACTTCCTC	660
AAACCAGACT TTTCAAACT GACTAGCACT GGTCTCCTCT ATGCTCTGGG ACAATCTTTC	720
TTTGCCCTCT CACTAGGGGT TACAGTCATG TTGACCTATG CTTCTTACTT AGACAAGAAA	780
ACCAATCTAG TCCAGTCAGG AATCTCCATC GTAGCCATGA ATATCTCGAT ATCCATCATG	840
GCAGGTCTAG CCATTTTCCA AGCTCGATCC CCCTTCAATA TCCAGTCTGA AGGGGGACCC	900
AGCCTGCTCT TTATCGTCTT GCCTCAACTC TTTGACAAGA TGCCTTTGG AACCATTTC	960
TACGTCCTCT TCCTCTGCT CTTCCCTTTT GCGACAGTCA CTTTCTCTGT CGTGATGCTG	1020
GAAATCAATG TAGACAATAT CACCAACCAG GATAACAGCA AACGTGCCAA ATGGAGTGT	1080
ATTTTAGGAA TTTTGACCTT TGTCTTTGGC ATTCCCTCAG CCCTATCTTA CGGTGTCATG	1140
GCGGATGTT ACATTTTGG TAAGACCTTC TTTGACGCTA TGGACTTCTT GGTTCCTCAAT	1200
CTCCTCATGC CATTTGGAGC TCTCTACCTT TCACTTTTAA CAGGCTATAT CTTTAAAAAG	1260
GCTCTTGCAA TGGAGGAACT CCATCTCGAT GAAAGAGCAT GGAAACAAGG ACTGTTCCAA	1320
GTCTGGCTCT TCCTTCTTCG TTTCTTCGTT TCGTCATTCC AATCATCATC ATTGTGGTCT	1380
TCATTGCCCA ATTTATGTAA TCAAAAAGGA CTTGAGTAGT GAACTCAGGC CCTTCTTTT	1440
TATGGATGGC TAACAATCAA TTCCAAACCT TGCCCTTCCA GAGTCCAAGC TTCAACATCA	1500
CTTGGTAGGA TAAAGTGGCT GCCTTTTGA ATTGGATAAT TTTCCCGTC AACAGTTAGC	1560

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TGACCTTGAC CAGCCAAGAC ACTCAATAAG CTGTAGTCAG CTGTCTTTTC AAAGTCAACT	1620
TTTCCAGTAA TTTCCCACTT GTAAACTGCG AAGAAATCAT TAGATACAAG GAGAGTGGAA	1680
CGCAATCAT CTGCTTTAAC AGTTACAGGA CGGCTATTTG CTGGCTCACC AATGTTCAAG	1740
ACATCGATGG ATTTTTC AAG ATGAAGTTCA CGCAAGTTGC CTTTGTATC CTTGCGGTCA	1800
AAGTCATAGA CGCGATAGGT GGTATCGCTA GACTGCTGGG TTTCAAGGAT TAAGATACCC	1860
GCCCCGATAG CGTGATAGT CCCGCTTGGT ACATAGAAGA AATCTCCAGC CTTAACAGGG	1920
ACTTTGGTCA ACAAGTCATC CCAGTTCTTG TCCTCGATT GCTGGCGGAG TTCTTCTTTT	1980
GACTTGGCAT TGTGACCGTA GATAATCTCT GAACCTTCAT CCGCTGCGAT AATGTACCAG	2040
CATTCTGTTT TTCCGAGTTC GCCTTCATGC TCGAGTCCAT AAGCATCGTC TGGGTGAACT	2100
TGGACACTGA GCCAGTCGTT GGCATCGAGG ATCTTGGTCA AAAGTGGAAA TACAGGTCTT	2160
GGACGATTGC CAAATAATTC ACGGTGTTCC GCATACAAAG TAGCAAGATC TGTTCCTCG	2220
TAACGACCAT TGGCAACTTT AGAGACTCCA TTTGGATGGG CTGAGATGGC CCAATATTCT	2280
CCGATTTTTT CACTTGGGAT GTCGTAGCCA AACTCATCAC GTAGCTTGGC TCCACCCAG	2340
ATTTTTTCTT GCATAACTGA TTGTAAAAAT AATGGTTCTG ACATGTCGAT CTCCTGTCTG	2400
ATTTTTCTCC CCTCATTATA GCAAAAAAG AGTTCGAATT GAACCTTTTT TTACATCTTA	2460
TAAAGCAGGG AGAAGATTTT ATAAAAATAG TAAACAAATG TGCTCTACCC GATGCTTGCA	2520
CCATGTCTAT AAATGACATC CTTGTACCAA TAGAAGGACT TCTTCTTGCT ACGTTTGAGA	2580
GCTCCGTTTC CTACATTATC TCGATCTACA TAGATAAAGC CATAGCGCTT ATTCATTTC	2640
CCTGTGCCAG CTGAAACCGG ATCGATACAG CCCCAGTCG TATAACCAAG CAAGTCAACC	2700
CCGTCTTGGT AAATGGCATC TCGCATGGCC TTGATGTGGG CCTCTAAGTA AGTAATCCGA	2760
TAGTCATCTG CTACATAACC ATTCTCATCC GGTGTATCCA TAGCACCAG TCCATTTTCT	2820
ACGATAATAC TAACTAAAA TCAAAAAGCA TTATATAATA GTGATATGAA ATCAACTAAA	2880
GAAGAAATCC AAACCATCAA AACACTTTTA AAAGACTCTC GTACAGCTAA ATATCATAAA	2940
CGCCTTCAAA TCGTTCTATA GTAAAATGAA ATAAGAACAG TACAAATCGA TCAGGACAGT	3000
CAATCGATT TCTAACAATG TTTTGAAGT AGGGGTGTAC TATTCTAGTT TCAATCTACT	3060
ATATTTCTGC TGATGGGCAA ATCTTATAAA GAGATTATAG AACTTTTATA GTAGTTTGAA	3120
ATAAGATGTG AACAACTCTA TCAGGAAAGT CAAATTAATT TATAGAAATA TTTTAGCAGC	3180
CAAGGTGTAC TGTATATAGT TCAATACACT ATAGACTGTA ATCAACAAC GATTGTGGCA	3240
AATGTAAAAA AATATGAGGA GTTCGGACTC GACTCTCTCC TTCAAGAAAC ACGTGGTGGT	3300
CGTAACCATG CATATATGAC AGTTGAGGAA GAGAAAGCCT TTCTTGCCCC CCATTGAAG	3360

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GCTACAGAGG CAGGAGAATT TGTTACAATT GATGCCTTAT TTCAGGCTTA TAAAAAGGAG	3420
TTAGGTCGTT CCTACACACG TGATGCCTTC TATCAACTGT TGAAGCGCCA TGGTTGGCGA	3480
AATATTACGC CACGTCCAGA ACATCCTAAG AAAGCAGACG CTCAAACCAT TGTTCGGTCT	3540
AAAAATAAAA TCTCAATCCA AGAAGGCAAG AAAGCGTTTT AAATATAGTA GACGTTTTTCG	3600
TAAGGTTTGC TTGATGTACC AAGCTGAAGC TGGTTTCGGT AGAATCAGTA AACTGGGATC	3660
TTGTGGGCT CCAATAGGAG TAGGTCCACA TATCCATAGT CACTATATAC GAGAATTTTCG	3720
CTATTGTTAT GGAGCTGTTG ATGCCTATAC AGGCGAATCA TTTTCTTAA TAGCTGGTAG	3780
ATGTAATACT GAGTGGATGA ACGCCTTTTT AGAAGAGCTT TCACAAGCTT ATCCTTTTAC	3840
TCGTTATGGA CAATGCTATA TGGCATAAAT CAAGTACCTT AAAGATTCGG ACTAATATTG	3900
GTTTTGCATT TATTCCTCCA TACACACCAG AGATGAACCC CATTGAACAA GTGTGGAAAG	3960
AGATTGTAAG ACGTGGATTT AAGAATAAAG CCTTTCGAAT TTTGGAAGAT GTCATGAATC	4020
AACTCCAAGA TGTCATACAA GGATTGGAGA AGGAGGTGAT AAAGTCCATC GTTAATCGGA	4080
GATGGACTAG AATGCTTTTT GAAAGCAGAT GAGTATTATA TGCAATTTCT TTATATAAAA	4140
AGACCGGATT GCTCCGATCT TTCAATAGTT CATATTCTCA ATTTCTATTT TAAAAATAGC	4200
TAAGGTTAAC GTCAAATGAC TACGCGACCT ATTTCATACG ATAAAAATCA AGCACTAGAC	4260
CAGCAGGTCC TTGAACTAAT AAGGACTCTG TTCCCAATC GGTACAGTT GGTCCGTGTA	4320
AAACCTTTAT ACCAAGCTCG TTCAACCGTT TGTAGTTCTG GTCTACATCC TCAACCTCGA	4380
TATGAATAAT GATTCCTGAC TGAAAGTTTT CCAAAGGAAC CAAATGATTT TGTGACAACA	4440
TAAGGCAGTG ACTACCAATC GTAAACTGAG CAAAACCATC ATTAGCATAA TCTGCCTTTT	4500
TATCCAAGAT ATGCTCCAAG TCAGCACAGA CTTGGGGAAC ATTTGAAACG ATAATATCTA	4560
ATTGATTTAA ATTCATTTAC TCTCCTCCAT AAAAAGACCG GATTGCTCCG ATCTTTTAAA	4620
GTTCGTCTCT ATGAAAATCA AAGAATAAAG TCTACAAGTT TCATATTGA TTTTCGGCGA	4680
GAGGAATTAT TTAATTGCGC GTGATTGCAA TCCTTCTTCT TCCAAGAAGA GACGGAATGG	4740
TACGAGTTCT TCTGCTTCGT ATTTTTCCTT GAAGGCTTTG ATAGCTTCTT CTGAGTGAAG	4800
TTTGGATCC AATTCAAGTA CTTCTACTGG AAGTGGACGG TGTGAGTGA TGGGAGCATC	4860
GATGACAACA GTTTTACCTT CTTTGTTCAA TTTAACAGCT TCTGCAACAA CTGCATCGAT	4920
GTCTTCGATA CGGTCAACTG TGAATCCAAC AGCTCCTTGA GCTTCGCAA TTTTAGCGTA	4980
GTGAGCGTTT GTGAAGTCTA CACCAACAA GTGTTTGTG GTATCTTCGT ATTTGTCTT	5040
GATGAAGCCG TACTCAGCAT TTGAGAAGAC AAGGTTGATA ACTGGAAGGT CGTATTGAAC	5100

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GTTTGTGATA ACGTCTGGGT AGCACATGTT GAATGCTCCG TCACCCATGA TGTTCATAC	5160
TTGGCGATCT GGATTGTCTT TCTTAGCAGC GATACCACCA GGAAGGGCAA TACCCATTGT	5220
CGCAAAGAGT GGAGATGTAC GCCACATGTT CTTAGGTGTC ATGTGAAGGT GACGAGTAGA	5280
TGTTTGAGTA GTGTTACCTA CGTCGATTGA GTAGATAGCG TCTTGATCAG CATGTTTGTT	5340
GATTGCATTG TAAACTTGAT ACAATTGCAA TTCACCCCTCA GTTTTACCTT CGAGTTTGTT	5400
CATGTAATCA CGCCAGTTTT GGTGTTCTT AACGTTTGCA CGCCACCATG GAGTTGATTG	5460
AACTGGGTTT ACTTTGTCAA GGATAGCTTT AGCTGCTTGA CCAGCATCAC CAAGGATTGA	5520
AGCGTCAAGG GCATGACGTT TACCAAGTTT GTAAGGGTCG ATATCGACTT GGATGAATTT	5580
TTCAGTGTTT TGAAATGCTT CGTAACTTC AGCAAATGGG AAGTTTGAAC CAAGGAAAAG	5640
AACTGTGTCT GCTTCAAAGA CCACCTTCGTT GGCTGGTTTC CAACCAACAC GGTAAAGCAGA	5700
ACCTGTCAAA CCTTCATAGT TCCATTGCAA AGCTTCAAAG TTTTACCAG TTGTGATGAT	5760
TGGTGCTTTG ATTTTACGTG ACAATTCAGT AATCACTTCA CCAGCTTTAA CACCACCAA	5820
TCCAGCATAG ATAAGTGGC GTTCAGCATT GTTCAAGATT TCAACAGCTT TGTCGATTTT	5880
AACTTCGTTT AAAGCAGGAG CGATGAATGA GCGTTCTGAT GAACCTGAAC CGTAGTATGA	5940
GTTTTCATCG ATTTCTTGA AACCAGGTT TACTGGAATT TCAACAACAG CTGGACCTTT	6000
TTTAGAAACT GCAGCAGGC AGGCTTCGTC AATTACTTTT GGCAATTGCT CAGCGTAAGC	6060
TACACGTTTG TTGTAAACAG CGATACCGTT GTACATTGGG TTTTGGTTAA GCTCTTGAA	6120
AGCATCCATG TTCAATTCGT TAACTGGACG TGATCCAAGG ATCGCTAGGA ATGGAGTGTT	6180
ATCCATAGCT GCATCGTAAA CACCGTTAAT CAAGTGAGTC GCACCTGGAC CACCTGAACC	6240
AACTGCAACC CCGATTGAGC CGCCGAATTT AGCTTGCTATA ACCGCTGCAA GAGCACCTGT	6300
CTCTTCGTGG CGAACTTGTA AGAAACGGAT ATCTTTGTCT TCAGCCAAAG CGTCCATCAA	6360
TGAGCTGAGT GTTCCTGATG GGATACCGTA GATTGTATCT ACGCCCCATG TTTTCAATAC	6420
GTTAAGCATT GCTGCAGATG CAGTAATTTT CCCTTGAGTC ATAATGATAA CTCTCCTTCA	6480
ATTTTTTTAA ACTTGGAGAA TACGATTACA TAGAATTGGA AACGTTCTCC AAATTTTAC	6540
TATTCCTAGT TATCATATTT ATGCTGACTT TTCTAAAAAT CTGCTCAAAA CTCTCTATTC	6600
TCTATTCTAA TACAGTTTTG AAAGTTCTGT CATTTCTGTT TTATAACAAA GAAATCTAGT	6660
CATTACTTTT AGTCTATTTT ACTAAAAAT AACAGAAGGG AACTGGTCAG AACAGATACA	6720
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ATATCTTAAC TCTTTTCAA AACTTTTAAA ATATTTTGTG TGGAAATTC AGAAATTTTA	21000
TGTCTATGAT AAAAATCCTT ATAACGGCAA TAAAAATAG ATATTATCCA AAGAAGATTT	21060



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TAAGTGCTAC AATAACTGTA TTATTTCTAG ATGGGAGGTT CTATTTTGG ATTGATCCAT	21120
TGTTGAACAA TATCTACCAC TATATCAAAA GGCATTCTTT CTGACCTTGC ATATTGCAGT	21180
TTGGGGAATT TTGGGATCCT TTCTGCTCGG TTTAATCGTT AGTATCATCC GACATTATCG	21240
AATCCTTGTT TTGGCGCAAG TAGCGACAGC CTACATTGAA TTGTCACGTA ATACGCCCCT	21300
TTTGATTCAA CTCTTCTTC TCTACTTCGG TCTTCCCGA ATCGGGATTG TCCTATCTTC	21360
AGAAGTCTGT GCAACGCTTG GGCTTGCTTT TTTAGGAGGC TCCTATATGG CAGAATCTTT	21420
CCGAAGTGGG CTGGAAGCCA TCAGTCAAAC CCAGCAGGAG ATTGGCCTCG CTATTGGTCT	21480
GACACCTCTA CAGGTCTTTT ACTATGTGGT TCTTCCGCAA GCAACAGCGG TGGCACTCCC	21540
CTCCTTTAGT GCCAATGTCA TTTTCCTTAT CAAGGAAACC TCTGTTTCT CAGCAGTGGC	21600
TTTGGCCGAC CTCATGTACG TCGCCAAGGA TTTGATTGGT CTCTACTATG AGACAGACAT	21660
TGCGCTAGCT ATGTTGGTAG TTGCTTATCT AATCATGCTG CTACCCATCT CACTGGTCTT	21720
TAGCTGGATA GAAAGGAGGC TCCGCCATGC AGGATTCGGG AATCCAAGTA CTCTTTCAAG	21780
GAAATAATCT CTTGAGAATC TTACAGGGAT TGGGCGTTAC GATTGGGATA TCCATCCTGT	21840
CTGTCTCTT ATCCATGATG TTCAGAACAG TCATGGGAAT CATCATGACC TCCCATTCTA	21900
GAATCATACG ATTTTAAACA CGATTGTATC TGGAAATTAT CCGTATCATG CCCAGCTGG	21960
TGCTACTCTT CATCGTTTAC TTTGGCTTGG CTCGAAACTT TAATATCAAT ATCTCAGGTG	22020
AGACTTCAGC TATTATCGTT TTTACCTCTT GGGGAACAGC TGAAATGGGA GACTTGGTAC	22080
GTGGAGCTAT CACTTCTCTC CCTAAACATC AGTTTGAAAG TGGACAGGCA CTCGGCTTGA	22140
CTAATGTTCA ACTTTACTAC CACATCATCA TCCCACAAGT CTTAAGAAGA CTGCTACCGC	22200
AGGCTATCAA TCTTGTCAC TCGATGATTA AAACCACTTC ATTAGTTGTT TTGATTGGGG	22260
TTGTGGAAGT GACCAAAGTT GGACAACAAA TCATCGATAG CAATCGCCTG ACCATCCCAA	22320
CTGCTTCATT TTGGATTAT GGAACCATTC TAATCTTATA TTTCGCAGTT TGCTACCCTA	22380
TTTCCAACT ATCCACTCAC TTAGAAAAAC ATTGGAGAAA CTAAATGTCT GAACTATCT	22440
TAGAAATCAA GGAATAAAA AAATCCTTCG GAGACAATCC CATCCTCCAA GGACTTCTC	22500
TAGAAATCAA AAAAGGGGAA GTTGTGTCA TCCTAGGGCC ATCTGGTTGT GGGAAAAGTA	22560
CCCTCCTTCG TTGCCTCAAC GGCTTAGAAA GTATTCAAGG TGGAGATATT CTCTGGATG	22620
GTCAGTCTAT CGTTGAAAAT AAAAAAGATT TTCACCTAGT TCGCCAAAAG ATTGGCATGG	22680
TCTTTCAAAG TTATGAACTC TTTCCCCATC TGGATGTCTT ACAAACCTC ATCCTAGGCC	22740
CTATCAAAGC TCAAGGAAGG GACAAGAAAG AAGTAACGGA AGAAGCTTTG CAATTACTAG	22800

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AGCGTGTCGG TTTGCTGGAT AAACAACATA GCCTTGCCCG TCAATTATCT GGTGGACAGA	22860
AGCAACGTGT TGCAATTGTC CGTGCCCTCC TAATGCATCC AGAAATCATC CTTTTTGACG	22920
AGGTGACTGC TTCGCTGGAT CCAGAAATGG TGCCTGAGGT GCTGGAACCT ATCAATGATT	22980
TGGCCCAAGA AGGCCGTACC ATGATTTTAG TAACCCACGA AATGCAGTTT GCCCAAGCCA	23040
TTACTGACCG GATTATCTTC CTCGACCAAG GGAAATCGC TGAAGAAGGA ACAGCTCAAG	23100
CCTTCTTTAC CAATCCGCAA ACCAAACGAG CCCAGGAATT TTTAAACGTC TTTGACTTTA	23160
GCCAATTCGG CTCATATCTA TAAAGGAGAT TCTTATGAAA CTATTCAAAC CACTCTTAAC	23220
TGTTTTAGCA CTTGCCTTTG CCCTTATCTT TATCACTGCT TGTAGCTCAG GTGGAAACGC	23280
TGGTTCAATCC TCTGAAAAA CAACTGCCAA AGCTCGCACT ATCGATGAAA TCAAAAAAAG	23340
CGGTGAACCT CGAATCGCCG TGTTTGAGA TAAAAACCG TTTGGCTACG TTGACAATGA	23400
TGGTCTTAC CAAGGCTACG CTACGATATT GAACTAGGGA ACCAACTAGC TCAAGACCTT	23460
GGTGTCAGG TTAATACAT TTCAGTCGAT GCTGCCAACC GTGCGGAATA CTTGATTTC	23520
AACAAGGTAG ATATTACTCT TGCTAACTTT ACAGTAACTG ACGAACGTAA GAAACAAGTT	23580
GATTTTGCCC TTCCATATAT GAAAGTTTCT CTGGGTGTCG TATCACCTAA GACTGGTCTC	23640
ATTACAGACG TCAACAACCT TGAAGGTAAA ACCTTAATTG TCACAAAAGG AACGACTGCT	23700
GAGACTTATT TTGAAAAGAA TCATCCAGAA ATCAAACCTC AAAAATACGA CCAATACAGT	23760
GACTCTTACC AAGCTCTTCT TGACGGACGT GGAGATGCCT TTTCAACTGA CAATACGGAA	23820
GTCTAGCTT GGGCGCTGA AAATAAAGGA TTTGAAGTAG GAATTACTTC CCTCGGTGAT	23880
CCCGATACCA TTGCGGCAGC AGTTCAAAAA GGCAACCAAG AATTGCTAGA CTTTCATCAAT	23940
AAAGATATTG AAAAATTAGG CAAGGAAAAC TTCTTCCACA AGGCCTATGA AAAGACACTT	24000
CACCCAACCT ACGGTGACGC TGCTAAAGCA GATGACCTGG TTGTTGAAGG TGGAAAAGTT	24060
GATTAGTCAT TAACTCTTAA AAGGAACTGG ATTTTAAGCT CCAATCCCTT TTTAAGATTT	24120
TACCTATAAC ATCTGAGTC TATCTAAGAT GTTCAATCTG AACACAGTGT ACATACTTTA	24180
TCTTCTATTG CATATACTTT ATCACAATAAG ATACGAATAT CCTCTTCACT ATGACTAGCA	24240
ATCAAAATG TTGTCCCTTT TTTACTAGAG AGCTTTCTAA ACAATGTTCT CATATTTTCT	24300
ACACTTGATT TATCCAAGGC ATTCATAGGT TCATCTAGTA AAAGAATAGA GGGATTCTCC	24360
ATAATTGCTT GAGCAATCCC TAGCTTTTTC CTCATACCTA GCGAATAAGT TTTAACTTTC	24420
TGGTCTTTT GCTCATATAG ACCAACTATT TTCAGTGTAT CATTGATTTC CTGATTACCA	24480
ACTACTCCTC GTATGCTTGC CAAATATTGT AAATTCTTAA AGCCACTATA ATAATTTATA	24540
AAACCAGGTT CTTCAATCAA AGCTCCCAA TTAGCTGGAA TTTTCTCTC AGGAACAATA	24600

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TTTTCCCAT TGATTAACAC TTCTCCATAA GACGGACTAT ATAAACCAGC TATTAATTTA	24660
AACAATACAC TTTTCCCTGA GCCATTCGCA CCAGTAATTC CTATAATTTC CCCCTGTTTA	24720
CAACTAAAGT TAAGGTTTTG AAAACACAT GTCTTTTTTA ATTTCAACTC AATATTTTTT	24780
AATGTAATTA TTTCAATCAT TCTATAAACC TCCTCTTTTG ACGAGTGAAA TAGAAAATGC	24840
TTTGAAAAAG AAAGACTAAA AATAGCAACT GAAGAAATAA ATCTCGTCCT ATATCTCCAT	24900
TCCCTCGATT CAAAATATAA AATAGATAAT TAGTTCGATT TCCTACAAAT AGACCACCAA	24960
ACACAATCAT GAGTAAAAAG AAATAACGC AAGCAAAGTT CG	25002

## (2) INFORMATION FOR SEQ ID NO: 49:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 11443 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 49:

CAGGTACGGT GAGGCGCAAC TAAATATAA TTTTCATCTT GATTAGGAAT TTTATCAGTA	60
TTATGATAGT GAGCATTGCC ATTGATGGAC CATAAGAGCA ATACAACTAA TCCACGCAAA	120
TAAGTATAAA ACATGCGATC TCCTTCGATT GTTTCTTGT TATTATTATA CCTATACAA	180
GGAGGGCTGG CAACTTTTC CCTTGACTAG ATACATATTT AGGATGAAAT TAGAATTCTG	240
TTAAAAAAA TGATATAATA GAATTTATGG ATAAAAATAA GATTATGGGA TTAACCCAAA	300
GAGAAGTCAA GGAAGACAG GCTGAGGGTT TGGTCAATGA CTTTACCGCA TCAGCCAGTA	360
CCAGCACTTG GCAAAATCGTT AAACGAAATG TCTTTACCTT TTTTAACGCT TTGAACTTG	420
CCATGCTTTT GGCTCTTGCC TTTGTGCAGG CTTGGAGCAA TCTGGTCTTC TTTGCTGTTA	480
TCTGCTTTAA CGCTTTTCT GGGATTGTGA CCGAGCTACG AGCCAAACAC ATGTTGGACA	540
AGCTCAATCT CATGACCAAG GAAAAGGTCA AAACCATCCG TGATGGTCAG GAAGTTGCTC	600
TTAATCCTGA AGAATTAGTG CTAGGAGATG TCATTGTTT GTCTGCAGGA GAGCAGATTC	660
CTAGTGATGC CTTGGTTTTG GAAGGCTTTG CGGAAGTCAA TGAAGCCATG TTAACGGGAG	720
AAAGTGATTT GGTGCAAAAAG GAAGTTGACG GCTTACTTTT GTCAGGAAGT TTCCTAGCCA	780
GTGGGTCAGT TTTATCTCAA GTTCACCATG TCGGTGCAGA CAACTATGCT GCCAACTCA	840
TGCTTGAGGC TAAGACCGTT AAACCCATCA ACTCCCGTAT CATGAAATCG CTGGACAAGT	900
TGGCTGGTTT TACTGGGAAG ATTATCATTC CCTTTGGTCT GGCTCTCTTG CTGGAAGCCT	960

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TGCTTTTAAA AGGCCTGCCT CTCAAGTCAT CCGTTGTAAA CTCGTCGACA GCTCTTTTGG	1020
GAATGTTGCC TAAGGGAATT GCCCTTTTGA CCATTACTTC GCTCTTGACT GCAGTGATTA	1080
AGTTGGGCTT GAAAAAGGTC TTGGTGCAGG AGATGTACTC TGTGAGACC TTGGCGCGCG	1140
TGGATATGCT CTGTCTGGAC AAGACGGGTA CCATCACCCA AGGAAAGATG CAGGTGGAGG	1200
CTGTTCTTCC GTTGACGGAA ACGTATGGTG AAGAGGCTAT TGCCAGCATC TTGACTAGCT	1260
ACATGGCCCA TAGTGAGGAT AAGAATCCAA CTGCCCAAGC CATTGCCAG CGTTTGTGG	1320
GAGATGTTGC TTATCCTATG ATTTCCAATC TTCCCTTCTC GAGCGACCGC AAGTGGGGGG	1380
CTATGGAGTT AGAAGGCTTG GGGACAGTTT TCTTAGGGGC ACCTGAGATG TTGCTTGATT	1440
CTGAAGTCCC AGAAGCTAGG GAGGCTTGG AGAGAGGATC ACGTGTCTTG GTCTTAGCTC	1500
TCAGTCAGGA GAAATTAGAC CATCACAAC CACAGAAACC ATCTGATATT CAGGCTCTAG	1560
CCTTGCTGGA AATCTTGGAC CCCATTCGAG AGGGAGCAGC AGAGACGCTG GACTATCTCC	1620
GTTCTCAGGA GGTGGGACTC AAGATTATCT CTGGTGACAA TCCAGTTACG GTGTCCAGCA	1680
TTGCCCAGAA GGCTGGTTTT GCGGACTATC ACAGCTATGT AGATTGCTCA AAAATCACCG	1740
ATGAGGAATT GATGGCCATG GCGGAGGAGA CAGCTATTTT CGGACGTGTT TCCCCTCATC	1800
AAAAGAACT CATCATCCAA ACGTTGAAAA AAGCGGGACA TACAACGGCT ATGACAGGGG	1860
ACGGGGTTAA TGATATCTTG GCCCTTCGTG AGGCGGATTG TTCTATCGTG ATGGCGGAGG	1920
GGGATCCAGC AACCCTCAG ATTGCCAATC TGGTCTCTT GAACTCAGAC TTTAATGATG	1980
TTCTGAGAT TCTCTTCGAG GGTCTGCGG TGGTCAATAA CATTGCCAC ATCGCCCCGA	2040
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TACTAGGTCG GTCAGAGTGG ATTTTGATTT TCCCCTTCAT TCCGATCCAG ATTACCATGA	2160
TTGACCAGTT TGTGGAAGT TTCCCACCAT TCGTTCTGAC TTTTGAGCGA AATATCAAAC	2220
CTGTTGAGCA GAATTTCTC AGAAAAATCCA TGCTTCGTGC CCTACCAAGC GCTCTCATGG	2280
TCGTCTTCAG CGTCCTGTTT GTGAAAATGT TTGGCGCGAG TCAAGGTTGG TCTGAGTTAG	2340
AAATCTCAAC TCTACTCTAT TATCTCTGG GGTCAATTGG TTTCTTATCC GTATTTAGAG	2400
CCTGCATGCC ATTTACCTTA TGGCGTGTC TCTTGATTGT TTGGTCAGTA GGAGGTTTCC	2460
TAGCCACAGC TCTCTTCCCA AGAATTCAAA AACTGCTTGA AATTTCAACC TTAACAGAAC	2520
AAACGTTGCC TGTTTATGGT GTCATGATGT TGGTCTTTAC CGTGATTTTC ATCCTGACCA	2580
GTGTTACCA AGCGAAAAA TAAATCAAAA CCACCAAGT GAACTGGTGG TTTGTTCTGC	2640
GGCTATAAGC CGCTTCTACC GGCAGGGCC AAAGCCCCAC CGAAATAGCT TCCTCGCGCA	2700
CCACTTTCCC GAGCAGGTGC TAAAGCACCT TAGTTACTTC CTCTTATTTA TTTCGCCAGT	2760

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AAACGGATCT ACTGACTCGA ATAACGTGAG CTGGTCTGCT ACTCTGTCTT CTTGTAATTG	2820
ATTCTGAATA TATTCAGCTA TCACTTTCTG ATTACGGCCT ACCGTATCTA CATAATAGCC	2880
TCTACACCAA AACTTGCGAT TGCCATATTT GTATTTTAAA TTCGCATGCT TATCAAAAAT	2940
CATCAAACCTG CTCTTGCCCT TTAATAGCC CATAAAGGAC GAAACACTAA GTTTCGGAGG	3000
AATACTGATA AGCATGTGAA TATGGTCTGA ACAAGCATTG GCTTCATGGA TTATTACACC	3060
CTTACGCTCA CATAAGTCAC GTATGATTCT TCCGATACTA GCTTTGTATC TGCCATAAAT	3120
GATTTGACGA CGATATTTGG GTGCAAAAAC AATATGATAT TTACAATTCC ATGTGGTATG	3180
TGATAAACTT TGATTATCCT CTCTCATGAG GTACCTCCTG TATGATATGT TGTAGTGGCG	3240
GAGAAACCAC TTCTATCTTA TCATTTTAGG AGGTTCTTTT TGTACCACG CTAAAAGCTC	3300
TATGGAACCA CTAGCATAGC TAGTGGTTTT CGGGAGACAA CAAGAAAGAC TGCAATCTGT	3360
GGATTGCAGT TTTTATACG ATGGATCTAT CGTAGATCTG ATGTGCAAGG CCTACGTGCC	3420
GATCATCTAT CGGTGAACCC AAGAGCGACC CTCAGCCTG CTTGGATTGA GGTAAATAGAT	3480
TCAAATATCT GTAGTTAGAC TATTTGAAGT TTGATGTAAG AAAGAGAAAG CGACAGATTG	3540
AAGTAATTTT AACTCTCTTC TATTGCTAGA ACAAATGGTC GGATAGGTTG GTAGTTTGAA	3600
AATGAAGATG CTATCTATTG TTAATGGA CATAGTGTTA TTTATTAGAA AATCGTTTGG	3660
TTTATTTCTT ATCAAATACG AAAAGCAACT TAAATATTC AACTAAAATA GATGTTATGA	3720
AGAAAAGTA AAATGATTTT GGCATAGTGA GGTCTGTTC TATTTGATAT CATATTTTGT	3780
ATAAAAACAA AAATGTCCAT TGCAAAGGAC AAAATGCGAA GTATATTATT TTTTGAAAGC	3840
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GTAGAAGCAT TCATTTTATC TGAAAAAGGC AGAGGTTTCA AATTAAATCC AAGAAGTTCC	4080
CTCGTGGACG TTGATGGGAA TTTTACAGAG GCTTTTGATC CTGAAGTAAG GCGTGAAAAA	4140
TTACTAGAAC GTCTCTGTT GACTGCTCCT AAGCCACATT CTATTTATGA TTTAGGAGAG	4200
GAATTCTACG TAAGCGAGTC AGTAGTACTA AAAGATCGTC AGATATTACA AGAGAGTCTA	4260
GCAATTTATG GGTAGATTT AAAAATGAGA CAACGAAAGC TTTTATTGA TGGGGATGAG	4320
GCTCAAATTC GTTCAGCCAT TCTAAATCTA CTGCCAATGT TTAATCAGTT GGATTTAGAG	4380
CAAATTACAC AGAATAAGGT TCAGCCTCTT GACGGAGAAC TTGCTCACTT TTGTTGGGA	4440
TTACTGATTA CACTTGAGAG AGAATTGGGG GTAAACATTC CCTATCCATA TAATATAAAT	4500

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ATTTTCTCTC ACCTGTATAT TTTTATCAGT AGGAATCGTC GTAGTACTAG TATTCATGTT 4560  
 GTAGCACCTT CAAAACCTAC TATTGTTGAT GAGAAAATTT ACAGTGCTCTG TCAAAAAATT 4620  
 ATTCAGAAA TTGAACAATA TTTTAGGATG AAGGTTGATG CAGTTGAGAT TGAATATCTT 4680  
 TATCAATACG TTGTATCTTC GAGATTGCAA AAACCATTTT CTCCGGGAA GCTTCCTTTT 4740  
 TCTCAGCGAG TTTTAGATGT CACTCATTAC TATTTTAGCC GTATGTGTAT GGACAATAGA 4800  
 GAGATTGAAA CGACAGATCC TGACTTTGTT GACTTGCGA GTCATATCAG TCCCTTACTG 4860  
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 TATCCTAATC TGGTTAAAGA GTTAACAACCT ATTTCTAAAG AAGTGAGTCT AGTATTTGGT 4980  
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 GAAAAGCGAG CACGTCCTCT AAAACAGTA GTGATGTGTA CATCAGGTGT CGGAACCTCA 5100  
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 AAGTTGTTGC CAAATTAGTT CGGGCTCAGA CATCTGATGA TGTGATTGCA GCTTTTGTGTT 6180  
 AATAAGAAAA AATTTTGGAG GGTATCCGTA TGAAAATTGT TGGTGTGCA GCTTGTACTG 6240  
 TGGGAATTGC CCACACTTAT ATGCACAGG AAAAATTAGA GAATGCCGCA AAGGTAGCTG 6300

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GACATGTGAT TCATGTTGAG ACTCAGGGGA CAATAGGGGT AGAAAATGAA TTGAGTCAAG	6360
AGCAGATTGA TGCAGCGGAT GTAGTTATTT TAGCAGTTGA TGTTAAGATT TCTGGTATGG	6420
AACGCTTTGA GGGTAAAAAG ATTATCAAGG TTCCAACAGA AGTGGCAGTC AAATCTCCCA	6480
ATAAACTGAT TGCTAAAGCT GTTGAGATTG TTACGAAATA ACTGAAAATA TTTAAGGAGA	6540
AAATATATGT TGAAACACTT AAACCTAAAA GGTCACTTAT TGACAGCCAT TTCCTATATG	6600
ATTCCAATTG TTTGTGGTGC AGGATTCTTA GTTGCCATTG GTTTAGCAAT GGGGGGTGGT	6660
GTTCTGTAGC CTCTGTAGC AGGAAAATTC ACTATCTGGG ATGCTTTAGC AACTATGGGT	6720
GGTAAAGCCC TTGGTCTCTT GCCAGTTGTT ATTGCTACAG GTTTGTCTTA CTCGATTGCT	6780
GGTAAGCCAG GGATTGCACC AGGTTTTGTT GTTGGTCTAA TTGCCAATTC TGTGGTTCA	6840
GGGTTTATCG GTGGTATCTT GGGAGGTTAT ATAGCTGGTT TCTTGGTTCA AGCGATTATT	6900
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TTTACCAACT GGTGACGAG CTTATTACAA AGCTTGGGAA GTGCTTCAAA TGGTTTGATG	7080
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AAAAAAAATA TCTATACTCA AGAGGAAATC GAAACATTGA AATCGGCTGT TCCTATGGGG	7320
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ATTGCAACAG GTATCGGTGG TGCTGTTGGT GGTGCTGTTT CTTTGACAAT GGGTGCTGAT	7440
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ATTTGTGCCT TGTTAGCTAA CATTGTAGTC ACAGGACTTG TCTACGCGAT TTTGAAAAAA	7560
CCAATAAAAC ATGCAGAACC AGTTATGACT GTTGAAGAAG AGATTGATTT GTCAGATATT	7620
GAAATTTTGT AAGAGGGTAA CGATGTCAAG AATTGAATTT TCACCATCTT TGATGACCAT	7680
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TCTGAATGGT CTTGCTTTTC GTTTGATGTA TAAAATTCAT GATGCAGGTC TAAAGGCTGG	7980
TGTTGTCCTT AATCCTGAAA CACCTGTTTC TACAATCTTT CCCTACATTG ATTTACTTGA	8040

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CAAAGCAACT ATTATGACTG TAGATCCAGG TTTTGCAGGA CAACGCTTTT TGGAGTCTAC	8100
CTTGTATAAA ATCCAAGAAC TCCGTCAGCT TAGAGTTCAG AATGGTTATC ACTACATCAT	8160
TGAGATGGAT GGTTCCTCGA GTCGTAAGAC TTTCAAACAA ATTGATGTGG CAGGACCAGA	8220
TATTTATGTT ATAGGTCGCA GTGGATTATT TGGTTTGGAT GACGATATTG CCAAAGCCTG	8280
GGATATCTGT TCTAGAGATT ACGAAGAAAT GACCGGAAAA ACAATGCCAA TCAAATAATG	8340
GTTTGAGAAG AAATTTATTA GTTAGGAGGA ATATATGTCA CTACAATCAG TTAACGCCAT	8400
TCGTTTTCTT GGCCTAGATG CTATTAACAA ATCTAATTCT GGTCAACCCG GAATTGTCTAT	8460
GGTGCTGCG CCAATGGCTT ATAGCCTATT TACAAAGCAC CTTAGAATTA CACCTGAGCA	8520
GCCAACTGG ATTAACCGAG ATCGCTTTAT CTTGTCTGCG GGTCTATGGT CAATGCTACT	8580
GTATGCTCTC TTGCATTAA CAGGGTATAA GGATGTATCC ATGGACGAGA TTAATAATTT	8640
CCGGCAATGG GGATCTAAGA CACCTGGTCA TCCTGAAGTG ACGCATACTG CTGGTGTGGA	8700
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GGCCAAAGTT TCTGGTAAAC CGAGTTTGAT TGAAGTGAAA ACGGTAATTG GTTACGGCTC	9120
ACCCAATAAA AGTGGTACAA ATGCTGTTC TGGTGACCA CTAGGAGCAG AAGAAACAGG	9180
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TTTGGTGTCT GATTACAAGG TTGCTTATCC CGAAGTTGCT AGTGAGATTG ACGCTATTGT	9360
AGCTGGAAAA TCCCCTGTAA CCATTACTGA AAAAGACTTC CCTGTCTATG AGAATGGCTT	9420
CTCTCAAGCA ACTCGTAATT CGTCCCAAGA TGCTATTAAT ACAGCAGCAG TTTTACCAAC	9480
CTTCTTAGGT GGATCGGCAG ACTTAGCTCA CTCTAACATG ACCTACATCA AGGCAGATGG	9540
CTTACAAGAT AAATATAATC CATTAAACCG CAATATTAG TTTGGGGTAC GTGAATTTGC	9600
CATGGGAACA ATCCTCAATG GAATGGCTCT TCATGGTGGT TTACGAGTTT ATGGCGGAAC	9660
CTTCTTTGTT TTCTCTGACT ACGTCAAAGC TGCTATTTCG CTATCAGCCA TTCAGGAGTT	9720
GCCTGTAATC TATGTCTTTA CCCATGATTC AATTGCCGTT GGTGAAGATG GTCCAATCA	9780
TGAACCAAGT GAACATTTGG CAGGTTTACG CTCAATGCCA AACTTGACTG TTATCCGTCC	9840



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AGCGGATGCC CGTGAACTC AAGCGGCTTG GCATCATGCC TTGACCACTA CCACCACTCC	9900
AACTGTCATT GTCTTAACCC GTCAAACTT GGTAGTTGAA GAAGGGACAG ACTTTGGTAA	9960
GGTCGCTAAA GGAGCCTACG TCGTGTATGA TACCCCGGGA TTTGATACTA TTATCATTCG	10020
TACAGGATCT GAGGTCAATC TAGCTATCAA AGCTGCTAAG GAATTGGTTT TACAAGGTGG	10080
TAAAGTACGT GTGGTATCTA TGCCCTCAAC CGAACTATTT GATGCTCAAG ATGCTACCTA	10140
CAAGGAAGAC ATTTTACCAT CTAAGACTCG TCGTCGTGTG GCCATTGAAA TGGCAGCGAC	10200
CCAAAGTTGG TACAAGTATG TTGGTTTGGG TGGCGCGGTC ATCGGTATTG ACATCTTCGG	10260
TGCGTCTGCC CCAGCTCAGA CTGTGATTGA TAATTATGGA TTTACGGTAG AGAATATCGT	10320
TGCTCAAGTT AAGTCCCTAT AGAAACCAAT TACAATGAAG ATACAGCTGT TGTCAGACTA	10380
GCAGATGTAG TGATAGACAC TAATCAGATG ATTGGTTATT TAAAACTGT AATGAAAATG	10440
TAATAATTTA TCTACGAAAG TTATAGTAGA TAGTATACAC AATAGAGTAT ACCCTGAAAC	10500
GGTTGCGAAG TACGCTAATC ACTTTGCTAC TGATCTAGAT AGTTTCTTTA ATCAATAAAC	10560
ACAGCATCCA CAGATTGACT TAGGATATTG TAAGTTTTTT GAAAGCTAGA GAGAAGGTCT	10620
CTAAATTTAA AAAACGCATA GTATAGGATG TTGAAATGAT GAACTGCACC CCAAAGTTA	10680
GACAGAAAAA AATCTAACTT TTGGGGTGTT TTTATTATGA AATTAACCTA TGATGATAAA	10740
GTTCAGTTCT ATGAACTTAG AAAACAAGGA TATATCTTAG AGAAGCTTTC AAATAAATTT	10800
GGGATAATA ATTCTAATCT TAGGTACATG ATTAAATTGA TTGATCGTTA CGGAATAGAG	10860
TTCGTCAAAA AAGGGAAAAA TCCTTACTAT TCTCCTGATT TAAAACAAGA AATGATTCAT	10920
AAAGTCTGAC ATGAAGGCTG GACTAAAGAT AGAGTTTCTC TTGAATACGG TCTCCAAGT	10980
CGTACGATAC TTCTTAACTG GCTAGCACAA TACAGGAAAA ACGGGTATAC TATTGTTGAG	11040
AAAACAAAAG GGAGAGTACC TGAGAGCGGA GAATGCCATC CTAAAAAAGT TAAGAGAACT	11100
CCGATTGAAG GAGGAAAAAG AGAAATAAGA AAGACAGAAA TTGTTCAAGA ATTAATGACT	11160
GAGTTTTCGT TAGATCTTCT TCTAAAAGCC ATTAACTAG CTCGTTGGAC CTACTACTAT	11220
CACTTGAAAC AGCTAGATAA ACCAGATAAG GACCAAGAGC TTAAAGCTGA AATTCAATCC	11280
ATCTTTATCG AACACAAGGG AGATTATGCT TATCGCCGGG TTCATTTAGA ACTAAGAAAT	11340
CGTGCTTATC TGGTAAATCA TAAAAGAGTT CAAGGCTTGA TGAAAGTACT CAATTTACAA	11400
GCTAGAATGC GACAGAACG AAAATATTCT TCTCATAAAG GAG	11443

(2) INFORMATION FOR SEQ ID NO: 50:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 5338 base pairs

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(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 50:

CCAATTACAT TATATTATCA AAATCGTCGA AACTGGCTCC ATGAATGAGG CAGCCAAGCA	60
ACTCTTTATC ACTCAGCCAA GTCTCTCCAA TGCAGTGC GAATTTGGAAA ATGAAATGGG	120
CATGAGATC TTTATCCGCA ATCCCAAGG AATCACCTTG ACCCGTGATG GCATGGAGTT	180
TCTCTCTTAT GCCCGTCAGG TTGTCGAGCA GACCCAGCTT CTGGAGGAAC GCTATAAAAA	240
TCCTGTGCCC CACCGCGAAC TCTTTAGCGT TTCGTCTCAA CACTATGCCT TTGTGGTCAA	300
TGCCTTTGTC TCTTTGCTCA AGAAAAGCGA TATGGAGAAA TACGAACTCT TCCTTCGTGA	360
AACTCGGACT TGGGAGATTA TCGACGACGT CAAGAACTTC CGCAGTGAGG TCGGGTCTCT	420
CTTCTTAAAC AGTTACAACC GTGATGTTTT AACCAAGATG CTGGATGACA ATCACCTGCT	480
AGCCCACCAT CTCTTCACAG CGCAACCGCA TATCTTTGTC AGCAAGACCA ACCCTCTGGC	540
AAAGAAAGAC AAGGTGAAAC TGTCTGATTT GGAGAATTTT CCTTACCTCA GCTATGACCA	600
AGGGACGCAC AACTCCTTCT ACTTTTCAGA AGAGATTCTT TCTCAAGAAC ACCACAAGAA	660
ATCCATTGTG GTCAGTGACC GTGCCACCCT CTTAATCTC TTGATTGGTT TGGATGGTTA	720
TACCAATTGCG ACAGGGATTT TGAACAGCAA CCTAAACGGA GACAATATCG TTTCTATCCC	780
ACTGGATATT GATGACCCGA TCGAGCTGGT CTATATCCAG CATGAGAAAA CCAGCCTATC	840
TAAGATGGGC GAACGCTTTA TAGACTATCT CCTAGAAGAA GTTCAGTTTG ATAGTTGAGA	900
AATGATAAGA ACCAATATGT AGGCTAGCAA CAACCTGCAC ATTGGTTCTT TTTACTTATA	960
ATTAAAAGTT TCCCCTGCCA ACTTATCAGC TAGCTTGGGA AAGAGAGTAT AAACTTATG	1020
GGCTAGGTTT AACAAAATCG GGAGATTGAG TTCTCGTTTG TTTTTCCTA TAATCTTGAC	1080
AATCTTTTGA GCCACTGCAT CTGGTTCTAG CAGGAAGCGA TCAACCGATT TAAGATAAGT	1140
TCCATCTGGG TCGGCTTGGT CGAAAAATCC TGTACGGATT GGTCTGGAT TGACTGTTGT	1200
CACATAGACT CCATAGGGCA TAAGTTCGAG TCGCAGAGCA TTTGAAAAAC CAATAGCCGC	1260
AACTTGGTC GCTGAGTAAA GACTAGACTT GCCAGTAGCT ATTAGACCTG CCATGCTGAC	1320
GATGTTGATG ATATGCCCTT TGCTGCTTTC CTTCATACGA GCCGCAAGGT GACGAGACAG	1380
ATTCATCAGG GCAAAGGTAT TGACCTCAAA CATCTGGTGA ATATCTTTAT CAGCAATCTG	1440
GTCAAATCCC TCAAAAATCC CGTAACCAGC GTTGTTAATC AAGACATCAA TCTTGCCATA	1500
GCGGAGATAA AGATCAGTTA CCAGAGCTTC TAGGGCTGAA TCGTCGGTAA TATCAATTTT	1560

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AATCAATTCT GCATGGGAAT AATTTCGTA GAGTTGGGCT AATTTTCCT TATTTCTACC	1620
AAGCAAGATG AGTTGGTCAT TGGGCAGGAG TTTGACCATT TCTTGAGCTA GACCACCGCT	1680
AGCTCCGTA ATGAGAATAG TAGGCATACT TATCCTTTCT GTGACTGCTA GATTTCCACT	1740
TCTTCCAAGT CTTTGACCAC ATGGACATTT TCAAAAATTG TGGCAGCGTC TTTCTTGAGT	1800
TTGCTAATAT CTTTGTAGAG GAAACGGGCA CTGATATGGT TGAGTAGGAG GCGTTTGGCA	1860
CCTGCTTCTA CCGCTACTTG TGCAGCTTGC ATATTAGTTG AGTGACCATG GTTACGAGCA	1920
ATTTTTCAT CACCCTTGCC ATAAGTGGAC TCATGAATA GGACATCTGC ATTGACAGCC	1980
AGACGCACAC TGGCACCCTT TTTTCGAGTG TCTCCTAAAA TAGTGATAAT CTTACCTGGA	2040
CGTGGCGCTG AGATATAGTC TGCTGCCTTG ATTTTCAGTTC CGTCTTCCAA AACAAGATCC	2100
TGGCCGTTTT TGATTTTACC AAAAAAGCGG CCGAACGGAA CACCAGCAGC CTTGAGTTTT	2160
TCAGCATCCA GCGTCCCTTC TAGATCCTTT TGCATGACAC GATAGCCAAC ACAGAAAATA	2220
GTGTGGTCCA GCTCCTCTGC ATACACAGTG AATTTATCGG TTTCAAGAAT TTTACCCAGA	2280
GAATCTTGGT CAAACTCATG GAAATGAATG CGGTAGGGCA GACGAGAACC TGACACACGA	2340
AGGCTGGTTA AGACAAATGA CTTGATTCTT TGAGGTCCGT AGATTTCCTA ATCTGTCTGC	2400
TCTTCATTGG CCTGAAAGGC ACGGCTAGAA AGGAAACCTG GCAAACCAA AATGTGGTCT	2460
CCATGCAGAT GGGTAATAAA GATTTTGCTG ACCTTACGTG GTCGAATTGT GGTTTCCAGA	2520
ATGCCGATTT GCGTACCTTC TCCACAGTCA AAGAGCCAAA CTTCGTTAAT CTCATCCAAA	2580
AGTTTCAGGG CGAGACTTGA AACGTTGCGG GCTTTAGAGG GCTGACCAGC CCCCCTTCCT	2640
AAAAATTGAA TATCCATTCT ATACTTTCTA ATTAATCAAT ATATAACATG GCTGTGCGGT	2700
TTTCCGATCG GAAATAGCGT TTGCCAGAAA AAGCAGCAGC TTCTTGCAAT AAATCCTCTT	2760
GGCTGTAGCC TTTGAGACGT TTTGACCAT CAGCCAATCT TTCCAAATCA GTCAAAGCTG	2820
TGAGACTTTC TAGGCTGATA ACTTCCTCGT CCTCGACAGG CTTTATGTAA ATCTTACCAG	2880
ACTCTTCAAA GACTAATTGA TGGGGGAAAA TTTGCGCAAT TTCAAAGAGC AAGTCATCCG	2940
AGATTTTCTC CTCATTTTCA AAGAAAATCC GACCAAGGCC GTCACTCTCA TAACAAAAAC	3000
CAAAGGATTT ACCAGACAGA TTAAGCCGAA TAAAAGGCTT ATTTTCTAGG GTGAAACTTG	3060
GCTCAGTATT GTAAAGATTC AGTTCTTGAC TGAGTTCTGC AAAATAATCC GTCGCAGCCT	3120
GAGGACTCTT TTTCTGATAG AGTTCTGCAA AGTAGGCATT AACAACTT GCGGAGGTG	3180
TAATAAGTGT TAACTGCTCC TGATCTGTTT TACCAGCTAG AAGCTGATCC AGATAGACCT	3240
TGTCCAGACT TGTATAACCT CCATACTTTA GAGCCAAAGT TTTAATATCA GTCATAAAAT	3300

			454			
TCTTCTAACC	TCCATTTATT	TTTCTCGGAA	ATGTAGCCTG	TAATCACTTC	GCCGTCTTCC	3360
TGATAATCAC	GTTCTTCCAG	AATTGCAACA	CTCTCTAAAT	CATGAATCTT	GTAGGACTTT	3420
GA AAAAGGCA	CTCGAGGGT	AAATGCTTCA	AAAATTTCTT	TAATCTTATC	TAGCAATAAT	3480
GCTTGCAAGT	TTTCACGACT	GTCTCAGAC	TTGGCAGAAA	TGAGGGTATA	TGGCGTTTGG	3540
GTAGGCGTGA	AATCCTCCAC	CAAATCCGCT	TTATTATAAA	GCGTCAAGTG	AGGAATATCT	3600
TCCATGTCCA	GGTCTTTCAT	GATGGAGAGA	ACCGTTTTTT	CATGCTCCTC	GTGTAAGGA	3660
TTGCTAGCAT	CGATAACATG	AACCAGAAGG	TCCACATGCT	TGCTTCTTTC	CAAGGTTGAC	3720
TTGAAACTGG	ACACCAACTC	TGTCGGCAAA	TCTTGGATAA	AGCCAACGGT	ATCTGTCAAA	3780
GTTACTTGGA	GATTGCCTCC	CAGATGAATA	CTCTTGGTTG	TCGCATCCAG	AGTCGCAAAAG	3840
AGCTCATCTG	CTTCATACTG	GGTCTTACTG	GTCAAGATGT	TCATGATAGT	TGATTTCCCA	3900
GCATTAGTAT	AACCAATCAA	ACCAATCTTA	AAAGTGCTAG	ACTCCAAACG	TTTTTCTCTG	3960
ACAGTCGCAC	GATTTTTCTC	AACCACCTTG	AGCTGGCGCT	CGATATCCGT	GATTTGATTG	4020
CGAACGCTAC	GACGGTTCAG	CTCCAGCTGG	CTTTCACCAG	GACCACGGGA	ACCAATTCCC	4080
CCTGCTGAC	GGCTGAGCAT	AATCCCCTGA	CCAACCAAGC	GAGGCAAAAG	GTATTGAGT	4140
TGGGCTAGGT	GGACTTGAG	CTTCCCTTCA	TGGCTTCGAG	CCCGCATGGC	AAAGATATCC	4200
AAAACTCAACT	GCATACGGTC	AATGACCTTA	ACACCGAGAA	CTTCCTCTAG	ATTGACATTC	4260
TGCCTTGGGG	TCAGACGATT	GTTGACGATG	ACAGTAGTGA	TTTCTTCTGC	ATCCACCATA	4320
AGCGCAATCT	CTTCCAACCT	ACCAGAGCCG	ACGAAGTCTT	TGGAATCATA	TTTTTCACGT	4380
TTTTGTCTGT	AGCTATCTAC	AACGACTGCC	CCTGCCGTTT	TCGCTAAACT	AGCCAATTCT	4440
TCCATGGAGA	GGTCAAAACT	GTCCATACCC	TGCAATTCCA	CACCAATCAG	CAGGACTCGC	4500
TCCTCTTTTT	TCGCCGTTTC	AATCATCTAA	AAACTCCTCT	ATCTGGCTTA	AAATGCGGTC	4560
TTGTACACCA	GATTCTCCAA	TCTGATAAAA	GGTGACCTGC	ATGCGATTAC	GGAACCAGGT	4620
CAGCTGACGC	TTGGCAAAAC	GACGAGTCGC	CTGTTTAAGA	CTCTCACTAG	CTTCCTCCAA	4680
GGTCTGCTCT	CCACGGAAAT	AAGGAAAGAG	TTCTTATAG	CCAATTCCTT	TAGCAGCCTG	4740
TACATTAGGG	GAATGGTCAA	ACAGCCACTT	GGCCTCATCC	AAAAGCCCAG	CCTCAAACAT	4800
CAAATCCACT	CGGTGGTTGA	TACGCTCATA	AAGTTGACTA	CGTTCATCAT	CCAAGCAGAT	4860
AATCAGCGGT	TCATACAAGG	TCTCTTGATT	TTCCAAATCC	TGACC AAAAT	GGGCAATTTT	4920
TAAGGCACGC	ATAGCACGAC	GACGATTAAA	CTGGGGAATC	TCAAGGCCTG	CTTGATCCAC	4980
CAAATGGGCT	AATTCCTCAT	CTGAATATGG	CTCCAAACTA	GCTCGATAAG	CTAAAATCTC	5040
CTCATGAGGA	GTCTCCCCAC	CTAGGTGGTA	ACCTTCTAGC	AAGCTCTGGA	TATAAAGTCC	5100

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AGTCCCACCG GCGATAATGG CTAGCTTGCC ACGGTTGTGA ATACCCTCAA TAGTCATCTT	5160
AGCTTCTGAA ACAAATCAA AAGCCGAGTA AGACTCGGT ATCTCTCTAA CATCGATTAA	5220
ATGATGAGGA ACAGCTGCCT GCTCTTCTGG ACTAGCCTTG GCCGTCCCAA TATCAAGTCC	5280
TCGATAGACT TGCTGGCTAT CTCCACTAAC CACTTCGCCA TTAAAACGCT TTGCGGGG	5338

(2) INFORMATION FOR SEQ ID NO: 51:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 19446 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 51:

CGGAAACCCA TCTAGTCTCC ATCGTTGGG AGACCAAGCA ACACGAATCT TAGATGCTTC	60
TCGCCAACAG ATTGCAGATT TAATCGGTAA GAAAAGCGAT GAAATCTTCT TTACCTCGGG	120
TGGAACAGAA GGGGATAACT GGCTTATCAA GGGTGTGCC TTGAAAAAG CTCAGTTTGG	180
CAAGCACATC ATTGTTTTCAG CCATTGAACA TCCAGCAGTC AAAGAGTCAG CCTCTGGTT	240
GAAAAGTCAA GGATTGTAAG TGGATTTTGC TCCAGTTGAT AAGAAAGGCT TGGTCGATGT	300
TGAGGCGTTA CAGGTTTGAT ACGGCATGAT ACAATCCTCG TTTCCATCAT GGCTGTGAAC	360
AATGAAATCG GCTCTATCCA ACCTATTGAG GCTATTTTTCAG AATTCTTGGC AGACAAGCCG	420
ACTATTTTCT TCCACGTTGA TCGGTTTCAG GCGCTTGCCA AAATCCGAC TGAAAAGTAT	480
CTGACAGAAC GGGTGGATTG CGCGACTTTC TCTAGTCACA AGTTCCACGG GGTTCGAGGT	540
GTGCGCTTTG TCTATATCAA ATCTGGCAAG AAGATTACAC CTCTTCTTAC AGGTGGTGGC	600
CAGGAGCGAG ATTATCGTTC GACAACTGAA AATGTGGCAG GGATTGCAGC GACAGCCAAG	660
GCCCTCCGTT TGTCTATGGA AAAGCTAGAT ATCTTTAGGA GCAAGACTGG GCAGATGAAG	720
GCAGTGATTC GCCAAGCTCT TCTGAACTAT CCGGATATTT TTGTCTTTTC AGATGAGGAA	780
AACTTTGCAC CTCATATTCT GACTTTTGA ATCAAAGGTG TTCGAGGTGA AGTCATCGTT	840
CACGCCTTTG AAGACTATGA TATTTTCATC TCAACAACCT CAGCTTGTTT ATCTAAGGCA	900
GGAAAACCG CCGGTACCTT GATTGCCATG GGAGTGGACA AAGATAAGGC CAAGTCAGCT	960
GTGCGTCTTA GCCTAGACTT GGAAAATGAT ATGAGTCAGG TCGAGCAGTT TTTGACCAAG	1020
TTAAAATGTA TTTACAATCA AACTAGAAAA GTAAGATAGG AGCATTTCATG CAGTATTTCAG	1080
AAATTATGAT TCGCTACGGA GAGTTGTCAA CCAAGGGTAA AAACCGTATG CGTTTCATCA	1140

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ATAAACTTCG TAATAATATT TCGGACGTTT TGTCTATCTA TACCCAAGTT AAGGTAACAG	1200
CAGATCGCGA CCGTGCCAC GCTTACCTCA ATGGAGCTGA TTACACAGCA GTTGCAAGAT	1260
CTCTCAAACA AGTTTTTGA ATTCAAAAC TTTCTCCTGT TTATAAGGTT GAAAAATCTG	1320
TAGAAGTTTT GAAGTCTTCT GTCCAAGAGA TTATGCGGA CATCTACAAG GAAGGTATGA	1380
CCTTTAAGAT TTCTAGCAAG CGTAGCGACC ACAACTTTGA ACTTGATAGT CGTGAACCTCA	1440
ACCAAAACACT TGGAGGGGCT GTATTCGAAG CCATTCCAAA TGTGCAAGTT CAAATGAAAA	1500
GTCCTGACAT CAATCTTCAG GTGGAGATTC GTGAAGAAGC AGCCTATCTT TCTTATGAAA	1560
CCATTCGTGG GGCTGGTGGT TTGCCAGTTG GAACTTCAGG TAAAGGGATG CTCATGTTGT	1620
CAGGAGGGAT TGACTCACCT GTAGCAGGTT ATCTTGCTCT TAAGCGTGGG GTGGATATCG	1680
AGGCAGTTCA CTTTGCTAGT CCACCATATA CTAGTCCTGG TGCCCTCAAG AAAGCGCAGG	1740
ACTTGACCCG TAAATTGACC AAGTTTGGCG GAAATATCCA GTTTATAGAG GTGCCTTTCA	1800
CAGAGATTCA AGAGGAAATC AAAGCCAAAG CGCCAGAAGC TTATTTGATG ACTCTAACTC	1860
GTGCTTTTAT GATGCGGATT ACTGACCGTA TTCGTGAGGT ACGAAATGGT TTGGTTATCA	1920
TCAATGGGGA AAGCTAGGT CAAGTAGCCA GCCAAACCTT TGAAAGTATG AAGGCTATCA	1980
ATGCTGTAC CAACACTCCC ATCATTCGTC CTGTGTTTAC CATGGACAAG TTGGAATCA	2040
TTGACATCGC CCAGGAAATC GATACCTTTG ACATTTCAAT CCAACCGTTT GAAGACTGTT	2100
GTACCATTTT TGCACCAGAT CGTCCAAAA CAAATCCTAA AATTAAGAAT GCGGAGCAGT	2160
ACGAAGCCGC TATGGATGTT GAAGGCTTGG TTGAGCGAGC AGTGGCTGGA ATCATGATTA	2220
CTGAAATCAC ACCTCAAGCC GAAAAAGATG AAGTTGATGA CTTGATTGAC AATCTGCTCT	2280
AATTCAGAAA ATCCAAAAGA ATAGCGAAAA TCAGTAAAA AAGTTAGTTT TTTCTCTAAA	2340
AACAGGTAAA AACTTAACCT TTTTATTTT TATGATATAA TGATATAAAA TTTTGAATAT	2400
AGAGAGTTTT CTGACAAATG ATCAATCCTA CTTTATCTA AAAATGAAAG AACACAACT	2460
CAAGGTTCTT TATACAGGTA AGGAGCGCCG TGTACGTATT CTTCTTCCTA AAGATTATGA	2520
GAAAGATACA GACCGTTCCT ATCCTGTTGT ATACTTTCAT GACGGGCAAA ATGTTTTTAA	2580
TAGCAAAGAG TCTTTCATTG GACATTCATG GAAGATTATC CCAGCTATCA AACGAAATCC	2640
GGATATCAGT CGCATGATTG TCGTTGCTAT TGACAAATGAT GGTATGGGGC GGATGAATGA	2700
GTATGCGGCT TGAAGTTCC AAGAATCTCC TATCCCAGGG CAGCAGTTTG GTGGTAAGGG	2760
TGTGGAGTAT GCTGAGTTTG TCATGGAGGT GGTCAAGCCT TTTATCGATG AGACCTATCG	2820
TACAAAAGCA GACTGCCAGC ATACGGCTAT GATTGGTTCC TCACTAGGAG GCAATATTAC	2880
CCAGTTTATC GGTTTGGAAT ACCAAGACCA AATTGGTTGC TTGGGCGTTT TTTTCATCTC	2940

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AAACTGGCTC CACCAAGAAG CCTTTAACCG CTATTTCGAG TGCCAGAAAC TATCGCCTGA	3000
CCAGCGCATC TTCATCTATG TAGGAACAGA AGAAGCAGAT GATACAGACA AGACCTTGAT	3060
GGATGGCAAT ATCAACAAG CCTATATCGA CTCGTCGCTT TGCTATTACC ATGATTTGAT	3120
AGCAGGGGGA GTACATCTGG ATAATCTTGT GCTAAAAGTT CAGTCTGGTG CCATCCATAG	3180
TGAAATCCCT TGGTCAGAAA ATCTACCAGA TTGTCTGAGA TTTTTCGAG AAAAATGGTA	3240
AGTTAAGAAA GGAAAAACG AAATGCATAT TGAACATCTT AGCCACTGGA GTGGTCATCT	3300
TAACCGTGAA ATGTACCTTA ACCGTTATGG ACATGGTGGG ATTCAGTTG TGGTCTTTGC	3360
TTCATCAGGT GGTAGTCACA ACGAATACTA TGATTTTGGC ATGATTGATG CCTGTGCTTC	3420
CTTTATCGAG GAAGGCCTTG TCCAGTTCTT TACCCTATCT AGTTTGGATA GTGAGAGCTG	3480
GTTGGCTACT TGGAAAAATG CTCATGACCA AGCGGAAATG CACCGTGCCT ACGAACGTTA	3540
TGTGATTGAG GAGGCCATTC TTTTATCAAG CACAAGACAG GTTGGTTTGA TGGCATGATG	3600
ACGACAGGTT GCTCTATGGG AGCCTATCAT GCACTCAATT TCTTCCTCCA GCATCCAGAT	3660
GTCTTTACCA AAGTGATTGC TCTCAGTGGT GTTTACGACG CACGTTTCTT TGTCGGTGAT	3720
TACTACAACG ATGATGCTAT TTACCAAAAC TCGCCAGTAG ATTATATTG GAACCAAAAC	3780
GACGGCTGGT TTATTGACCG TTACCGTCAG GCAGAGATTG TGCTGTGTAC GGGGCTTGGA	3840
GCCTGGGAAC AAGATGGTMT GCCATCCTTT TACAAGCTCA AAGAAGCCTT TGACAAGAAA	3900
CAAAATCCAG CCTGGTTTGC TGAATGGGGA CATGATGTCG CCCATGACTG GGAATGGTGG	3960
CGTAAACAAA TGCCTTATTT CCTCGGTAAT CTCTATTTAT AAAAGGAGTT ACCTATGAAT	4020
TACCTTGTTA TTTCTCCCTA CTATCCACAA AACTTTCAAC AGTTTACCAT CGAACTAGCT	4080
AATAAAGGCA TCACAGTCTT GGAATTTGGT CAAGAGTCTT ACGAGCAATT GGATGAGCCC	4140
TTGCGCAATA GCTTGACCGA GTATTTTCGT GTTGATAATC TTGAGAACAT AGATGAAGTC	4200
AAACGTGCAG TTGCTTTTCT CTTTATAAAA CATGGTCCAA TTGGCCGCAT CGAGTCTCAC	4260
AATGAATACT GGCTTGAGCT AGACGCAACA CTCAGAGAAC AATTCAATGT TTTTGGTGCC	4320
AAACCAGAGG ATCTCAAAAA GACGAAATAT AAGTCTGAAA TGAAGAACT TTTCAAAAAA	4380
GCAGGTGTTT CTGTGGTACC TGGAGCTGTT ATCAAGACGG AAGCAGATGT TGATCAAGCA	4440
GTGAAAGAAA TCGGTCTTCC AATGATTGCC AAACCTGATA ATGGAGTGGG AGCAGCCGCA	4500
ACCTTTAAAC TTGAGACAGA AGACGATATC AATCACTTCA AGCAAGAATG GGACCATTCA	4560
ACCCTTTATT TCTTTGAAAA ATTTGTCACT TCCAGCGAAA TCTGTACCTT TGACGGGCTC	4620
GTGACAAGG ATGGAAGAT TGTCTTCTCA ACAACCTTTG ACTACGCCTA TACACCGCTT	4680

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GACCTCATGA TTTATAAGAT GGACAATTCT TATTATGTGC TCAAGGATAT GGATCCTAAA	4740
CTGCGCAAGT ATGGGGAAGC AATTGTCAAA GAATTTGGTA TGAAGAACG GTTTTCCAT	4800
ATTGAGTTCT TCCGTGAGGG GGACGATTAT ATTACCATCG AGTACAATAA CCGCCCTGCA	4860
GGTGGTTTTA CCATTGATGT TTATAACTTT GCTCATTCCT TGGACCTTTA TCGTGGCTAT	4920
GCAGCTATTG TCGCAGGAGA GGAGTTCCCG GCGTCAGACT TTGAACTCA GTATTGTTTG	4980
GCTACTTCTC GCCGTGCAAA TGCTCACTAT GTTTATTTCAG AAGAGGATTT GCTTGCCAAA	5040
TATAGCCAGC AGTTCAAGGT TAAAAAAGTC ATGCCAGCTG CCTTCGCGGA ACTTCAAGGA	5100
GATTACCTGT ATATGCTGAC CACTCCGAGT CGACAAGAAA TGGAGCAGAT GATTGCAGAT	5160
TTCCGACAAC GTCAAGAATA AGAACTATCG GATTAAGGAA ATTAATCTCC TTAATCCTTT	5220
TGTTTTGTCT GATAAAAAAT AAGAGCATCC CAACAAGGTA GCTATCATAA AACTTGTTCG	5280
ATAACTATTT GAAGCAGGAT TAGGTGGTCA GAAATTAAT TTTAATATTT CAATTGAGTC	5340
ATAGTATTGT GTTTGCGTAT CCTTAAATCA GCTAAAAGGA TCCATGACGA CACCTATACG	5400
ATATAGTTTT CAAGATACCA AACAAGTCTA TTAATATTCA ATGAAAATCA AAGAGCAAAC	5460
TAGGAAGCTA GCCGCAGGTT TCTCAAAACA CTGTTTTGAG GTTGTGGATA GAACTGACAG	5520
AGTCAGTATC ATATACTACG GCAAGGTGAA GCTGACGTGG TTTGAAGAGA TTTTCGAAGA	5580
GTATAAATA TTCAGGTGAC GCATAGATAT AGTTAATGTA AGCTTTGTTT GAAATCTGAT	5640
AAAATAATGA TATTACTAAG TTTTAAAAAC TAAAGAAAAG GGAAGATATG ATTACAGGCG	5700
AATTAAAAA TAAATCGAT CAGCTGTGGG AAATCTTTG GACAGAAGGA AACGCAAATC	5760
CTTTAACAAA TATTGAACAG TTGACTTATC TCTTATTAT GAAAGATTG GATAGTGTCTG	5820
AGCTTGACG TGAAGTGAT GCTGAATTC TAGGGATTCC TTATGAGGGA GTTTTTCCAA	5880
AAGATAAACC TGAATACCGT TGGTCAACTT TAAAAATAT AGGAGATGCT CAGGAAGTTT	5940
ATCGTTTAAT GACTCAGGAG ATTTTCCGT TTATTAATAA TCTCAAGGGG GATACAGATG	6000
ATACAGCCTT TTCACGATAT ATGCGAGAAG CTATTTTCA AATAAATAA CCTGCTACGC	6060
TTCAAAAGGC AATTCTATC TTAGATGTTT TTCCAAC TAGGATTAGAT GTAGATTTTG	6120
ATAATGACAA ACAAAGTATT ACTGATATCG GAGATATCTA TGAATATCTG TTATCAAAAT	6180
TGTCGACCGC AGGTAAAAAT GGACAGTTCC GTACACCTCG TCACATCATC GATATGATGG	6240
TTGAGTTGAT GCAACCGACT ATCAAAGATA TCATCTCAGA TCCCGCTATG GGTTCGTCTG	6300
GCTTCTTAGT ATCTGCTAGC CGTTACTTAA AGCGTAAGAA AGATGAATGG GAAACCAATA	6360
CAGATAATAT CAATCATTTT CATAATCAGA TGTTTCATGG AAATGATACG GATACGACTA	6420
TGTTGAGACT TGGGGCGATG AACATGATGC TACATGGAGT AGAAAATCCA CAAATCAGTT	6480



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ACCTTGACTC GCTGTCTCAA GATAATGAAG AAGCCGATAA ATATACTTTG GTTTTAGCAA	6540
ATCCTCCTTT TAAGGGCTCA CTTGACTACA ATTCAACCTC TAATGACCTT CTTGCAACCG	6600
TAAAAACCAA AAAACAGAA TTACTCTTTC TTTCTCTTTT CTTGCGAACT TTAACCAG	6660
GTGGACGAGC AGCAGTTATC GTACCTGATG GTGTCTTTT TGGTTCGTCT AAAGCTCATA	6720
AAGGAATTCG TCAGGAAATT GTAGAGAATC ATAAGCTTGA TGCTGTAATC TCAATGCCTA	6780
GTGGTGTGTT CAAGCCTTAT GCTGGAGTTT CAACTGCCAT TCTCATCTTT AAAAACTG	6840
GTAATGGTGG TACTGACAAA GTCTGGTTT ACGATATGAA AGCGGATGGT TTAAGTTTGG	6900
ATGATAAGCG ACAACCGATT AGCGACAATG ATATTCCAGA TATTATCGAA CGCTTTCATC	6960
ATCTTGAAAA AGAAGCAGAA CGTCAGAGAA CGGATCAATC TTTCTTTGTT CCAGTTGCTG	7020
AGATAAAGGA AAATGATTAT GATTGTCTA TCAATAAATA TAAAGAGATT GAGTATGAAA	7080
AAGTTGAGTA TGAACCAACA GAAGTCATAT TAAAGAAAAT CAATGATTTA GAAAAAGAAA	7140
TTCAAGCTGG CTTGGCTGAA TTGGAAAAAT TACTCAAGTA GGGAGGTGGC TGTATGAAAA	7200
AAGTGAAGTT GGGGAAGTC TTATCTCTAA AAAAAGGCAA GAAAGCCACT GTACTTGCTG	7260
AACAAACAAC TCTAAGCCAA CGTTATATTC AAATAGATGA TTTAAGAAAT AATAATAATT	7320
TAAAATTCAC TGAAAGTTTA AATATGACTG AAGCACTCCC AGATGATATT CTGATAGCAT	7380
GGGATGGAGC TAATGCAGGA ACAGTTGGTT ATGGATTATC GGGAGCTGTT GGTAGTACAA	7440
TTACGGTCTT AAAAAAGAAT GAGCGATACA AAGAAAAAAT TATATCAGAT TACTGGGAG	7500
TCTTTTGGAA AAGTAAATCG CAGTATTTAC GAGATCATTC AACAGGTGCA ACAATTCCTC	7560
ATTTAAACAA GAATATATTA CTTGATTTAC AATTAGAATT GCTAGGTATC GAAGAACAAG	7620
AGAACATTAT CTGTATTCTT AATACGATTA AAAGGCTTAT TACTAAAAGA AAATTTAGT	7680
TAGATGAACT AAACCTGCTC GTCAAATCCC GATTTAACGA GATGTTTGGG GAAAATAAAA	7740
TATTTGAAAG CATTGATAAC TTATTTGATA TTATAGATGG TGATAGGGGC AAAATTATC	7800
CTAAATCAGA TGAGTTGTTT AGTGAGGAGT ACTGTTTATT TTTAAATACA AAGAATGTTA	7860
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TAATATTACG TCCCAAGACA CCAATCTAA ATCAGAAATT TATTATCCAT GTTTAAGGA	8100
ATAATAATTA TAGTCGAGTG ATATCAGGAA GTGCTCAGCC TCAGTTACCA ATTACAAAAT	8160
TAAAAAAAT ACTTCTCCCC CTCCCCCAC TAGCCCTCCA AAATGAGTTC GCAGACTTTG	8220

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TAGTCCAGGT CGACAAATCA CAATTTGCTT GTGAGATAGC TATAAAAGTG TGGAGAAATA	8280
GCTTGAAATT TAGTATAATA TAGCTAACT ATTTGTTAA AGTGAGAAAA AAATGGGAAA	8340
TTTTAGCTTT CTTTTAAAA ATGACGAATA TGAATCTTT TCAAAACCTT GCATTGAAGC	8400
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GCAGGCTGTC CATTTGATAT ATAGTCACGA TTCATATTTA GAAGCTCCCT ATCGTGCTAC	8520
TCTATCTTCT TTAGTATGGG ATGATGATTT TAGGGATATC GTAGATTCTG AACTCCACAA	8580
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AGCCTCTGTC AATCCAGAAG TAGGGGAAGT ACAGGTCAAA GAATATGCTG AAGCTTTGGA	9180
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GATGGATAGA CGTCATCTTC AAAAACCCTG TGAGGATATT TCTAGTAAAA TTAGGGACGA	9360
TATTTCCGGG CGTCACTACC AAAACATGC CATTGCAAGC GTTTGTGAAG CTTTCTCTGA	9420
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TAGAACTTCC TTGGTTAAGC AAGCATATGA TTCGTTTGA AAATTACTCC CAGATCTTTC	9600
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CAAGTCCATT TTTGATTATT TTGATGCAAG AATTGTAGGC TTAACAGCTA CTCGCGTCA	9840
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ATATGATTTG GAAGAGGCTG TTAAGACGG ATATTTAGTA GCCTATCATT CTATCGAAAC	9960
CAAACTGAAA CTACCTACGG ATGGTCTACA TTATGATGAT TTGTCCGAAG AAGAAAAGGA	10020

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TGTACCAGAG GTTGTTAATT TAGTCTTCTT CAAGAAAGTA CGCTCTAAAA CTAAGTTTGT	10440
GCAGATGATT GGTGAGGAA CCCGTCTATG TAAAGATTTA TTGGACCTG AGCAGGATAA	10500
GGAAACTTC TTGGTATTTG ATTATGGGGA CAATTTTGAT TATTTTCGTG CAGATCCAAG	10560
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TCAGCAGCTT GTCTCGGAAC TTCAAGGTCG TATAGAGAGC TTAAATGAGT TGGACTTCAG	10740
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GAAATAATAC TCAATGAAAA TCAAAGAGCA AACTAGGAAA CTAGCTGCAG GCTGCTCAA	12000
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ATTGTTTCATG TAAACATGGG CACCATATG GAAAAAGAGA TGCTTGTTA TATGAGTAGG	13500
AAGAGCATGG AACATCTGGT AACATGAAG TGGTTTGACA TTCCAATCCT GAGAACCATG	13560

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AGTAAAGACA ACCTCTGCCT TTACTTTATG GGCATTGAGC AGATAATTGC GGTCA TGCCA	13620
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TTGGTGAGCT TCATTGCCAC GGATATAGTC GCCAGCTAAG AGATTACGAG AATAGGTTAA	13740
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CATTTATAGG TGA AAATGGT ATAATATAGT GAGAAGGATA GAGGAGAAGT GTAAATTGAT	15300

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CGCACAACTA GATACAAAAA CAGTCTATAG TTTTATGGAA AGCGTCATTT CGATCGAAAA	15360
GTATGTGAGA GCAGCTAAAG AATACGGCTA CACTCATTG GCTATGATGG ATATTGACAA	15420
TCTTTATGGC GCTTTCGACT TTCTAGAGAT TACAAAAAAA TACGGCATTC ATCCTTTGCT	15480
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AAGAAAGCAT GGCAGGAAG AAGTGACTGT TCTGGATCCA GTACTGGAGG ATATTTTGGC	17100

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TCCAACCTAC GGCATAATGC TCTATCAGGA GCAGGTTATG CAGGTTGCCC AGCGACTTGC	17160
CGGATTTAGT CTTGGGAAAG CCGATATTTT GCGTCGGGCT ATGGGGAAAA AGGATGCCTC	17220
TGCCATGCAT GAGATGAGGG CTTCTTTAT TCAAGGTTC TTAGAAGCTG GTCATACTGT	17280
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TCCACTACAA GCTATTGCAA GTAAGGCTAT TTACCCGATT ACCCCAATCG GAAATTTGTC	17940
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TGGTGACGGA TCTTACCACG GCGCTATGCG TTTGACTGAA CATGGCTTCC CAGCTATTGG	18840

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TCTTCCAGGT ACAATCGATA ACGATATCGT TGGTACTGAC TTTACAATCG GTTTTGACAC	18900
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TGAAGGTGTG ATGTCAGCGG CTGAATTGG TCAAAAACCT AAAGAAGCTG GAGATACAAG	19200
CGACCTTCGT GTAACAGAAC TTGGACATAT TCAACGTGGT GGTCTCCAA CTGCGCGTGA	19260
CCGTGTTTGG GCGTCACGTA TGGGTGCACA TGCTGTTAAA CTTCTTAAAG AAGGTATCGG	19320
TGGTGTTGCG GTTGGTATTC GTAACGAAAA AATGGTTGAA AATCCAATTC TTGTTACTGC	19380
AGAAGAAGGG GCATTGTTTA GCCTTACTGC AGAAGGTAAG ATTGTGGTTA ACAACCCAGC	19440
TACAAA	19446

## (2) INFORMATION FOR SEQ ID NO: 52:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 16593 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 52:

TCGTAATAT GCTCTGTTT TGGATTTGT TTCTTAATCT GTTTGGCAAG TGCCTTCATC	60
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GCATAGTTAC GGAGTAAATC TAGGTAGACT GCATTTTCAT CTCCACGGAA GCTATAGTAG	240
AAGTGAACCT GTTTATCTAA AATAGGATGT TCACGGATGT AAGAGATGAA GGGGGTGATC	300
CCAATACCTC CAGCAATCCA AACCTGATTT TCTCGTCCTT CTTCTATGAT CATGTGTCCG	360
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AAGGGATGCG GAGCACTTTC AAAGCCTTCT TGGAAAATCT TTAGAAAGGC AAATTGTCCT	540
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CGTTTGAGAT GGTAATTTT CCCTAGATAG GGAAGGAAA TCTTTTGATA TAGAAAAATG	660
ATATAAAAC CAGCTAGTAA GCCTAAAAGG GCATAGCTAC CAACAAGAAA ACTTAGAAGA	720
TTAAATGTAA GGAGACGATT GCCCATTATC ATGTAGATGT GAAAGAGTCC TAAATATAG	780



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GCTAGGTAAA CCAGGCGGTG AATCCATCGC CAAGCTTCGT ATTGGATGTA TTTGCCTAAA	840
TAGGCGACAA GGATGATGCT GGCAAAGATA TAGATGGCAA GATTGCCAAA CTGAGCAGCT	900
AAGCGAGAGC CCCACAAACC GCCCATACTA AAGTTATGAA AGATTAGTAG GATGATTGAG	960
AGAAAGGCTG TGAATTTGTG GACGGTGTAG ACCTTCTCCA AACTGTGAAA CCAGCTTTCT	1020
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GGAATCATGA ATTGGGGAGA AGTGTTTCATC CAAGTCAAAA GAGTCAAGAT AAAACTAGCT	1140
ATGATAAAGA GTAGTCCTTT GACTGATTTC ATAGAAAATT CCATTTTCATT TAGATTTCTGA	1200
TTTGTGTGTA ATAAATTTGT TACATTTTAT CATAGAAAAT GTATGGTGTG AAATTGAGGT	1260
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GAGCCGACCA AGACTTAGTC ACAAACATCA AGTCTACTCC AGAGATGATA GCTACAGTAG	2280
AGGTGTTCTT GATGAGGTTA ACAATTTGGT TGGTCAATGG AGGGAGAATG ATGCGGAAGG	2340
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TTTTCTATCT CTCATAATTT ACCTGACAAA AACTATGGTG GTGACTTGCT AGTTGAGAAT	15180
GATACAGAGA AATTGACCA ACTGCTAGAT GCGGAAACGG ACGTGGCAGT TTATGGTCAT	15240
GTTCACAAGC AGTTGCTTCG TTATGGAAGT CAAGGGCAAC AAATCATCAA TCCAGGGTCG	15300
ATTGGCATGC CCTATTTTAA TTGGGAGGCG TTAAAAATC ACCGTTCCCA GTATGCCGTG	15360
ATAGAAGTTG AAGATGGGA ATTACTCAAT ATCCAATTC GTAAAGTTGC TTATGATTAC	15420
GAAGCTGAGT TAGAATTGGC CAAGTCCAAG GGGCTTCCCT TTATCGAAAT GTATGAAGAA	15480
CTGCGTCGTG ACGATACTA TCAGGGGCAC AATCTGGAAT TATTAGCCAG CTTAATAGAA	15540
AAGCATGGGT ATGTAGAGGA TGTGAAGAAT TTTTGTGATT TTTTGTAAAG GTTTCCTAAA	15600
ATAGCCAATG CAAACTAAAA AAGCGATTTG CTGGTCCAAT CGCTTTTAGT ATATCTTATA	15660
CTCAATGAAA ATCAAAGAGC AACTAGGAA GCTAGCCGTA GGTGCTCAA AGCACAGCTT	15720
TGAGGTTGCA GATAAAGCTG ACGTGGTTTG AAGAGATTTT CGAAGAGTGT TATTGTAAGT	15780
GAGATTGATC TGGGAGGTAA GAACCACTA GATAGGTATT GCTGAGTTT TCAAGGGTTC	15840
CGTCTTGATA GAGTCTTTG AGCGCTTTAT CAAATTGCTC TTTAACTCT TTTTGGTCGC	15900
TTGAGAAAAAT GATATAATTG CTGGGGCTAT CTGCAGAAG TAAATCAACG ACTGAGAGGT	15960
CTAAACCACG GTCCTTGATA ATCTTTTGAA CGGATACCTT GTCAAAACT AGGAAATCAA	16020
ACTCTCCGTT AGCAAGGTCT AGGATTCGTT TACCAATATC CTCACCAGAA AAATTAATTG	16080
TAGCGGGATT ATCAGTGTGT TTCTGATTCC AGTTATTGAT GAATTGAGCG TTAGAAGTTC	16140
CGGTATCCTC TTGTGTGTT TTACCAGCGA TCTGGTCAAG AGAAGTCAAA GGATTTTCT	16200
TGTTGCTGAC AAGGACGAGG GGATTGTTGG AAATTGGAAG CGAGTAAAG TATTTTTCAG	16260
CACGCTCTTT TGTGTAAGT AAGTTATTGG CCGCAGCCTG ATAGTGACCA GAATCAAGTC	16320
CTGGGAAGAT GCTCTCCAG GCGGTCTTT GGAATTGAAT CTCGTAGTCG CTGAGTTTCT	16380
CATCTACTGC CTTTAAACT TCGATATCAA AGCCTGTCAG ATTGCCCTTG TCTTCGTAGT	16440
CAATGGTGG CACGTCGCCA GCTGTAGCAA GGACGATTGT CTTTGAGCG CTAGTCTCTT	16500
TGGGTGTAGC TTGATTCTCA CAGGCAACCA AAAATGGTAG GATAGCTAGT AATAGGCTAA	16560
ATTTTTCAT ACTGTCTCCA TTCAAATGTA AAG	16593

(2) INFORMATION FOR SEQ ID NO: 53:

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- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 3510 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 53:

GGGATATCCT TATATCCTTG TTCCTGGAAC CATGTGCGGA ATTGCTCAAC AGTTTTTTCA	60
CCTTGAATTC CTGGTGCAAT GACAGTAAGA ATTTGGAAT CACGATCTGG TTTCGCCGCT	120
AGTTCCATCA ACTCTGGCAT ACTTTTCTTG CATGGACCAC ACCATGAAGC CAAAACTTC	180
AAGTAAACCT TTTTACCCCT AAAATCAGAT AACTTAACCT CTTTGCCATC CATGGATTGC	240
AATGTGAAGT CTGGAGCATC TTTTCCAACA GCAATTGTG GTACAGTCGT TGTGTGTTT	300
GGCTGTGTG CTGCTTGAGT CTTTCTAGTT TCTTCTCAC CACAGGCCAT CAATACAACT	360
AATGACAAGA GACTTAAGCC AGCAACATT ACTTTTTTCA TTGTCTCTT TTTATTCAA	420
AATTCCAGCT AGAACATTTA CTGTCTTAA TAGTAACAAA ATTCCCATTA AAACAATGAG	480
GAAACCACCA ATTTTCTTTA GTAGCATCAT ATGACGCTTG ATTTTACTAA AATATGGCAT	540
GACTAGACCT GAAGCTAGTG CCAATACCAA GAAAGGAAGG GCCATGCCaG AGTGTAATG	600
AGAGTATAAA TCGCTCCTTG CCAAGCGCCA TTGCCTCCAG AAGCCGCAAG TGCTAAACA	660
GAACCTAAAA CTGGACCAAT ACAAGGTGTC CAACCAAAGC TAAAGGTAAT ACCAAGTAAA	720
AAAGCTGACC AATAACGATT AGAATCTGAT TTTTAAAGG TAAACTTTT TTGAACCTCT	780
AATTCTTCA AATGAAAAAT TTCCATCTGG TGAAGACCCA AAATGATAAT AATAGCTCCC	840
ATGCCATATC GAAACCAATT TGCATAGAGA ATATGACCAA AGTAACCAGC ACCAAAGCCT	900
AGAATAAAGA AAATGAGAGA GATACCAGCG ATAAAGCAAA GTGTCGAAT CAAGCCTGAC	960
CAGAGAACCT TTCTCCCAA CAAAGAAAAG CTTTGTGCAC TTTCTTGATC ATCCAATAAA	1020
ATCCCAGCAT AGACTGGCAG AAGAGGAAAA ATACAAGGAG AAAAAAGGA TAAACACCT	1080
GCTAGAAAAA CAGAGATTAA AAATACTATC GTTTCCAATA AAGAACCAAC TTTCTTAATA	1140
ATTCTAATCC TATTTTACTA TATTCATTT TATTTGTAAG CTTTCTGCTA CGCAAAATCG	1200
TATCGGGCAC TATTTGACCA ATCTTTCTT TTGCTAGTCA AGGCGGATCT TATCCCCAA	1260
AATAGCCAAA AAGCAACGAC AAGGATTACT CATCGCTGCT TTTGTGAACG AAAATGTCTT	1320
TTAGGTCTGA CATTTCAATA ATCATGTTT ACTTGAGTTT GTCAAGGATT GCTTTAAGCT	1380
CCTCTACTAG TTTAGTTTCT GTCTCTGCTG AGCCATTTTC TTCTTTCACG AAATCAAGGG	1440
TTTCTTGAGG AAGGTTTTGG GCTTTGGCAA GGACTTTTTT ATCCGCTTTT TCTGCATCTA	1500

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GCTGTCCTAG AACCTTGATC AATTCCTGTC TTAATTGCTG GATTTCTGAC TCTTTCTTAC	1560
GGCGAATCAG CCAGAAGGCA ATCACGCCTA GGAGGGCAAG TAGACTGACC ACAATCACTC	1620
CTGCCCGAAC TGAGTTTGTT TCAGTCATCT TATCTGAATC CTTACTATCT TCCGTTCCCT	1680
GTTTTGCATC CTTCTTGTC TGTGCAGGCT TGCTGTCGCT AGCATTGCT TTCACATCTT	1740
TGAGAGAGTC CAAGGCAGCC CAGCCTTCAC AGACTCTACT GCAGTATGCA GACCTTACTC	1800
TGTCAAGGCA CTATCTCCG GAGCTTTTGG AGCATCTAGG AGGACAGCCT TGGTTGCATC	1860
GATTTTCGGA TCAGATACTG TTGCCAAAGC TTCAAGCGT TGGTCTAACT CTTGACTCAA	1920
GGCACGAAGT TCAGACTTGT CAACTTGCTC TTGAGCTTGT GTGCTCGTTG AGCTAGCCGA	1980
AGCGCTTGCT ACCACTCTAG GATCTTGAGT CGGAGCTGAG CTTGGAGCTG GGACAGGGCT	2040
TGCAGGTTGA CTAGGAACAG TTATGGTATA TTGAACTAG AATAGTACAT ATGGACTTCT	2100
AAAACATTGT TAGAATTCGA TTTTACTGTC CTGATCGATT TGTCTATTTC TTATTTTCAAT	2160
TTACTATAAT AACCGATGGT GTGGTTAATG TTGGTAAGAG AAACCTCTGA AACCAAGCTT	2220
CAAAAAAGTC GCTCGTCATC GTCTCTTCGT AAGTCATTGG AGCGATTAAT TCACCATTTG	2280
TTAGACCTGC AACCAAAGAA ATCCTCTGAT ATCTTCTTCC AGATACTTTG CCTCTTATTA	2340
ACTGACCTTT TAATGAGCGA CCATATTCTC GATAAAAAATA AGTATCGAAT CCTGTTTCGT	2400
CAATCTAAAC AGGTGCTAGG TGCTTTAAAC TATTAAAATT CTTAAGAAAT AAGGCTACTT	2460
TTTCGGGTC TTGTTTCATG TAGGTGTTGGT TCTTTTCTTC GAGGTAGCC CATAGCTTTG	2520
AGCGCATAGT GGATGGTAGT TGGATGACAG CCAAATCAG AAGCTATTTC AGTCAAATAA	2580
GCCTCTGGAT TGTCAGTAAG ATAGTTTTTA AGTCTATCTC TATCAACTTT TCTTGGTTTT	2640
GTTCTTTTFA CTTGGTGGTT TAGCTCTCCT GTTTTCTCTT TTAGCTTTAA CCAGCCATAA	2700
ATGGTATTAC GTGAGATTG GAAAACGTGT GATGCTTCTG TTATACTACC TATTGCTCA	2760
CAATAAGAGA GAACTTTTTT ACGAAAATCT ATTGAATATG CCATAAGAAG ATTATACCAC	2820
ATTGTGTACT ATTTTGGTT CATTTCACTA TAACACAAA TAGATTATTA TTACATAACA	2880
AAAAAGAGGT CTAAACCTCT TAACTCAATT ACTCCGCCAG TAGGACTCGA ACCTACGACA	2940
TCATGATTAA CAGTCATGCG CTACTIONCAA CTGAGCTATG GCGGATTAAA GCTAAGCGAC	3000
TTCCCTATCT CACAGGGGGC AACCCCAAC TACTTCCGGC GTTCTAGGGC TTAACCTCTG	3060
TGTTCCGGCAT GGGTACAGT GTATCTCCTA GGCTATCGTC ACTTAACCTCT GAGTAATACC	3120
TACTCAAAAT TGAATATCTA TTCAATTAA GAAAACCGTT CGCTTTCATA TTCTCAGTTA	3180
CTTTGGATAA GTCCTCGAGC TATTAGTATT AGTCCGCTAC ATGTGTCGCC ACACCTCCAC	3240

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TTCTAACCTA TCTACCTGAT CATCTCTCAG GGCTCTTACT GATATATAAT CATGGGAAAT	3300
CTCATCTTGA GGTGGkTtCA CACTTAGATG CTTTCAGCGT TTATCCCTTC CCTACATAGC	3360
TACCCAGCGA TGCCTTTGGC AAGACAACTG GTACACCAGC GGTAAGTCCA CTCTGGTCCT	3420
CTCGTACTAG GAGCAGATCC TCTCAAATTT CCTACGCCCG CGACGGATAG GGACCGAACT	3480
GTCTCACGAC GTTCTGAACC CAGCTCGCGT	3510

## (2) INFORMATION FOR SEQ ID NO: 54:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 20986 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 54:

CGGAGAAAAA CATGGCTAAG TCAAACCTTG AAAAAGTAGA ATCAGTTGTT GGCTGGGTC	60
GTGATAAGAA AATCACAGGC TACCGTATCT CTAAGAAAC GAATGCGCGT GAAATGTCTA	120
TCATTGCTCT GCGCAGGGT CGTGCAAAG TAAAAATAT TTCATTTGAA ACAGCCCTAG	180
GCCTAATTGA TTTCTATGAA AAAAATTATG AAAAATTGA AGATTAATCT TTGGATAACG	240
GCGGATTCTT GACCTTCAAG TAGTAGAGAT AGAGAATCTG CCTTTTCATT TTGAGGACAG	300
CAAAAAGACT GCACGGTTGA TGCAGCCTTT TCTTTTATT TGAGATAGCG TTGAAGGAAC	360
TCTTTTGTTT GGTCTTCTTT AGGATTGGTG AAGAGGTCTT CTGGTTTACC TTCTTCAGCG	420
ATCACGCCCT TATCCATAAA GATAACACGG TGAGAGACAT CACGGGCAAA TTCCATTTCA	480
TGGGTTACGA CAATCATGGT CAAGCCTTCC TGAGCCAGGT CCTGCATGAT TTTGAGGACT	540
TCTCCAACCA TTTCTGGATC GAGAGCTGAT GTTGGTTCAT CAAAGAGAAT AGCGTCCGGA	600
TTCATGGAGA GGGCACCAGC GATGGCCACA CGTTGTTTTT GACCACCTGA GAGTTGTTTT	660
GGTTTGGCTT GCCAGTAGCG TTCTCCCATG CCGACCTTTT CCAGGTTTTT TTTGGCAATC	720
TTTTCAGCTT CTGTGCGTTC GCGTTTTAGG ACAGTTGTCT GAGCGACGAT TGTGTTTTCA	780
AGAACATTGA GATTTTCAA GAGGTTAAAG GATTGGAAAA CCATCCCAA CTTTTCACGG	840
TATTGCGTGA GGTTCATAGC TTTTTCGAGG ACGTTTGTG CATGATAAAG GATTTGTCCA	900
TCAGTTGGTG TTCAAGTAG GTTAATGGAG CGTAGGAAGG TCGATTTTCC GCTTCCAGAG	960
CTTCCGATGA TAGAGATGAC CTCTCCCTTG TGGACAGTGA GTGAAATGTC TTTTAGCACT	1020
TCGTTTGTG CATAGGATTT TTTGAGGTGT TTAATTCAA GGATTGCTTG TGTCAATTAT	1080
TCAAATCCTC CGTTTGCAAT TGGTTAGCAC CTGTAGTGTA GGTATCCATG TCCATTCTGC	1140

GCTCGATAAA GCGTAGGATA CGTGTTACGG TGAAGGTGAG GACAAAGTAA ATCACGGCGA	1200
TGATTGTAAA TGTCTGGAAG TATTGATAGG TTTGTGTTGC CACGGTATTT CCTGAGAAAT	1260
AAAGTTCGAC AACAGAGATA ACGTTCAATA CAGATGTATC TTTGATATTG ATGACAAATT	1320
CATTACCACT TGCAGGTAGG ATGTTACGGA CTACCTGAGG TAGGACAATC TTACGCATGG	1380
TCTGGTTATG GGTACATACCA AGAGCAGTCG CAGCTTCAAA TTGTCCCTTG TCAACTGCTA	1440
GGATACCACC ACGGACGATT TCAGTCATGT AGGCACCGGT ATTGATTGAA ACGATGAAGA	1500
TAGCAGCCAG TGTACGGTCA AGGTTGATCC CGAAAGCTTG GGCAGTTCCA TAGTAGATAA	1560
CCATCGATTG AACCAATCATT GCGTACCAC GGAAATTTTC AATGTAGACA TTGAGAACCC	1620
AGCCGACTAG TTTTGTAGG CCGTAAATGA CTTTGTTTTC AGAGAGAGGA GCAGTACGGA	1680
AGACACCAAT GGCAAGTCCA ATAATGAGAC CTATGATGGT TCCGACGATA GAGATTAAAA	1740
GAGTGATACC AGCACCACGC AAGAGTTGTT GCCAGTTTTC AGAAAGAATT TTAGCAACTT	1800
GGCTAAAGAA ACTACTGCTA GTCTCTTCAG TTGTTGTAGC TTCGGCAGGT TGTTCCTTGA	1860
TCATACGATC CATCAAGGCA ACTTGGTCAT CTTTGTAAAT GGTTTCAATG CTGGCATTGA	1920
TTTGGCTAAT ACGATTGTCA TTTTACGAA GCGCGATAGC GATAGCTGTA TCTTCTTCCC	1980
CAGTTTTGAA ACCAGGTTCT ACTTGAATCA TCTTGAACCT AGAGTTCGCA GCTTCAGCAG	2040
TCAGTGCTTC TGGACGTTCA GAAACATAAG CATCAATGAC ACCAGCCTCA AGAGCTTGTC	2100
GCATTTGAGC GAAGTCTCCC ATGGCTGTTT CTTTTTTCAG ACCTGGGATT TGTGCAATCA	2160
AGTTATAAAG GTAGACCCCT TGTGAGAAG TGATTTTTC ACCGTTAAAG TCATCCAAAG	2220
ATTTAGCACT TCGTAGGCA GAATCTTTT TGACAAGCAA AACTGGTTCG CTAGTATAGT	2280
AACTGCTCGA AAAGGCAATT TCTTGTTCG GTTCTGCAGT TGGACTCATA CCTGCGATAA	2340
TCATGTCAAT CTTACCAGAA GTAAGGCGAG GGACTAGACC TTCCCACTTG GTTTTAACAA	2400
CCAAAGGTTT TTTACCTAAG TCCTTAGCGA TTTTCTTGGC GATTTGAACA TCGTATCCGT	2460
TGGCATACTG ATTGGTCCCA TCGATTTTGA CAGCTCCGTT GCTATCATCA TCCTGGGTCC	2520
AGTTAAAGGG AGCATATGCT GCTTCCATAC CGATGCGTAA ATATTTCATCG GCTTGAGCAA	2580
CATTGACAAG TCCTAGCATC AGCAAGAGAC TTGTGAAAAT AGATAAGTAY ATGTGGCTCA	2640
TGATTTCTCC TATTCTGATC TATTAATAAA TAACTGTCTC CTATTTTATC GAAAAATGCG	2700
TAATTTTTC AATAAGTAA GTCTTACTT ACGAAAAAT GCTATAATGA TAAGAAAGAT	2760
AAAAAGGGG CTTAGTTGAT GAAAAAACT TTTTCTTAC TGGTGTTAGG CTGTGTTTGC	2820
CTTCTTCCAC TCTCTGTTT TGCCATTGAT TTCAAGATAA ACTCTTATCA AGGGGATTG	2880

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TATATTCATG CAGACAATAC GGCAGAGTTT AGACAGAAGA TAGTTTACCA GTTTGAGGAG	2940
GACTTTAAGG GCCAAATCGT GGGACTTGGA CGTGCTGGTA AGATGCCTAG CGGGTTTGAC	3000
ATTGACCCTC ATCCAAAGAT TCAGGCCGCG AAAAACGGTG CAGAACTAGC AGATGTGACT	3060
AGCGAAGTAA CAGAAGAAGC GGATGGTTAT ACTGTGAGAG TCTATAATCC AGGTCAGGAG	3120
GGCGACATAG TTGAAGTTGA CCTCGTCTGG AACTTAAAAA ATTTACTTTT CCTTTATGAT	3180
GATATCGCTG AATTAAATTG GCAACCTCTG ACAGATAGTT CAGAGTCTAT TGAAAAGTTT	3240
GAATTCATG TAAGGGGAGA CAAGGGGGCT GAAAACTCT TTTTCCATAC AGGGAAACTT	3300
TTTAGAGAGG GAACGATTGA AAAGAGTAAC CTTGATTATA CTATCCGTTT AGACAATCTT	3360
CCGGCTAAGC GTGGAGTTGA GTTGCATGCC TATGGCCTC GGACCGATTT TGCTAGCGCT	3420
AGGGATCAGG GATTGAAAGG GAATCGTTTA GAAGAGTTTA ATAAGATAGA AGACTCGATT	3480
GTTAGAGAAA AAGATCAGAG TAAACAATC GTTACTTGGG TCCTCCCTTC GATCCTTTCC	3540
ATCTCCTGT TATTGAGTGT CTGCTCTAT TTTATTTATA GAAGAAAGAC CACTCCTCA	3600
GTCAAATATG CCAAAAATCA TCGTCTCTAT GAACCACCAA TGAATTAGA GCCTATGGTT	3660
TTATCAGAAG CAGTCTACTC GACCTCCTTG GAGGAAGTGA GTCCCTTGGT CAAGGGAGCT	3720
GGAAAATCA CCTTTGATCA ACTTATTCAA GCTACCTTGC TAGATGTGAT AGACCGTGGG	3780
AATGTCTCTA TCATTTGAGA AGGAGATGCA GTTGGTTTGA GGCTAGTAAA AGAAGATGGT	3840
TTGTCAAGCT TTGAGAAAGA CTGCCTAAAT CTAGCTTTT CAGGTAAAAA AGAAGAACT	3900
CPTTCCAATT TGTTTGGGA TTACAAGGTA TCTGATAGTC TTTATCGTAG AGCCAAAGTT	3960
TCTGATGAAA AACGGATTCA AGCAAGAGGG CTTCAACTCA AATCTTCTTT TGAAGAGGTA	4020
TTGAACCAGA TGCAAGAAGG AGTGAGAAAA CGAGTTTCCT TCTGGGGGCT CCCAGATTAT	4080
TATCGTCCTT TAACTGGTGG GAAAAAGGCC TTGCAAGTGG GTATGGGTGC CTTGACTATC	4140
CTGCCCTAT TTATCGGATT TGGTTTGTTC TTGTACAGTT TAGACGTTCA TGGCTATCTT	4200
TACCTCCCTT TGCCAATACT TGGTTTCTA GGGTTAGTTT TGTCTGTTTT CTATTATTGG	4260
AAGCTTCGAC TAGATAATCG TGATGGTGT CTAATGAAG CGGGAGCTGA GGTCTACTAT	4320
CTCTGGACCA GTTTTGAAAA TATGTTGCGT GAGATTGCAC GATTGGATCA GGCTGAACTG	4380
GAAAGTATTG TGCTCTGGAA TCGCCTCTTG GTCTATGCGA CCTTATTTGG CTATGCGGAC	4440
AAGGTTAGTC ATTTGATGAA GGTTCATCAG ATTCAAGTGG AAAATCCAGA TATCAATCTC	4500
TATGTAGCTT ATGGCTGGCA CAGTACGTTT TATCATTCAG CAGCACAAT GAGCCATTAT	4560
GCTAGTGTG CAAATACAGC AAGCACCTAC TCTGTATCTT CTGGAAGTGG AAGTTCGGT	4620
GGTGGCTTCT CTGGAGGCGG AGGTGGCGGC AGTATCGGTG CCTTTTAAAG AGAGCTACCA	4680

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TAGACTGAAA AAGTATGATA TAATGGAAGA TAGAAAAAG ACAAACTATA AGAAAAGTCA	4740
ATAGTTTTAT CTAACATATT TCTTATTTCA ATTTGATGAT TTGGCGATGA TTTTAGAGCA	4800
CGGCAAAAAG CCCTTGAAAA AGTCCATTTT TTCAAAGGTA ATCCTGTGTT AATTTCAGAA	4860
ATTACATCAC TTTTGTTCG TCAAATGGCA GCTCTTTTAT AGGATATAAA ACAGGGTTCG	4920
GATAAGTTTT TTTGCAAGGT GGATGATGGC TACATTGTAA TGTTCCTT ATTCTAACTT	4980
AGTCTTAAGA TAGGCCTTAG AAGCAGGTGA AAAGCGAGGG CATGCTTTGG CAGCTTGAT	5040
GAGTGCCAC CGCAGATGAG GGAACCCCG TTTGACCATT CTCCAGCTA AATCAATCTG	5100
ACCTGACTGA TAAATAGAAG AATCCAGTCC AGCGAAAGCT TGTAATTGAG CAGGATTATC	5160
AAAGGCATGA ATATTTGAA TCTCGGCTAA AATGACCGCC CTAAACGATC CCCAATCCCA	5220
GTAACCGTCG TGATGACCGA GTTGAATCA GCCATCGAGT CATTGATACA TGTTCGGCC	5280
TTGTCAATGA GCCTCTTGA ATGCTTGATG ATTTGGAATT CACGAGCAGG AGATGTTGTT	5340
CCGATAGAAC GAGGTGCGAC TGAGAGGATA TCCTGAATTT TAGAAGCGGT CAATCGCTTA	5400
ATTTCTATCA GCTTATCAA TCCTGCCTCA ATCCTTTTCT GAGGATTAGG GTAGCGTGTC	5460
AAGAGTTGGT AGGTATATTC TGAATGCTTT CCAACGATTT TATCCAATC AGGAAAGATG	5520
ATATCAAGAC AACGAGTGTA TTGTACTTTC CAATCAGACT GTTTTCTTG AGACGATGAA	5580
TATGTCTAGC CAGTATTTT AGGTCTACTT GCCGATTATC GTTTGAAAT TGTTCACGAT	5640
TGGGGTCAGA AAGAAGTTTA AGAGCGATGC CATGAGCGTC TTTCTTATCC GTTTTAGTCT	5700
TGCGAAGTGA TAATGATTTG GCAAATTCCT TGATGAGCAA AGGATTGTAG GTGTAACTT	5760
TATATCCTTG TTCATGCAGG AAGTTCAGTA GATTAAAGGC ATAATGTCCA GTATCTTCAA	5820
GAGCGATGAG ACAGTCTGG TTGATCTGTC GAATAGACAG ATCTAAGAGT TCAAAACCAG	5880
CTTTATTATT TGAAAAGTG AGTGGTTTAA GAACAGTTT TCCTGGAACA TTCAAGGCTG	5940
TAACATCGTG TTTATTTTGA GCGATATCAA TGCTACATA AAGCATGGGA GTACCTCCAG	6000
ATATAGTATT TCAAGTCTAC TTGGTTATCC ACGAATTTT TGCTTGTTA CCTTAGACGA	6060
GATCAAACGT CTATGCGTTA TCAAATCAT TACCAATTGA AACAAAGCT GTGGTTAGAG	6120
CCTTTCGAA ATCGTCAAGC GATTGGAGGA AATGAACTAA TCCATAGTGG CTATTCCAA	6180
GTATACCACT TGGGCTTGG CAGTAGCTAA CTGCGCTAAA TATAATATAG GGAGTAATCT	6240
ATGTATCTTA TTGAAATTT AAAATCTATC TTCTTCGAA TTGTTGAAG AATTACGGAA	6300
TGTTTCCGA TTTCCAGTAC AGGTCACTTG ATTTTAGCAG AGGAATTCAT CCAATACCA	6360
AATCAAAATG AAGCCTTTAT GTCCATGTTT AATGTCGTGA TTCAGCTTG TGCTATTTTA	6420

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GCAGTTATGG TGATTATTT TAACAAGCTC AATCCTTTTA AACCGACCAA GGACAAACAG	6480
GAAGTTCGTA AGACTTGGAG ACTATGGTTG AAGGTCTTGA TTGCTACTTT ACCTTTACTT	6540
GGTGTCTTTA AATTGATGA TTGGTTTGAT ACCCACTTCC ATAACATGGT TTCAGTTGCT	6600
CTCATGTTGA TTATCTACGG GGTTCCTTC ATCTATTTGG AAAAGCGCAA TAAAGCGCGT	6660
GCTATCGAGC CAAGTGTAA AGAGTTGGAC AAGCTTCCTT ATACGACCGC TTTCTATATC	6720
GGACTCTTCC AAGTCTTGC TCTTTTACCA GGGACTAGCC GTTCAGGTGC AACGATTGTC	6780
GGTGGTTTGT TAAATGGAAC CAGTCGTTCA GTTGTGACAG AATTACCTT CTATCTTGGG	6840
ATTCCTGTTA TGTTTGGAGC TAGTGCCTTA AAGATTTTCA AATTGTGAA AGCCGGAGAA	6900
CTCTTGAGCT TTGGGCAATT GTTTTGTCTC TTGGTCGCGA TGGGAGTAGC TTTTGGCGTC	6960
AGCATGGTGG CTATTCGCTT CTTGACCAGC TATGTGAAAA AACACGACTT CACCCTTTTT	7020
GGTAAATACC GTATCGTGCT TGGTAGTGTT TTGCTACTTT ACAGTTTGT CCGTTTATTT	7080
GTATAAGAAA AACCTTGAAG GGGCAACTCT TCAAGGTTTT ATACTCTTCG AAAATCTCTT	7140
CAAACCGCGT CAGCTTTATC TGCAACCTCA AAACAGTGT TTGAGCAGCn CTGCGGCTAG	7200
CCTCCTAGTT TGCTCTTGA TTTTCATTGA GCTTTAAAAT CCAGTCATGG TAATCCCCAA	7260
TAGGCGGACA CCTCTTCTT TCTTGCTTAA TTCTTCATAG AGTTGCAGGG CTATTTGGCT	7320
TATCTGACTA GCATCTGTG TTTTGTGAGC AAGACTTTTT CGTTTGGTAA GAGTTGAAAA	7380
GTCTCGTAG CGGATTTTCA AAATGACAAT TTTTCCAGCT TTTTCTTGTT GATGTAGATT	7440
GAGAGCGACT TTTTCTGATA GAAGAGTCAG CTCTTTTTTG ATATCTTCCT CAGCAAGGAG	7500
AATCTTCCCG TAGGTTTTCT CTTGCGGAT TGATTTACGG ATGCGATTGG ATTGACTGG	7560
AGAGTTGTGA ATGCCACGAG CCTTTCGATA CAGATCATAG CCTAGTCTAC CAAAACGGTC	7620
TATTAGGGTT ACCTCAGGAA CTTCAAGTAA ATCAGCACCA GTAAAAACGC CCATTTGATG	7680
AAGACGTTCT ACTGTCTTTT TTCCTACTCC ATGAAATTTG GAAATATCCA TTTGTTTGAG	7740
AAAATCCTCA GCCTGTTTCA GTAGAATCAC TGTCAAACCA TGTGGTTTTT GATAATCACT	7800
CGCCATTTTA GCTAAGAATT TGTGTAAGA AACGCCGCG GAAGCAGTTA GATGGAGTTC	7860
TTGCCAGATA TCTTTTTGAA TGAGGCGAGC AATTTTGACC GCTGACTTGA TACCGAGTTT	7920
ATTTTCTGTC ACATCCAAAT AGGCTTCGTC AATGCTCATG GGTTCATCA AATCTGTATA	7980
GCGCTTAAAA ATAGCTCGAA TCTGGAGTCC CACAGACTTG TATTTCTCAT AATCCCTGA	8040
GATAAAGACA GCCTGGGGAC AACGTTTATA AGCTTCCTTG GAACTCATGG CAGAATGGAC	8100
ACCAAAAGCT CTGCGCTCAT AACTACAGGT AGAAACGACT CCCCCTCCAC CTGTTTGCCG	8160
AGGGTCGCTT CCAATAATGA CAGGTTTTCC TCTGAGTTTA GGATTATCCC TGATTCCAC	8220



TGCAGCAAAA AAGGCATCCA TGTCAATATG GATGATTTTT CTTGACAAAT CATTTAACAA	8280
AGGAAAAATC AACATGCCTA GCACCTTTTT ATACTCTTCG AAAATCTCTT CAAACCACGT	8340
CAGCTCTATm TGCAACCTCA AAACAGTGTT TTGAGCAATC TGCGGCTAGC TTCCTAGTTT	8400
GCTTTTCGAT TTCCATTGAG TGTACTGCT TATTYTCITT TATTATACCC TTTTTCCTGA	8460
AAAAAAGAAA AAAGGACTTT ATTTTTCCTAA AAATATAATA CAGTTTGAAA TAAAAATAG	8520
ACTGTTTTAG AAAAGAAAGT GTAAAAATAG GGAATTTTCA CTTGTTGAAA TCGGTTACTA	8580
TATGGTATAC TTGTCTTATG AATGTAACAG ATGACTGTTA CTAGAAAAAA GAGGACATTA	8640
ATATGGTTGT TAAGACAGTT GTTGAAGCAC AAGATATTTT TGACAAAGCT TGGGAAGGCT	8700
TCAAAGGCGT AGATTGGAAA GAAAAAGCAA GTGTATCACG ATTTGTACAA GCTAACTACA	8760
CACCTTATGA TGGAGACGAA AGCTTCCTTG CAGGACCAAC AGAGCGTTCA CTTACATCA	8820
AGAAAAATGT AGAAGAACT AAAGCACACT ACGAAGAAAC TCGTTTCCCA ATGGACACTC	8880
GTCCAACATC TATCGCTGAT ATCCCTGCTG GATTTATCGA CAAAGAAAAT GAAGTTATCT	8940
TCGGTATCCA AAACGATGAA CTCTTCAAAT TGAACCTCAT GCCAAAAGGT GGTATCCGTA	9000
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GTGCGGCTCG TCACGCACAC ACTGTAACGT GTCTTCCAGA TGCATACTCA CGCGGACGTA	9180
TCATCGGTGT TTACGCACGT CTTGCTCTTT ACGGTGCAGA CTACTTGATG CAAGAAAAAG	9240
TAAATGACTG GAATGCAATC AAAGAAATCG ATGAAGAAAC AATCCGTCTT CGTGAAGAAG	9300
TAAACCTTCA ATACCAAGCA TTGCAACAAG TTGTTGCGCT GGGTGACCTT TACGGGGTTG	9360
ATGTTGCGCA ACCAGCGATG AACGTGAAAG AAGCAATCCA ATGGGTAAAC ATTGCTTTCA	9420
TGGCTGTCTG CCGTGTGATT AACGGTGCTG CTACATCTCT AGGTGCTGTA CCAATCGTAT	9480
TGGACATCTT TGCAGAACGT GACCTTGCTC GTGGTACATT TACTGAATCA GAAATCCAAG	9540
AATTCGTTGA TGATTTGCTT ATGAAACTTC GTACAGTTAA ATTTGCTCGT ACAAAGCTT	9600
ATGACCAATT GTACTCAGGT GACCCAACCT TTATCACAAC TTCTATGGCT GGTATGGGTA	9660
ACGACGGTCG TCACCGTGT ACTAAGATGG ACTACCGTTT CTTGAACACT CTTGACAACA	9720
TCGGTAACTC ACCAGAACCA AACTTGACAG TTCTTTGGAC TGACAAATTG CCATACAACT	9780
TCCGTCGCTA CTGTATGCAC ATGAGCCACA AACACTCTTC TATCCAATAC GAAGGTGTAA	9840
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TTGATCCAGA AAATGAAGAA CAACGCCACA ACATCCAGTA CTTGCGTGCT CGTGTAAACG	9960

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ACTTGAAGTC ACTTTCTAGC CTTGACTTTA GTTATGCAGC TGACGGTATC TCATTGACTA	10680
CACAAGTATC ACCTCGCGCT CTTGGTAAGA CTCGTGATGA ACAAGTTGAT AACTTGGTAA	10740
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AGTAAGTTTG GCAATGTTCC ATCAAAATCG GATACATAAA GAGGTTTTTT AATTTTTC	13500

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GCGGTCTTTA GTCTTCAAAA ACAACATCCG GATTATCCAG ATATTTATGG AGCTATTGAT	16980
CAAAATGGCA CTTATCAAAA TGTGAGAACA GGTGAAGATG GTAAGTTGAC CTTTAAAAAT	17040

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ATACAGGGGA AGAAACCCCTT GTATATCTTG ATGCTTGTG CCATTTTGGT GTTTGGTAGT	20760
GGTTATTGTC TTACGAAAA ACCAAATAAC TGATATTCAA TGTACATCAT TATGAATAGG	20820
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ATGTGGCATG AATCATCAAT AACGGATATG AGGCTGGGCA GATTGTGCCA GCCTCATTTG	20940
GGGTATTGT TTGTAAACG ATAGGACTGG TCTGGTAATC ATTTTA	20986

(2) INFORMATION FOR SEQ ID NO: 55:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 21040 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 55:

CCCAGCAAAA AGCCATCCGA AGATGACTTT TTTGCTATTT AATTTCTGTA TAAGTTACTT	60
CCAAGCCACG CTTAACAGCT GGACGATTGG CAATTTTTC TGCCCATTTT ACTAGATTTT	120
GATAACTTGA GGCATCCAAG AATTTTGCAG AACCTTGGTA AAGATTTCCT TGAACATACT	180
GTCCATACCA AGACCAGATA GCAATATCTG CAATCGTATA GTCATTGCCT GCAATATAAG	240
GTTCCTGAGC CAATTCCTTA TCCAATAAAT CCAACTGGCG TTTCACCTCC ATCGTAAAC	300
GGTTAATAGG ATATTCCAAT TTTTCAGGAG CATAATTGAA GAAATGTCCA AATCCCCCAC	360
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CCTTCACACC ATTTGGTGT TCCAGTGAAT AAAGCTGAAA AGCTTGTCT CCTTTGGCA	720
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TACTAGCTTC ATCCTGCCAT ACGGTCGGTA ATTGATATGC TGACATCCGA AACCTCCCTT	840
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TAATCATTGA GAAGCTTCCA GCCATAACAA TTCCCCATTG TGACAAGTCT AGTTTGGTTA	960
CGTGGAAGAT TCCTTCAAGC GGTCTACAA CGATTGTTGC CATGAGAAGG ATAAAGGATA	1020



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CCAAGATGGA CCAGTTAAAG GTCTTAGACT TGAATGGGCC AACTGTCAAG ATGGATTTGGT	1080
AGACAGACTT GACATTGTAG GCATGGAAGA GCTGAATCAA ACCAAGGGTT GCAAAGGCCA	1140
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CAGAGTATTG ACCAACGACT TTTTCAAAT CTTCATCTGA CAGTTCATTG AGTTCAGCAC	1800
CAGTTAAAAC GTGACCTTCT GTATCGTTTG CGTCAATGAT TCCCAAACGT TTGGCAATGG	1860
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GACAACGTTT TAAGAGTTGG TCTGGCGCAC CCTTGACTGC TACAAGGAAA CGACCATCTG	2220
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CAGATTCAAC TGTCAGGCT GCTTCTTCAA TTTTAAGAGA GTTGGCTTCT ATCAAACGTA	3060
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GTATCATCGT TTAGGGCATT GGTACATAG ACATTGTCAA TTATGCCTCG ATGGTCTACA	16140
ATATGACTCT CTCCAGCCAC TTCTGTCCCA TCCTGAAAGA CTGCATGAAG GGTCAAAGGA	16200
TGGTCACTGG AAGGATAAAT TTCCCTGTT GTATGGAAAA ATTTGCTCAA TAACTGCATG	16260
GCATTATAGG TTGAACCCCTG CATTTCTGAC AAGCCAGCAA TGATGAGATT TCCCAATGGA	16320
TGGCCAGCAA AGGCTCCGGC ATCCTCAGAG AACCGATACT GAAAGACCTT CTCATAAAAC	16380
TTAGGCATAT CCGACATGGC CACAAGGACA TTACGAAGAT CACCTGGCGG TGTCAACTGT	16440
TGCATATTTT TTCGGAGTTC ACCTGAAGAA CCACCATCAT CTGCCACCGT CACGATAGCT	16500
GCGATTTCCA CATCTTTTTC CCGCAGACTT TTTAGAATGA CGGGACTTCC AGTCCCTCCA	16560
CCAATCACCG TTATCTTTGG TTTTCTCATG AACGGTTTAC CGTTTCTTTT CTGCGGTCTT	16620
TGTCGCGATG CCCTTCATTA ACAGACCAAT TCTTGATAA GTCTGCGCC AAGCGTTTAG	16680
CAAATGCCAC ACTACGGTGT TGTCCACCCG TACATCCCAT GGCAATGGTC AAAACGGACT	16740
TACCTTCCTT TTGGTAACTT GGCAGAATCG GCTCAATCAA GGCCAATAAA TGTGATAAAA	16800
AGTCTTCTGA CTCAGGATGG TTCATGACAT AATCATAAAC AGGTTTCATCC ACACCCGTTT	16860
GGTTTCTCAG TTCTGGTAAA TAATAGGGAT TTGGCAAGAA ACGGACATCA AAGACCAAGT	16920

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CCGCATCAAT CGGGATTCCA TACTTAAATC CGAAAGACAT GACTTCGATA CGGAAAGACT	16980	
GGGCTTGTTT TTGGTCTGAA AACTGCTCTG CAAGGGTTTT GCGCAGCTCA CGTGGAGTGA	17040	
GTTCACTCGT ATCCACCACA TTTTGGCTCA TATTTTTCAG AGGTGCCAAG AGTTCACGTT	17100	
CCAACTTGAT TCCATCTAAA ATACGACCGT CTGCTGCTAG TGGGTGACTC CGTCTGGTTT	17160	
CCTTGTAACG AGCGACCAAT TCCTTATCAG CCGCATCCAA AAAGAGGATT TTGAAATCCA	17220	
AACCATCTTG ATTTTCCAAC TCATCCAAAA CAGCTTGAAT CTCTGAAAAG AAAGAACGGC	17280	
TACGCATATC CACTACCAAG GCCAACTTAG GATTGTCTTC CTTAATTTC AACCAGCTGCA	17340	
AAAACCTAGG CAAGAGAGCT GCGGCATAT TATCAATGGT GAAATAACCT AGATCCTCGA	17400	
AGGACTGAAT GGCTACAGTT TTCCCTGCGC CACTCATCCC TGTACAATC ACCAAGTGAA	17460	
GTTGTTTCTT TGTATCTTTT TTCTCCTTAT ATCAAAAGAA GTTTGGCAAC ACCAAACTTC	17520	
AACCTAGCTT TCCAATCTCT GCGATGACTT CAATTTTCGAC TTTTACATCA CGAGGAAGAC	17580	
GAGCTACCTC CACAGCTGAA CGAGCTGGGA ATTCTCTTTT GAAGGCCGTT TGTAAACCT	17640	
CATTAAAAGG AACAAAGTCG TTCATATCGC TCAAGAAGCA AGTTGTTTTG ACAACATGGT	17700	
CAAAGTCTGT TCCTGCTTCT GCCAAAATAG CACCGATGTT TTTCAAGACT TGCTCTGTCT	17760	
GTTCCTGGAT ATTCTCTCCT ACAATTTCCC CAGTTTCAGG GGATAGGGGA ACTTGACCGC	17820	
TAGCAACAA AAGGTTGCCA ACGATTTTTT CTTGAACATA GGGTCCGATA GCCTTTGGGG	17880	
CCTTATCTGT ATGAATGTTT TTTGCCATTT TCTTTTCTC ACAATTTTTC TAAGATTGCA	17940	
TCCCAAGCCT CATCCATCCC TGCCTTACTG ACAGATGAAA AGAGGATGAA ATCGTCACTC	18000	
GGGTCAAAGT TTAATTTCTT TTTGATTGCT GATTTCATGCT TGTTCATTT ACCACGAGGA	18060	
ATCTTGTCGG CTTGGTCCG CACAATGATG ACTGGAATCT CATAATACTT GAGAAATTCG	18120	
TACATCTGCA CATCATCTGC TGACGGGTCA TGACGAAGGT CAACTAGACT GACAACCGCA	18180	
CGGAGATTTT CCCGAGTCGT TAAGTACTCC TCAATCATGC ACCCCCACTT TTCACGTTCC	18240	
TTTTTAGAAA CACGAGCATA GCCATAACCA GGCACATCCA CAAAGCGCAT CTTGTCTATCA	18300	
ATGTTAAAA AGTTCAGGAG CTGGGTTTTT CCAGGTTTTT CTGATGTACG GGCGAGATTC	18360	
TTACGGTTCA ACATAGTGT GATAAAGCTG GATTTACCAA CATTTGAACG CCCTGCTAGG	18420	
GCAATCTCTG GCAGTTCATC CTGCGGATAG TGGGACTTAT TAGCTGCACT GAGCAAGATT	18480	
TCAGCATTGT GTGTATTAAG TTCCATAGTC ACCTCTAGGC TGTTTCTAGG ATCGGTTTAT	18540	
CCGTTCCATC TACAGTTTCT TTAGTGATGC GAACCAATTT CACATTTTCC TGACTCGGCA	18600	
CCTCAAACAT GACATCTAGC ATGGTTTCTT CGATGATGGA GCGAAGTCCA CGCGCCCTG	18660	
TCTTCCGTTT GATTGCTTTA TTAGCAATCT CTTGAAGGGC TTCGTCGTCA AATTCCAAC	18720	

CAACATCATC ATAAGAAAGC AAGGTTTGGT ATTGTTTCAC CAAGGCATTT CTTGGCTCTT	18780
TCAAGATGCG AACCAAGTCA TCAACGGTCA ATTGCTCAAG AGCCGCAAAA ACAGGCAAGC	18840
GTCCAATCAA CTCAGGGATA ATACCAAATT TTTGAATGTC TTCAGCGATG ATTTCTTGCA	18900
TGTATGAGCT GTTTTCGTCA ATCGCCTTAT TATTTTGACC AAATCCGATG ACTTTTTCAC	18960
CCAGACGTTG TTTGACAATT TCTTCAATAC CATCAAAAGC ACCACCCACG ATGAAGAGGA	19020
TATTTTGTGT ATCCACTTGA ATCATCTCTT GTTGTGGATG TTTGCGTCCA CCTTGAGGCG	19080
GTACGCTAGC AACAGTTCCC TCAATAATCT TGAGAAGGGC TTGTTGCACC CCTTCACCAG	19140
AAACATCACG TGTGATAGAC ACATFCTCAC TCTTCTTGGC AATCTTGTC AATTCATCCA	19200
CATAGATAAT GCCACGCTCT GCACGTTTGA TGTTAAAGTC AGCAACCTGC AAGAGTTTGA	19260
GGAGGATATT TTCCACATCC TCACCCACAT AACCAGCCTC CGTCAGAGCT GTCGCATCCG	19320
CAATAGCAAA AGGTACATTC AAGCTCTTAG CCAAGGTCTG GGCAAGGAAA GTTTTCCCTG	19380
AACCAGTTGG GCCAATCATC AAAATGTTTG ACTTCTGCAA ATCCACATCT TCTGACTCTT	19440
CGCGTGTATC GTGGAAATTG ATGCGTTTGT AGTGGTTATA AACCGCCACT GCCAAGGCAC	19500
GCTTGGCAGC ATCTTGACCA ATTACATAGT GGTTC AAGAT ATGGAGGAGT TCAATTGGTT	19560
TTGGCACCTC AGACAAGTCT GCCAAGACTT CCTCAACCAA TTCTTCTCGA ATGATTTCTT	19620
GAGCTAAGTC CACGCATTCA TTACAAATAA AAGCATTGTT GCCAGCAATT ATTTTGTGA	19680
CTTCTTCTTG GTTTTGGCCA CAAATGAGC AATAAACCAT CATATCATTT TTTCTATTTG	19740
TAGACATGAT TTCCTTCCAT TCTATACTGT CATCTATCT AAAATAAGGT CATGTAAAAA	19800
GCATGAATAC TATTGACCAG ATTGGTAAAG GCATTTAACC AAAGGAGGAT AGAAAGCCCG	19860
TAACGCTTTT TACGAAAAGC TTGTGCTCCT GCCAGAAAGC AGATGAAACA CAGAAAAGCC	19920
GTGAATAGAC CAAATAAACT CCGTTCCATT AGACTTCCTT TCTCTTGCGG TATTGGATGG	19980
TAAATCATA AGGATTCTTC TCATCTTTGG CGTAAATTT GCTTGAACT GTCTCAAAAA	20040
GAGACAAGTC AAGTTCTTCA GGGAAATAGG TATCTCCTTC CACCCGAGCA TGAATGTGAG	20100
TGACAATCAC TTATCAAGG TAAGGTTC AAGCCTGAAA AATTTGCTTC CCACCGATAA	20160
TGTAGAGATT CTTTCTTGA GCCTGATACC AGTCAAGAAC AGACTGGACG TCCTGAAAAG	20220
TAGCAACCCC ATCTATCTTT TCTTCCGGAT TACGCGTCAA AATCAAGGTT TCCCGTTTGT	20280
GAAGCAAGCG ACGCCCCATC CCATCAAAGG TCACACGCC CATCAAGATA GCATGATTCA	20340
GAGTTGTTTC TTAAAGTGC TGCAATTCTG CTGGCAAATG CCAAGGCAGA CGATTTCTCT	20400
TACCAATCAC ACCCTCTTCA TCCTGGGCCC AAATAGCTAC GATTTTCTTA GTCATGCTTC	20460

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CATCCTTTTC ACTGATAGTA CTATTTTATC AAAAAACTCA AAAAAAGACT GGTTTGGAAT	20520
AGCTTACAAA ATAGAAAAAA TCTGTAAGAA ATTTCTTACA GATTTATCTA TGTTCCTTA	20580
TTTCTTACAA ACCAGGTGCT TGTCCAAGTT CGGCTGCAAG CATCCAAATT GTTTTATCTG	20640
TTTCAGTTTT AGCGCCTGCA AAGATACCGT TTGTACATC GTCACCTTCT TCATCAGTGA	20700
CATCCAAACC TTTTGGAAA AGTTCTGACA AGTAACGGTA GATAACAAGA ACACGTTCCA	20760
AGCTTTCTTC AACATTACGG TATTCACCAG CTTCTTCTTC GATTTCACTA TTTTGAAGGA	20820
ACTCTGTCAA TGTAGAGAAT GGGCTTCCAC CGAGTGTAAT CAAGCGTTCA CTGATTTTAT	20880
CCAATTGACC GTCAAGAGCT TCCATGTACT CATCCATTTT TGGATGCCAT ACAAGGAAAC	20940
CACGACCATG CATATACCAG TGCACCTGGT GCAAAGCAAC GTGAGCTACA TACAAATCAG	21000
CAACAGCTTG GTTCAAGACT TCCTTTGTTT TTGCCAATGC	21040

(2) INFORMATION FOR SEQ ID NO: 56:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 2387 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 56:

ATTCTTAATA CGATTAAAAG GCTTATTACT AAAAGAAAAT TTCAGTTAGA TGAACATAAC	60
TTGCTCGTCA AATCCCGATT TAACGAGATG TTTGGGGAAA ATAAATATT TGAAAGCATT	120
GATAACTTAT TTGATATTAT AGATGGTGAT AGGGGCAAAA ATTATCCTAA ATCAGATGAG	180
TTGTTTAGTG AGGAGTACTG TTTATTTTAA AATACAAAGA ATGTTACTAA AAACGGATTT	240
TCATTGATA CAAAGCAATT TATCACTAAA ACAAGGATA AATTACTTCG AAAAGGCAAA	300
CTTGAGCGTT ATGATATAGT CTTGACAACA AGAGGTACTG TTGAAATGT AGCGTACTAC	360
GATGAATTAA TAAATATAA ACATTTACGT ATAAATTCAG GTATGGTAAT ATTACGTCCC	420
AAGACACCAA ATCTAAATCA GAAATTTATT ATCCATGTTT TAAGGAATAA TAATTATAGT	480
CGAGTGATAT CAGGAAGTGC TCAGCCTCAG TTACCAATTA CAAAATTAAA AAAAATACTT	540
CTCCCCCTCC CCCCCTAGC CCTCCAAAAT GAGTTCGCAG ACTTTGTAGT CCAGGTCGAC	600
AAATCACAAT TGGCAATCCA AAAATCTCTG GAAGAACTTG AAACTTTGAA GAAATCTCTG	660
ATGCAGGAGT ATTTTGGCTG ATATTCTGCC ATTGTAATTA CGGTAATGAT TTGTTATAAT	720
ACTTCAAAGG AGGAAATCAG ATGGTAGTAA AAACAAGAAA ACAAGGAAAT TCAATCACCA	780
TTACGATTCC AAGTGAATTT AATATTCCAA GTGGTGTTAA ATACGAAGCG AAATTGTTAC	840

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CAAGTGGTGA GATTATCTTT ACTCCTGAAG AATTGGGGCA GCAGGTTTCT TATGTATCTG	900
ATGATGCCTT TGACTTAAAT TTAGATAAAA TATTTGACGA ATACGACGAT GTTTTCAAAG	960
CTTTGGTGGA AAAATGACAA TCTATTTGAC AGAAAAGCAA ATTGAAAAAA TAAATGCTTT	1020
AGCAATTCAA CGGTATTCTC CAAATGAGAA AATTCAAACA GTTAGTCCTT CTGCCTTAAA	1080
TATGATTGTG AACTTACCAG AACAAATTTGT CTTTGGGAAG CCTCTTTATC CAACAATTTT	1140
TGATAAAGCA ACGATACTAT TTGTCCAATT GATAAAGAAG CATGTTTTTG CTAATGCTAA	1200
TAAAAGAACT GCTTCTCTCG TTTTGGTCAA ATTTTACAA TTAAACGGCT ATCGTTTTTC	1260
TGTAACGGTA GAAGAAGCAG TAAAAATGTG TGTAACCATC GCAGTAGAAG CTTTAACTGA	1320
TGAAAAAATG ACAAGCTACT CCAATGGAT TTCTGAACAT TCTGTTAGAG AAAAGGTCAA	1380
AAAGTAACCT AGTATGCTGG ATTTGAATGA GCACAAGAAA ATAAATGAAC AGACAATATT	1440
AGAATCTCTG AATGCAGAAA CTGATATTGT CTCTTTTAT TGATGAATAA GAAAGTGAGA	1500
AATTATGGAA TCAAAAGTTA CAATTATCAT GCAAGAAATG TTACCTCTTT TAAATAATGA	1560
ACAATTACTA GCGTTGAGAG AGAGTTTAGA ACATCATCTA GTAGACGGAA AAAAGCAGCA	1620
GAAGTATTCG AATAATAACC TGTGCAACT ATTTATTACC GCCAAGCAGG TAGAGGGCTG	1680
TAGCTCAAAA ACAATTCGTT ATTATCAGAG GACGATTGAA AACTTGTTTA ATGCTATTAA	1740
AGAGTCTGTG ACACAACTCA CAACAGATGA TTAAAGGAGT TATTTAGCAA ATTACCAGTC	1800
TGAAAAGGAT TGTAGTAAGG CAAATTTAGA CAATATTAGG CGTATATTGT CTCTTTTTTT	1860
TGCTTGGCTT GAGCAAGAGG ATATATCATT AAAATTCCCA TTCGACGGAT ACAGAAAATT	1920
AAGACTGAGC AAAATGTGAA GGAAACTTAT ACTGATGAAC ATTTGGAAT TATGCGTGAT	1980
AACTGTGAAA ATTTGAGAGA TTTGGCAATA ATAGACCTAC TAGCATCGAC AGGTATGCGT	2040
GTAGGGGAGC TTGTACAGTT GAATCGTTCA GATATTGATT TTGAAAACAG AGAGTGTGTT	2100
GTCTTTGGTA AAGGAAAGAA GGAGAGACCA GTATATTTTG ACGCTCGTAC GAAAATTCAT	2160
TTAAGAAATT ATCTTAACGA CAGAAAAGAT AGTCACCCTG CTCTTTTGT AACGCTAGTT	2220
GGAAAAGTCC AGAGGCTTGG AATTGCTGGT GTAGAGATTC GCTTAAGAAA GTTAGGAGAC	2280
AAACTCGGCA TACAAAAGGT TCACCCACAT AAGTTCAGAA GAACTTTAGC GACTAAGGCA	2340
ATTGATAAAG GTATGCCTAT CGAACAAGTC CAAAACTGC TAGGTCA	2387

(2) INFORMATION FOR SEQ ID NO: 57:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 10669 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double

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(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 57:

ATATTAAAGC GACTTTCTGT GCGCTAGGGA AAAATGTTCC TGGGAATGAG GACTTGGTGA	60
AGAGGATAAA ATCTGAAGGT CATGTTGTTG GAAACCATAG CTGGAGCCAT CCGATTCTCT	120
CGCAACTCTC TCTTGATGAA GCTAAAAAGC AGATTACTGA TACTGAGGAT GTGCTAACTA	180
AAGTGCTGGG TTCTAGTTCT AAACATCAGC GTCCACCTTA TGGTGCTATT ACAGATGATA	240
TTCCGAATAG CTTGGATTG AGCTTTATCA TGTGGGATGT GGATAGTCTG GACTGGAAGA	300
GTAAAAATGA AGCATCTATT TTGACAGAAA TTCAGTATCA AGTAGCTAAT GGCTCTATCG	360
TTTTGATGCA TGATATTCAC AGTCCGACAG TCAATGCCTT GCCAAGGGTC ATTGAGTATT	420
TGAAAAATCA AGGTTATACC TTTGTGACCA TACCAGAGAT GCTCAATACT CGCCTAAAAG	480
CTCATGAGCT GTACTATAGT CGTGATGAAT AAGCAAGAAA AAATAGGTCT GTTAGATATT	540
TGACAGACTT ATTTTTTACA GAATATAGTA CTACTTAAAA AATGTTTTAT GCTATAATTG	600
ATGAATAAAA TAGAAGGAGA AGCATATGAA TACCTATCAA TTAAATAATG GAGTAGAAAT	660
TCCAGTATTG GGATTGGAA CTTTTAAGGC TAAGGATGGA GAAGAAGCCT ATCGTGCAGT	720
GTTAGAAGCC TTGAAGGCTG GTTATCGTCA TATTGATACG GCGGCGATT ATCAGAATGA	780
AGAAAGTGTT GGTCAAGCAA TCAAAGATAG CGGAGTTCCA CGTGAAGAAA TGTCGTAAC	840
TACCAAGCTT TGAATAGTC AGCAAACCTA TGAGCAAACCT CGTCAAGCTT TGGAAAAATC	900
TATAGAAAAA CTGGGCTTGG ATTATTGGA TTTGTATTG ATTCAATTGC CGAACCCAAA	960
ACCGCTCAGA GAAATGACG CATGGAAAAC TCGCAATGCG GAAGTTTGA GAGCGATGGA	1020
AGACCTCTAT CAAGAAGGGA AAATCCGTGC TATCGGCGTT AGCAATTTTC TTCCCATCA	1080
TTTGGATGCC TTGCTTGAAA CTGCAACTAT CGTTCCTGCG GTCAATCAAG TTCGCTTGGC	1140
GCCAGGTGTG TATCAAGATC AAGTCGTAGC TTAAGTGTCT GAAAAGGGAA TTTTATTGGA	1200
AGCTTGGGGG CCTTTTGGAC AAGGAGAACT GTTTGATAGC AAGCAAGTCC AAGAAATAGC	1260
AGCAAATCAC GGAAATCGG TTGCTCAGAT AGCCTTGGCC TGGAGCTTGG CAGAAGGATT	1320
TTTACCACCT CCAAATCTG TCACAACCTC TCGTATTCAA GCTAATCTTG ATTGCTTTGG	1380
AATTGAAC TGATCATGAG AGAGAGAAAC CTAAAAACG ATTGCTGTTT AATCGGGTGC	1440
TCCACGAGTT GATGATGTGG ATTTCTAGAA AATCATAAAA AGAATTGTAC ATTATTCTAA	1500
TTTTTGATAT AATAGTCAGC AGGAAAGAAA GTCTTATGGC GTTCTTCAAG CGAGCTTGGG	1560
ATAGTGGGAG CCAAGTAGGG CAAAATAAAG GGCTGGCGCT TTCTGTAGTA TTTTCAAAAA	1620

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CAATGAAGTA ATAAATTAGG GTGGAACCGC GTTCTGACG CCCCTAGGTT AAATCAACCT	1680
AGGATTGTCA GATGTGGTTC TTTTGCTTAT TCAGTCTATT GTGTGAAAGA AAGGAGAGCC	1740
GTGGACAACC TTTATCTTGT AAAAGACGAT AGTCAACTAG CTACATTTTCG TGATTTTGTA	1800
GTAAGAAATA CTGAAAAGTT GAAAGATTAT CAATCTTTTT TAAAGAATGA ACTTGCAGTC	1860
TGTGATTAC CGCAAGCTGT TATTTGGTCA GATTTTAATG CTGCTACACA GATTATTAGG	1920
GAAAGTGCTG TTCCAACCTA TACAAATAAT AGACGAGTGG TTATGACGCC TGATTTAGCT	1980
GTTTGGAAG AATTGTATTT GTATCAGTTG ATGGACTACG AGTGTCTGA GCAAACCTCA	2040
GCAATAGAAA GTCACATCA TTTCTTATCT GAAAATTTCC TCTTACAGAT TGTAGGACAT	2100
GAGTTAGCTC ATTGGTCGGA CATTTTTTAG ATGATTTTGA TGGTTATGAC TCTTATATCT	2160
GGTTCGAAGA GGGGATGGTT GAATATATTA GTCGCAAGTA TTTCTTGACA GAAGAGGAAT	2220
TTCAAGCGGA AAAAATTTGT AATCAATCTC TCGTAGAACT TTTTCAGAAG AAGTATAGTT	2280
GGCATTCAAT GAATGATTTT GGTCTTCGA CTTATGATAA GAACTATGCA AGTATTTTTT	2340
ATGAATACTG GCGCAGCTTT TTGACAGTAG ATAAGTTGGT AGAAAATTTA GGTAGTGAC	2400
AAGCGGTCTT AGATTCTTAT CATTTATGGG CAAATACAGA AAAAATTTT CCCTTGTTAG	2460
ATTGGTTTGT TCAGCAGAAA TTAATTGAAA AAGAAATATA AAAACTAAAG GAGTAAACAA	2520
TGTCTAAGAA ATTAACATTT CACTGCATCA GTGGCAGAGA CCTCCTTACA GTCGGGCTGC	2580
TCCACGCTCA GCACTAGAGT GCCTGAGCTA GACGCAGTAC TAACTCGTCT TGCCTCGTAT	2640
GATCGACGAG GCAGACTCGT GTCGCAAGTA ATTATTTTTT ATTAAGGAGT ATTCAATGTC	2700
TAAGAAATTA ACATTTCACT GCGTCAGTGG CAGAAACCTC CTTACAGTCG GACTGCCCTA	2760
CGCTCAGCAC TAGAGTGCCT GAGCTAGACG CAGTACTAAC TCGTCTTGCC TCGTATAATC	2820
GACGAGGCAG ACTCGTGTCT CAAGAAATTA TTTTATTATTA AGGAGTATTC AATGTCTAAG	2880
AAATTAACAT TTCAAGAAAT TATTTTGA CT TTGCAACAAT TTTGGAATGA CCAAGATTGT	2940
ATGCTTATGC AGGCTTATGA TAATGAAAAA GTGCGGGGA CAATGAGTCC TTACTCTTC	3000
CTTCGTGCTA TCGGACCTGA GCCATGGAAT GCAGCTTATG TAGAGCCATC ACGTCGCTCT	3060
GCTGACGGTC GTTATGGGGA AAACCTAAC CGTCTCTACC AACACCACCA ATTCCAGGTG	3120
GTCATGAAGC CTTCTCCATC AAATATCCAA GAACTTTACC TTGAGTCTTT GGAATAATTG	3180
GGAAATCAAT CTTTGGAGCA CGATATTCGT TTTGTTGAGG ACAACTGGGA AAACCCATCA	3240
ACTGGTTCAG CTGGTCTTGG TTGGGAAGTT TGGCTTGACG GAATGGAAAT CACTCAGTTC	3300
ACTTATTTCC AACAACTCGG TGGATTGGCA ACTGGCCCTG TGAAGTCGGA AGTTACCTAT	3360

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GGTTTGGAGC GCTTGGCTTC TTACATTCAA GAAGTAGACT CTGTCTATGA TATCGAGTGG	3420
GCTGATGGTG TAAAAACGG AGAAATCTTT ATCCAGCCTG AGTATGAGCA CTCAAAATAT	3480
TCATTTGAAA TTTCCGACCA AGAAATGTTG CTTGAAAAC TTGATAAGTT TGAAAAAGAA	3540
GCTGGTCGTG CATTAGAAGA AGGCTTGGTA CACCCTGCCT ATGACTATGT TCTCAAATGT	3600
TCACATACCT TTAATCTGCT TGACGCGCGT GGTGCCGTAT CTGTAACAGA GCGTGCAGGC	3660
TATATCGCTC GTATCCGTAA CTTGGCCCGT GTCGTAGCCA AAACCTTTGT CGCAGAACGC	3720
AAACGCCTAG GCTACCCACT TTTGGATGAA GAAACAAGAG CTAAACTCCT AGCAGAAGAC	3780
GCAGAATAAA GAGAGTGACA AATTACGAAA ATGGGCGAAC AGAGTGAGCC CTGAGCCAGT	3840
TGCCGCAGTG ATGAAGGTAT CCTTAGTGAA ACTAAGGATA CTAGGCAAAA TTGGAGACTT	3900
TTGGCTCCAA TTTTAGCAAT GAAACAACGA AGTTGGTTGC TTGCGTGCCA ATCACATAAG	3960
GCAAACCTGA AAATAAAAAG ATACTTTTCG GAGAAAAAC ATGACAAAA ACTTATTAGT	4020
AGAACTCGGT CTTGAAGAAT TACCAGCCTA TGTTGTTACG CCAAGTGAAA AACAAC TAGG	4080
CGAAAAATG CGAGCCTTCC TCAAGGGAAA ACGCCTGTCT TTTGAAGCCA TTCAAACCTT	4140
CTCAACACCA CGTCGTTTGG CTGTTCTGT AACTGGTCTT GCAGACAAAC AGTCTGATTT	4200
AACAGAAGAT TTCAAGGTC CAGCAAAGAA AATTGCCTTA GATAGTGATG GAAACTTCAC	4260
CAAAGCAGCT CAAGGATTG TCCGTGGGAA AGGTTTGA CTGTAAGATA TCGAATTCCG	4320
TGAAATCAAG GGTGAAGAAT ATGTCTATGT CACTAAGGAA GAAATTGGTC AAGCAGTTGA	4380
AGCCATTGTT CCAGGCATTG TGGATGTCTT GAAGTCACTG ACTTTCCTG TCAGCATGCA	4440
CTGGGCGGGA AATAGCTTTG AATACATCCG CCCTGTTTAC ACTTTAACTG TTCTCTTGGA	4500
TGAGCAAGAG TTTGACTTGG ATTTCTTGA TATCAAGGGA AGTCGTGTGA GTCGTGGCCA	4560
TCGTTTTTTG GGACAAGAAA CCAAGATTCA GTCAGCATG AGCTATGAAG AAGACCTTCG	4620
TAAGCAGTTT GTAATCGCAG ATCCATGTGA ACGTGAGCAA ATGATTGTTG ACCAAATCAA	4680
GGAAATTGAG GCAAAACATG GTGTACGTAT CGAAATTGAT GCGGATTTCG TGAATGAAGT	4740
CTTGAATTTG GTTGAATACC CAACTGCCTT CATGGGAAGT TTTGATGCTA AATACCTTGA	4800
AGTTCAGAA GAAGTCTTGG TGACTTCTAT GAAGGAACAC CAGCGTTACT TTGTTGTTCTG	4860
TGATCAAGAT GGAAACTCT TGCCAAACTT CATTTCTGTT CGTAACGGAA ACGCAGAGCG	4920
TTTGAAAAAT GTCATCAAAG GAAATGAAAA AGTCTTGGTA GCCCGCTTGG AAGACGGAGA	4980
ATTCTTCTGG CGTGAAGACC AAAAATTGGT GATTTCAGAT CTTGTTGAAA AATTAAACAA	5040
TGTCACCTTC CATGAGAAGA TTGGTTCTCT TCGTGAACAC ATGATTGCTA CGGGTCAAAT	5100
CACTGTACTT TTGGCAGAAA AAGCTAGTTT GTCAGTGGAT GAAACAGTTG ACCTTGCTCG	5160



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TGCAGCAGCC	ATTTACAAGT	TTGACTTGTT	GACAGGTATG	GTTGGTGAAT	TTGACGAACT	5220
CCAAGGAATT	ATGGGTGAAA	AATACACCCT	TCTTGCTGGT	GAAACTCCAG	CGGTGGCAGC	5280
TGCTATTTCGT	GAACACTACA	TGCCTACATC	AGCTGAAGGA	GAACCTCCAG	AGAGCAAGGT	5340
CGGCGCAGTT	CTAGCCATTG	CAGACAAATT	GGATACGATT	TTGAGTTTCT	TCTCAGTAGG	5400
ATTGATTCCA	TCAGGTTCCTA	ATGACCCTTA	TGCCCTTCGT	CGTGCAACTC	AAGGTGTGGT	5460
TCGTATCTTG	GATGCCTTTG	GTTGGCACAT	TGCTATGGAT	GAGCTGATTG	ATAGCCTTTA	5520
TGCATTGAAA	TTTGACAGTT	TGACTTATGA	AAATAAAGCA	GAGGTTATGG	ACTTTATCAA	5580
GGCTCGTGTT	GATAAGATGA	TGGGCTCTAC	TCCAAAAGAT	ATCAAGGAAG	CAGTTCTTGC	5640
AGGTTCAAAC	TTTGTGTGG	CAGATATGTT	GGAAGCAGCA	AGTGCTCTCG	TAGAAGTAAG	5700
CAAGGAAGAA	GATTTTAAAC	CATCTGTGA	ATCACTTCT	CGTGCCCTTA	ACCTGGCCGA	5760
GAAGGCAGAA	GGGGTTGCTA	CGGTTGATTC	AGCACTATTT	GAGAATGACC	AAGAAAAAGC	5820
TTTGGCAGAA	GCAGTAGAAA	CACTCATTTT	ATCAGGACCT	GCAAGTCAGC	AATTGAAACA	5880
ACTTTTTCG	CTTAGCCAG	TCATTGATGC	TTTCTTTGAA	AATACTATGG	TAATGGCTGA	5940
AGATCAGGCT	GTCGTCAAA	ATCGTTTGGC	AATCTTGTC	CAACTAACCA	AGAAAGCAGC	6000
TAAGTTTGCT	TGTTTAAACC	AAATTAACAC	TAAATAAAAT	TTGATAAACG	GACTTTATCT	6060
TATTACAAAG	GAGAAGAAAT	GGATCCGAAA	AAAATTGCTC	GTATCAATGA	GCTTGCTAAA	6120
AAGAAAAAAA	CAGAAGGCTT	AACACCAGAA	AAAAAGTGG	AACAAGCCAA	ACTACGTGAG	6180
GAGTACATCG	AAGGTTATCG	CCGCGCTGTT	CGTCACCACA	TTGAAGGAAT	CAAAATTGTG	6240
GACGAAGAAG	GAAACGATGT	TACACCAGAA	AACTACGCC	AAGTACAACG	TGAAAAAGGA	6300
TTACATGGCC	GTAGTCTTGA	TGATCCAAAT	TCATAATAAT	ACTCTTCGAA	AATCAAATTC	6360
AAACCACGTC	AGCTTCACCT	TGCCGTACTT	AAGTACAGCC	TGCGGCTAGC	TTCTAGTTT	6420
GCTCTTTGAT	TTTCATTGAG	TATATGTATT	CTTCTTTT	ACAAAGATAG	ATGAAACGAT	6480
AACAAGAGA	CTAGCAGTTT	GTGTTTGCTA	GTCTTTTTC	GCTAAAAAG	GAACCATAAT	6540
GGTTCCTAAA	AACTATCATT	AGTAACTTGC	ACCGGCTGTA	GCGTCTGCGT	CACCACCGTG	6600
GCCTCCAGCA	TCCCCTGAAT	CAGAAGCGCC	AGAAGTAGCA	TCGGCGTCTC	CATGACCTCC	6660
GGCAGCAGGA	GCAAATGGTC	CGCTACCACC	CACCAAACGT	TGACCAGTCT	CTTTTAGGTA	6720
CCAGTCAAGC	CATGGTTGGA	AGTTAAAGAC	GATTTTCATTG	ATACCAGCGT	ATGATCCATC	6780
AGGATAGTAC	ATTGCTTGGT	AGTTGTGAGT	GTTGATAACA	CCTGCAGGAG	AACCTGGAAC	6840
GATCGTACGG	ACGTATTCTT	GGTTTCCGTT	GCGAAGTGTT	CCGATAACCC	ACTCTACGTT	6900

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CTTCATACGT GCTGGTGGAA GAGAACCATG AACAGTCGAC ATACGGCTAC CTGATTGAGG	6960
TGGTACACGT TTAGCGAACA TAGTGTCTGG ATCTTGGTGA GCGTTGTTGT AGTAGAGGAA	7020
TTGGTTGTTG TCGTCAGCGT ATGTCAAATC AAATGGCATA GCTTTCAAGA ACATATCAAT	7080
TTGGTTAACT GTTAGGATAC CGTGGTCCAA TTTGACATAG GTATCACCAG AACAGCACC	7140
AGTGAATGCT GCAACTTTTT CTACCCATTC TGGATCGTCA GGGTCAACTT CTGTGATGGT	7200
TGTAGCGATT GGTTTTCCAC AATCCAAGTC TTCTGATTCG ATTGGTTTTG GTTTTTTCAA	7260
TTTCGAAACG ACTCCTACGT ATTTAACAAA GTTATCTAAG CAAGTTTCAA GGAATTTAAC	7320
AGTGCCTTCG TTGGTGATAT TTCCGTTGTT ATCAAAAGCT TCCTTAGCTT TACCAAGAAG	7380
GAATTCGTTA CCTGGAAGCG TGTAGGCATT AACACCTGGA GCATCAAGGA TTTTACGAAG	7440
GTGAACCTGA GCACGTGATG TTCCTTGGTC ATAGTATGAT GCACCCACAA TCATAACAGG	7500
CTTGTTTTCA AATGGATGAA CTTCTGATGA AAGCCATTCA AGTACAGATT TGAGTGAAGC	7560
TGAGATAGTG TGGTTATGCT CAGGAGTAGC AATGATAACA CCATCTGCAC GAGTAATTTT	7620
GTTATATAAA TAACGTAATT GGAAACTTTC ATCCCATTTT TCATCTTGGT TAAACATTGG	7680
AACTTCGTCA ATTTCAAGAA CTTCTAATTC AAATTTGAGT TTGAAGTAGC GACGGATAAA	7740
TTCCAAGAGC TTACGGTTAT ATGATTGATC GTAGTTTGAT CCAACAAGTC CAACAAATTT	7800
CATTCTTTTT GGTCTCCTAT CTTACAAATT TTCCAGTCA AAGTCTTCAG CATCTTTGCG	7860
AAGTAATCTT TGTGCATTAC GTAATTTTTC TGTGATTTTT ACAAGATAC GGAAGTCATC	7920
AAAGATGGCA TCCAATTTCT TGATAACATC AAGGTCAACC AAGTCGCCAC TTGGGTTAAA	7980
TGCTTGAAGA GAGTGTGAGA GCAAGAATTC ATCTGGAAGA ACATTTGCCT TGATTTCAGG	8040
AGCATTCAAG ATTTGACGAA GTTGCAATTG GGCACGAGAT GAACCAAGCG TACCGTAAGA	8100
AGCACCTGTA ATCATGATTG GTTTGTTCAA AAGTGGGTAA ATACCATAAG ACAACCAAGC	8160
AAGAGCGCTC ATCAAAACAG CTGGAATAGA GTGATCATA TCAGGAGTAC CGATAATAAC	8220
GCCATCTGCC TCTTCGATTT TAGCAGCAAT TTCCAATATT TCAGCAGGTA CTTGCTTGTC	8280
AGCTGGTTTG TTGAAGACAG GAATGGCCTT GATTTCACA AGTTCAATTT CAGCTTTGTC	8340
AGTAAAGTGT TTTTGCATGT ATTGAAGCAA TTGACGGTTT GTAGAACGTT TTGAATTTGT	8400
TCCAACAATA GCAATAAGTT TTAACATGAG ATTTCTTTTC TCTTTTACA TAATACAATT	8460
TTAAATTC ATTGAAACAG TTGTCTCTAT AGAGTAGGAA TTCCTGAAGA ACAGCTTAGG	8520
TGGCCTTCTT TATCGATGAG GATGACTTCG ATGCCCTCCA AACTTTCGAC TTGCCAGAGG	8580
ATAGAAGCAG GTCITTCTCC AAAGAGTCGA GTCGTCCAGA TTTCGCCATC GACTGATTTA	8640
TCAGAGATGA TTGTTAGACT CGTAGTTCC GTTCAACAG GATATCCTGT TTGACTGTCA	8700

AAAATGTGAT GGTAATCTTG TCCATCGACG GTCAGGTGAC GTTCATAAAT GCCTGAAGTC	8760
ACGACAGATT TATTGACAAC AGGGATGGTC ATTAAATGAT TTCCCTTAGG ATTGGCTGGG	8820
TCTTGAATCC CGATTTGCCA TGGGTTATCC CCTCTTGCCT GATTTTTTCC AATGGTCAGG	8880
ATATTCCCTC CCAGATTGAT CAAGGCAGAA GTCACCCCTT CTTTCCTAAG AAATTGGGCA	8940
ACCTTATCCG CACTGTATCC TTTGGCTAAA CAACCTAGAT CGATCTTCAT TCCTTTCTGT	9000
TTTAAAAACA CAGTAGAAGT AGAAGAATCT AACTCGATAC CATGAGGATT GATTAGAGGC	9060
AGCACCGATT CAATTTCTTG AGGCTGGGCG ACCTTGGCAT CTGAAAAACC GATACGCCAG	9120
GTTTGAATTA AGGGACCAAT GCTGATATTG AGGTGGCTAG AGAGCGCTAG GCTATGCTCT	9180
AACCCAAGTG AAATCAGCTC AAACAGGTCT GGATGAACCG TGACGGGGGC TATTCCTGCT	9240
TGATAATGA TTCCATCAA CTCAGATTCT TGACTATTGG CGTTGAAGCG GTATTCAAAT	9300
TCTTTGAGCA AGTCAAAGGA TTTTGGAGA AAGATATCGG CTTGCTCATC CACTAATGAA	9360
ATAGTGATAG TAGTCCCAT TAGCCGTTCA GAATGTGAAC GAAGAGTCAA GCTACCAACT	9420
CCTTCTCTT ATAGAAAATA AGTTGTAATA TCAAATAATC ATCTAAATTG AAGCCCTTAC	9480
ATTTCAATTT CATGTTATTA TAATACCATA AAGTTAGAAT TTTCACAAAC AAAATTGGA	9540
AAAAGTCAAG AAATATGCTC ATAAAATTCA TCAGGCTTGA AAACAGGATA AATGGGGAAT	9600
TATTTTTGAT AAAAAATGCT GAAATAATAG TACCCCTT GTAAACGCTA ACGGTAAATG	9660
GTATACTAGT AAGGTAAATT TAGAATGAAG GCAGGAAATT TTTATGAGTA AAATCGTTGT	9720
AGTCGGTGCT AACCACGCTG GTACAGCATG TATCAATACC ATGTTGGATA ATTTTGGAAA	9780
TGAGAACGAA ATTGTTGAT TTGACCAAAA CTCTAACATC TCTTCTCTAG GATGTGGAAT	9840
GGCTCTTTGG ATTGGTGAAC AAATTGACGG TGCTGAAGGC TTGTTCTATT CTGATAAAGA	9900
AAAATTGGAA GCTAAAGGTG CTAAAGTTTA CATGAACTCA CCTGTTCTTT CAATCGACTA	9960
TGATAACAAA GTAGTTACAG CGGAAGTTGA AGGAAAAGAG CACAAAGAAT CATACGAAAT	10020
ATTGATTTTC GCTACAGGCT CTACACCAAT CTTGCCACCA ATCGAAGGTG TTGAAATTGT	10080
TAAAGGAAAC CGGAATTTA AAGCAACTCT TGAAAACGTA CAATTCTGTA AATTGTACCA	10140
AAATGCTGAA GAAGTTATCA ATAACTTTC TGACAAGAGC CAACACCTCG ACCGTATCGC	10200
CGTTGTTGGT GGTGGTTACA TCGGTGTTGA ACTTGCTGAA GCCTTTGAAC GTCTTGGAAA	10260
AGAAGTTGTC CTTGTTGATA TCGTTGATAC TGTCTGAAC GGTTACTATG ACAAAGACTT	10320
CACACAAATG ATGGCGAAGA ACTTGAAGA TCACAACATC CGCTTGGCTC TAGGTCAAAC	10380
TGTTAAAGCA ATCGAAGGTG ACGGTAAAGT TGAACGCTTG ATTACTGACA AAGAAAGCTT	10440

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TGACGTGGAT ATGGTTATCC TTGCAGTTGG TTTCCGTCCA AACACAGCCC TTGCAGGTGG	10500
TAAGATCGAA CTCTTCCGCA ACGGTGCCTT CCTTGTAGAC AAGAAACAAG AAACATCTAT	10560
CCCAGACGTT TACGCTGTTG GTGACTGTGC GACTGTTTAT GACAATGCTC GTAAAGATAC	10620
AAGCTATATC GCTCTTGCTT CAAATGCTGT GCGCACTGGT AACGTTGGT	10669

## (2) INFORMATION FOR SEQ ID NO: 58:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 7542 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 58:

CGCGCTAATA GATACTTTAT GATAGAATAA AGAACAAGAT TGACAAGTAA GAGGAAACAT	60
TATGCAAAAT CAAACACTCA TGCAATACTT TGAATGGTAT CTGCCCCACG ACGGTCAACA	120
CTGGACCGGT CTGGCTGAAA ATGCTCCACA CCTAGCTCAT CTGGGGATCA GTCACGCTCG	180
GATGCCACCA GCCTTCAAGG CAACCAACGA AAAAGATGTC GGCTATGGGG TCTATGACTT	240
ATTTGACTTA GGAGAGTTCA ACCAAAAAGG GACTGTCCGC ACCAAGTATG GTTTCAAAGA	300
AGACTATCTT CAAGCCATTC AAGCCCTTAA AGCACAGGGA ATTCAACCTA TGGCCGATGT	360
AGTTCTCAAC CACAAGGCTG CTGCCGATCA CAGGGAAGCC TTTCAGGTTA TCGAAGTTGA	420
TCCTGTAGAC CGTACAGTTG AACTTGGAGA ACCCTTCACC ATCAATGGCT GGACTAGTTT	480
TACCTTCGAT GGTGCGCAAG ATACCTATAA TGGCTTCCAC TGGCATTTGGT ACCACTTCAC	540
CGGTACAGAC TACGATGCCA AACGCAGTAA ATCTGGGATT TATCTGATCC AAGGGGACAA	600
CAAGGGCTGG GCCAACGAGG AATTGGTCGA TAACGAAAAC GGAAACTACG ACTACCTCAT	660
GTATGCCGAC CTAGACTTTA AACATCCTGA AGTCATCCAA AACATCTATG ACTGGGCTGA	720
TTGGTTCATG GAAACGACTG GTGTAGCTGG TTTCCGTTTG GATGCCGTTA AGCATATTGA	780
CTCTTTCTTT ATGCGCAACT TCATCCGCGA TATGAAGGAA AAATACGGTG ACGATTTCTA	840
TGTTTTTGGT GAATTTTGA ACCCAGACAA GGAAGCCAAT CTGGACTATC TCGAAAAAAC	900
GGAAGAACAC TTTGACCTTG TCGATGTTTG TCTCCACCAG AATCTCTTTG AAGCCAGTCA	960
AGCTGGCGCA AACTATGACC TTCGTGGCAT TTTCACAGAT AGCCTGGTTG AACTCAAGCC	1020
TGACAAGGCT GTGACTTTTG TCGACAACCA CGATACCCAA CGAGGACAAG CCCTTGAGTC	1080
TACCGTTGAA GAATGGTTCA AGCCAGCAGC CTATGCCCTC ATTTTGTGTAC GCCAAGACGG	1140
CCTTCCATGT GTCTTTTACG GAGACTACTA TGGGATTTC A GGCAGTATG CTCAGAAGA	1200

TTTCAAAGAA ATCCTTGACC GCCTCCTAGC CATCCGAAAA GATTGGCCT ATGGAGAACA	1260
AAATGACTAC TTTGACCATG CTAACGTAT CGGTTGGTA CGTTCAGGTG CTGAAAATCA	1320
ATCCCCAATC GCAGTCCTTA TCTCAAATGA CCAAGAAAAC AGCAAGTCAA TGTTTGTGG	1380
TCAAGATGG ACTAATCAAA CCTTTGTAGA TTTACTTGGT AACCACCAAG GTCAAGTTAC	1440
AATTGATGAG GAAGGTTATG GACAATTCCC TGTCTCAGCT AGATCCGTAA GTGTCTGGG	1500
AGTCAATACC ATCTAATAGC TCATAATAAC CAAGCTAGGT CCAAGCGGAT TTGGCTTTT	1560
TGTATTACACA AAAAGACCTA CCCAAATGGA TAGATCTTTA CTTGATTACA ATTTACCTGC	1620
TACTGCATCC AACAAATCTT GGATCTTAGG TTGGTTGCTT CCTCCTGCCA TGGCCATATC	1680
TGGTTTACCA CCACCACGTC CATCGATGAT TGGTGCTAAT TCTTTGACAA GGTTTCCTGC	1740
ATGAAGTCT TTTGTCTTGC TTGCTACAAG GACATTGACT TTGTCAACGA TAGCGGCAAC	1800
TAGGACAAGA AGATCAGAGT AGTCTTTTTG TTCCAGTTA TCTGCAAAAG TACGAAGGGC	1860
ACCGGCATCG GATACAGACA CTTGACTAGC AATGTAACGA TGACCGTTGA CTTCCTTAAC	1920
ATCTTTGAAG ATATCGCCTG CGGCTGCAGC TGCGGCTTTT TCTTTCAACT CAGCATTTT	1980
TTTTTGAAGT TGACGAAGTT GTTCTTGAAG TCCTTCTACC TTGTGAGGTA CTTCTTGAC	2040
TTGAGGTGCT TTCAAGGTTG CTGCGATAGC TTTAAGAGCA TCCTCTTGTT CACGATAGGC	2100
TTCAAAGGCT TCCTTACCAG TCACTGCCAA GATACGGCGA GTTCCTGAAC CGATTCTTC	2160
TTCTTTGACA ATTTTGAAGA GACCAATCTC AGAAGTGTG TCAACATGAG TACCACCACA	2220
AAGTTCAATA GAGTAGTCAC CGATAGTCAC GACACGAACT TCCTTGCCGT ATTTCTCACC	2280
AAAGAGGGCC ATAGCTCCCA TTTCTTTAGC AGTGTCAATA TCCGTTTCAA CTGTCTTCAC	2340
TTCAAGTGCT TCCCAAATTT TCTCGTTAAC TTGCTGTTC ATCGCACGAA GTTCCTCAGC	2400
AGTTACTGCT TGGAAGTGGG TAAAGTCAAA GCGAAGGAAT TCAACTTCGT TAAGAGATCC	2460
TGCCTGTGTT GCGTGGTTTC CAAGGATATT GTGAAGGCA GCGTGAAGCA AATGAGTCGC	2520
AGTGTGGTTT TTCATGACAC GGTGACGGCG ATTGCTATCA ATTGCCAAGG TATATTCTTG	2580
GTTCAGGCA AGCGGTGCAA GGACTTCAAC TGTATGAAG GCTTGACCAT TTGGGGCTTT	2640
CTGAACATTG GTCACAGTAG CCACAACCTT ACCTGACTCA TCCAAGATTT GTCCGTAGTC	2700
AGCTACCTGT CCACCATTT CAGCATAAAA TGACGTTTCC GCAAAGATAA GAGAGGCAGT	2760
TCCTTCTGAA ACAGCTCCTA CTTCTGCATT GTCAGCAACG ATAGCTACCA ATTTAGAAGA	2820
CAATTGGCTA GCATTGTAGT TGAAGACACT TTCTACAGTG ATGTTTTGAA GAGTTTCATT	2880
TTGCATACCC ATTGAGCCAC CTTTGACAGC TGACGCACGC GCGCGTTCTT GCTGTCTTT	2940

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CATGGCTGCT TCAAAACCTT CACGGTCTAC AGTCATACCA GCTTCTTCAG CGATTTCCTC	3000
AGTCAATTCA ACTGGGAACC CATAAGTATC ATAGAGTTTG AAGACATCTG AACCAGCGAT	3060
AACAGATTGA CCTTTTCTTT TCAAGTCTGC TACAATGCCT TGGGCAAAGT GTTGACCTGA	3120
GTGAAGGGTA CGGGCAAATG ATTCTTCTTC GCTCTTAACG ATTTTCTCAA TAAAGTCACG	3180
TTTCTCAAGC ACTTCTGGGT AGTAGCTTTC CATGATTTTT CCAACAGTTG GAACCAATTT	3240
GTAAGGAAA GGCTCGTTGA TACCCAATTT TTGACCATGC ATAGAAGCAC GACGGAGAAG	3300
ACGACGAAGA ACATAACCAC GACCTTCATT TCCTGGAAGG GCACCATCAC CGATAGCAAA	3360
TGAAAGAGAA CGAATGTGGT CTGCGATAAC CTTGAAGCTC ATGTTGTGCG CATCTTGGTC	3420
ATAAACCTTA CCAGACAATT TCTCGACTTC ACGGATAATC GGCATGAAGA GGTCCTTTC	3480
AAAGTTGGTC TTAGCCCTTT GGATAACGGC CACCAAACGC TCCAAACCAG CGCCCGTATC	3540
AATGTTCTTA TGTGGCAATT CCTTGTATTC GCTACGAGGA ACAGCAGGGT CTGCGTTAAA	3600
TTGTGACAAA ACGATGTTC AGATTTCAAT ATAACGGTCG TTTTCAATAT CTTCTGCAAG	3660
CAGGCGAAGA CCGATATTTT CTGGGTCAA GGCTTCCCA CGGTCAAAGA AGATTTCTGT	3720
ATCTGGTCCA GAAGGTCCCG CACCGATTTC CCAGAAGTTG TCCTCAATTG GAATCAAGTG	3780
ACTTGGATCC ACTCCACTT CAATCCAGCG GTTGTAAAGAA TCTTTATCGT CTGGATAGTA	3840
GGTCATGTAA AGTTTTTCAG CAGGGAATC AAACCATTC AAGGCTCATA	3900
AGCCCAAGTG ATAGCTTCGT CACGGAAGTA ATCCCGATA GAGAAGTTCC CCAGCATTTT	3960
AAACATGGTA TGGTGACGCG CGGTCTTCCC TACGTTTTCG ATGTCGTTGG TACGGATAGC	4020
CTTTTGGGCA TTGGTAATAC GTGGATTTTC AGGGATAATG GTCCCGTCAA AGTATTTCTT	4080
AAGGTTGCT ACCCCAGAGT TGATCCACAA AAGAGTTGGG TCATTTACAG GAACCAAAT	4140
TACTGATGGT TCTACTGAGT GACCTTGGT CGCCAGAAA TCAAGCCACA TTTGGCGTAC	4200
TTGTGCACTA GATAGTTGTT TCATATTGTC TCCTTATTC CTTGTTAAT GTGATTGGCT	4260
TTCCAGCATT TCCACATAGT CAATCGCGAC ACAGAGGAA ATGACTAGGT CTGCATAAGC	4320
GTCTTCAAGA ACCGTTACGG TATAGGTAGA AGTCAGATGG AAGAGTTCCT TCTTAATTTT	4380
CGCAATCAAC TGATCGCGAT CATCCAGCAA TTGAAATTC AAATCCAGA TATTGCCCTC	4440
GATACGAAGA CCTAGATTAT CAAACTCATA CTTATCTCGC CAGAAGGTCA ACTTCTTACG	4500
AATGACAAAA CTCGAGCCAT CCCGAAGCTG AATTTCAAAA CGAGGAAGCA AGGTCAAGAT	4560
TTCTTTACTA ATCTCACTGA CTTGTTACAC AGCCGCATCA TAGATGGTAA AGGTTTTAGG	4620
AATCTTAAAA AATGATCCCT CCACCTGATA GGCAATTTCT CCCCTGTCAT CCTTGATAGC	4680
GAAGCGTTCT CCTCCAAGAC GAACTTTTG TTGACAAGA AATGTTTCA TCAACACCTC	4740

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CAAAAATCAA AAGACAAGCT CATATCACGA AGGGCGAAAA ACCGCGGTAC CACCTTCATT	4800
CAATGAACCT GTCATTCTCT TGTTCCTATG CAATTGTATG ATTGAGTAGC ATGACTTCCT	4860
AGCTTAGATG GCTCGCAGCA CCGCCATTTC TCTGGACTAA GACAAGTGAA AATCAATTCT	4920
CAACTTCTCT ATTATAACGT TTTTAAAGC TTGCGTCAAC TGGAAATGAT CTCCGTTGAA	4980
TTAGACCAAT TCCCTACATC TCTGATTACT TTTTCAGGAT ATATTTTTTC TTAGTGCCAT	5040
TTTTCTTTT ATCCCAAATT TTCATATTAC TAAACACAGC TACTAGAATA TTTCCAAATA	5100
TAAAGGTGCC TATACCCAA TATATGGACT CAGTTGTTAG GTATTGTGCA TCCAAGCCAT	5160
CCTTTAAATG GAATAGTATA GCAGTTGGT TAACAATCAT AAAGTTGGC CAGAAACTTT	5220
TTTTGAAAA AGTAGACATT TTCATTATTT GTTGCCGCTT TCTGTAAGGT TAATACTCAA	5280
TAAAAATCAA AAAGCAAAT AGGAAGCTAG CCTCAAGCTG TACTTGAGTA CGGCAAGGCA	5340
ACGCTGACGT GGTTTGAAGA GTATAGGCTT AGTATACTAC TAGGCAAGCA AATAAACAAA	5400
TAAACAATA GAATAGAAAA AGATAGGGCT CTAAAACTG ACTTCTATTC CTTAAAAACG	5460
AACCAGCTTG ACTGATTCGT CTTCTACGT TTATCTCCTA CTTCCGATAC ATTTTAAACT	5520
GTAGGAAGAG GTCGTATAT TTCCCTGTCC ATTTATGGTC AAATTTCTCA TAAACTTCTA	5580
GGTGTTCAT GGTTCACAA TCGGGATAGA AGGCCTTATC TTCTTTGTT TCCTCTGGGA	5640
GCAATTCCTT CGCTGGTAGG TTGGTGTG AATAGCCGAC ATACTCCGCA TTTTGGAGAG	5700
CATTTTCAGG TTTCAACATA AAGTTGATAA AGGCATAGGC TGAGTTTGG TTTTAACTG	5760
TTTTGGGAAT GACCATATG TCAAACCAA GATTGCTGGC CTCTGTCGGT ACCACATAAC	5820
GTAGATTTTC ATTTTCTCT AACATTGGC TGGCTTCACC AGAGAAGGTC ACGCCGATTG	5880
CAACATTATT CTGAATCATA TAGCCCTTCA TCTCGTCCGC AACGATAGCC TTGATATTTG	5940
GAGTCAGTT GTAGAGCTTA TCCACTGTCT CTTCCAAGTG CTGCAGATCC TTGGAGTTGA	6000
GGCTGTAGCC GAGGGAATTG AGTCCTAGTC CCAGCACCTC ACGCGCCCCA TCAAAGAGCA	6060
TGATAGAATT CTTATCTCC GGCTTCCAAA GGTATCCCA ATGCTCAGGC GCTTCATCTA	6120
CCATGGTTTC GTTGTAGACA ATTCCTAAGG TTCCCAGAA GTAAGGGATG GAGAATTTAT	6180
TACCTGGGTC AAAGGACTGG TTGAGAACT CTGGTCCGAT ATTTTCGATT CCTTCAATTT	6240
TTGAATAATC AAGCGGAACC AAGAGGTCTT CGTCCTTCT CTTGTTAATC ATGTATTCAC	6300
TTGGAATGGC AATATCGTAG GTCGTTCCAC CCTGCTTTAT CTTAGTGTAC ATGGCTTCGT	6360
TGGAGTCAAA AGTCTCGTAC TGAACCTGAA TTCTGTTC TTCTGTAAAC TGAGTCAAGA	6420
GTTCAGGATC GATATAGTCT CCCAGTTAT AGATAACCAA TTTTGGACTA TCTCGACTAT	6480

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TGATTTTACT ATCTAAATGA GTCGCAATTC CCCACAAGAC AAGGATAATC GCTGCAATTC	6540
CTGCTAAAAA TGAATAGATT TTTTTCATGC TTGCTCCTCC TTCTCACGAG AGATAAAGTA	6600
ATAACCTACA ACTAGGATAA TACTAAAGAG AAAGACTAGA GCAGACAGGG CATTGATTTC	6660
TAAGGAAATC CCCTTGCGAG CACGAGAGTA AATCTCGACT GATAGGGTTG AAAAGCCATT	6720
TCCTGTTACA AAGAAGGTCA CGGCAAAGTC ATCTAACGAA TAGGTGAAGG CCATGAAATA	6780
ACCAAGTAATG ATAGACGGAG TCAGGTAAGG AAGCATGATT TCCTTGAACA TCTGAAATTG	6840
ACTAGCTCCC AAGTCATAGG CCGCATGAAT CATGTCGCCA TTCATTTCCT TGAGTCGAGG	6900
CAAGACCATC AAGACCACGA TAGGAATGGA GAAGGCCACG TGACTIONATA GAACGGTCAA	6960
AAAGCCAAGT GAAAACTTGA GTTGGGTAAA GAGAATCAAG AAGCTAGCAC CAATCATAAC	7020
GTCAGGCGCA ACCATGAGGA TATTATTGAG TGATAGAAAG GCTTCTTGGT ATTTCTTACG	7080
AGACTGGTAG ATGTAAATGG CACCAAAAAGT CCCGATAATG GTCGCTATCA AGGCTGATAG	7140
GAAGGCCAAG AAAAATGTCT GAGCCAAAAT CAGCATGAGT CTCCCATCTC CAAACATGGT	7200
TTCAAAGTGA GTCCAGCTAA AACCTGTAAA GCTATTCTATA TCATCACCAG CATTAAAGGC	7260
ATAGCCAATC AAGTAAAGA TAGGCAGGTA GAGGACCAGA AAGACCAGTC CCAGATAAAG	7320
GTGCGCAAAT TTTTTCATCG TTCTCTCCTT TCCTTAGTCA CCCACATGGT GATGAACATG	7380
GTCAGGATGA GAATCACACC GATGGTTGAA CCCATACCAT AGTTGTCATT GGTAGAAAA	7440
TTCTGCTCAA TAGCCGTCCC CAAGGTGATA ACGCGTCCC ACCAATCAAA CGGGTCAGCA	7500
TGAAGAGACT CAAACTTGGG ATAAAGACCG ACTGAACCCC GG	7542

## (2) INFORMATION FOR SEQ ID NO: 59:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 9223 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 59:

AAAACCAAAT TCCGGTATTT TAACCTATGC TGTAATACC ATGAAGCTG TCATGACAGA	60
TCAGGTCTAT AACATTAAGG TTGAGACAGA AAATGGAAAT TATGTTGGTG AAGCTAGCCA	120
TGTTTGGTGC CTTTIGACAA ATTACTTCGC TGATAAGAAA ATCTTTGAAG AAAACAAGGA	180
CGGCTATGCC AACATTTTGA TTCTGAAAGA TGCTCTATA TTCTCCAAAT TATCCGTCAT	240
TCCTGATTTA TAAAAGGGG ATGTTGTCGC AAATGATAAT ATCGAGTATA TCAAAGCGCG	300
TAATATTAAA ATCTCTTCAG ATAGTGAATT GGAGTCAGAT GTTGACGGAG ATAAATCAGA	360



TAACCTACCT GTAGAAATCA AAGTCCTAGC TCAGCGAGTA GAAGTATTTT CAAAACCGAA	420
AGAGGATTAG TATATAGAGA AAGCCTTTTT TAAGGCTTTT TGTATACTTT AAAAGATAGT	480
TCCTTTAACA ACGGACATTC CTTGCAAATA GTTTTACAAA AATAGTATAC TGGATTCAAT	540
GAGTTTGAAA ACGTTTGCGT AAAATTIGAA TGAATACTTT AGGAGACAAA TTGATGGAAT	600
TGAGTGCTAT TTACCATAGG CCTGAGTCGG AGTATGACTA TCTTTATAAG GATAAGAAAC	660
TCCATATTCG AATTCGAACT AAGAAAGGGG ACATTGAAAG CATCAACTTG CACTATGGGG	720
ACCCTTTTAT CTTTATGGAG GAGTTTATC AGGATACAAA AGAAATGGTC AAGATAACTT	780
CTGGTACCTT ATTTGACCAT TGGCAGGTG AAGTGTCAGT TGACTTTGCA CGTATCCAGT	840
ATCTCTTTGA GCTCAGAGAT ACAGAAGGTC AAAATATTTT GTATGGCGAT AAAGGGTGTG	900
TGGAAAATTC TCTAGAAAAT CTTTATGCAA TTGGGAATGG ATTTAAGTTG CCTTAGCTTC	960
ATGAGATTGA TGCCTGCAAG GTTCTGACT GGGTTTCAAA TACGGTATGG TATCAGATAT	1020
TTCTGAAAG ATTTGCCAAT GGCAATGCTC TATTAAACCC AGAAGGGACT TTAGACTGGG	1080
ATTCATCTGT CACACCTAAG AGCGATGATT TCTTTGGTGG TGATTACAG GGGATTATTG	1140
ATCATATGAA TTACTTGCAA GACTTGGGTA TFACTGGACT ATATCTTTGT CCCATCTTTG	1200
AATCTACAAG CAATCACAAG TACAATACGA CAGATTACTT TGAAATTGAC CGTCATTTTG	1260
GAGACAAGGA GACCTTTCGG GAACTGGTGG ATCAAGCGCA TCATCGTGGC ATGAAAGTCA	1320
TGCTGGATGC GGTATTTAAT CATATTGGTT CGCAATCTCT TCAATGGAAA AATGTCGTCA	1380
AAAATGGTGA ACAGTCTGCT TATAAGGATT GGTTCATAT TCAACAATTC CCAGTGACAA	1440
CTGAAAAGCT AGTTAATAAG AGAGACTTAC CCTATCATGT TTTTGGTTTC GAGGACTATA	1500
TGCCTAAGCT AAATACAGCC AATCCAGAGG TCAAGAATTA TCTTTTAAAG GTTGCAGCTT	1560
ATTGGATTGA AGAGTTAAT ATCGATGCTT GGCCTTTGGA TGTGGCTAAT GAGATTGACC	1620
ATCAGTTCTG GAAGGATTTT CGTAAGGCAG TTTTAGCTAA AAATCCTGAT CTTTATATCC	1680
TAGGAGAAGT CTGGCATACA TCTCAGCCTT GGCTAAATGG AGATGAGTTC CATGCCGTCA	1740
TGAATTATCC TTTATCTGAT AGTATCAAGG ACTATTTCTT ACGAGGAATT AAGAAGACAG	1800
ACCAGTTCAT CGATGAAATC AATGGAGAGT CTATGTATTA CAAGCAGCAG ATTTTCAAGG	1860
TCATGTTTAA TCTCTTGGAT TCACATGATA CAGAGCGAAT CCTGTGGACG GCCAATGAAG	1920
ATGTTCAACT GGTAAATCA GCCTTAGCCT TTCTCTTTT ACAAAAAGGA ACACCGTGCA	1980
TTTATTACGG AACCGAGCTA GCCTTGAAGT GAGGACCAGA TCCAGATTGT CGTCGTTGTA	2040
TGCCTTGGGA ACGTGTATCA AGTGACAATG ATATGCTGAA CTTTATGAAG AGGCTGATTA	2100

516

AAATTCGGAA ATACGCGTCA GTAATCATTT CGCATGGCAA GTATAGCCTT CAAGAAATCA	2150
ACTCTGATCT AGTAGCTCTG GAATGGAAAT ACGAAGGACG GATCCTCAAA GCAATATTCA	2220
ACCAATCAAC AGAAGATTAT CTTTGTAGAGA AAGAAGCAGT AGCACTAGCA AGCAATTGCC	2280
AAGAATTGGA TAATCAGCTT GTCATCTCTC CAGATGGATT TATGATTTTC TAAAACTAG	2340
TTGATGAAGA TTATGGTACA TTTCATACCT TATATAGTAT AATAAGGCTA GTTACTAAAC	2400
TTGTAAAGGA GAACTTAAAT GAATTGTAGA GGACATGAAA CAAGACAAAG AATTGTTAGA	2460
GATTTTGAAG TTCAGCCTAA AGCACATATT AAGCTGTTAG CAAATCAACA AAAACATAGT	2520
GATGCAGGAG CAACTATTGA AGATGAATAT TATGTATTTA TCGCTGAGAG TAAATTTGAT	2580
GGCAAGAAGG AAGTTATTCA GTGTTGCATG GGTGCGGCAA GGGATTTTTT AGAACTAATT	2640
AATCACAAAG GGCTACCTCT TTTTAATCCG CTTGTAGGTG ATTCTCATGT AAATAATAGA	2700
CAAGAATATG ACAATACAGG GAGTGGAAAT TTATAACCTG AAAAGTGGA TGAACTGCA	2760
AAGCAGCTTT ATAATGCTAT AATGTGGTTG ATTATTTTAT GGAATGCTAA GCCGGATACA	2820
CCTTTATTTA ATTTTAAAGA CGAAGTAATT AAGTATAAAA CATATGAGCC TTTTGAAAGC	2880
AGTATAAAAA GAGTAAATAC TACTATAAAG AATGGTAGTA AAGGGAAAAC TCTGACTGAG	2940
ATGATTAATG GCTACAGAGC GGATAACGAT ATTAGAGATG AAATTTGTAA CTTAATATT	3000
CTGAAAAATA AAATTCGTGA TATGAAAAAC CAACAAGGAA ATACAATGGA ATCTTACTTT	3060
TAGTTATTGT TGAATTTTGG GTATTCTATA AAATATCCTA ATTGAGATT AAATAGTAGA	3120
CTATACAATA TAGTTAAAT ATCAGTAAAA ACAACACTTT ATTGAGGTAT TGGATACGCT	3180
TTGCTAATAG CCTAATAATC ACATGTGGAG TGTGCTACA ACGAAAAAGG TGATAATCCT	3240
TGATTTCAAG CTATTTTATA AGCATTTTGT CTTGTAGAT AAAGGCAATT TTGACAATAA	3300
AAATCCTAAA AGGTGAATCG TTATAGATGT ATTTGTAGAT ATCGTTTGCG CATCGAAAAA	3360
ATTAATACAA GAATAAATAT TTATAGCTCT TTAGGTGACT TTTATAGAAG TAAAGTTTAG	3420
GATAGAAAAA CAAGAAATAA CGCACCATT TTGGTGCGTT ATGCTTTTTT ATGCTATAAT	3480
GGATTTATAA AAATAAAGGA GTTTGCTATG ATTGAAAGA ACATAAAATC CTTGCGTAAA	3540
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AGTCGTTATG AAAATGGAAC GAGTTCAGTC TCTACCGAAT TAATAGACAT CATTGTGTCAG	3660
AAGTTTAATG TATCTTATGT CGATATTGTA GGAGAAGATA AAATGCTCAA TCCTGTTGAA	3720
GATTATGAAT TGACTTTAAA AATTGAAATT GTGAAAGAAA GAGGTGCTAA TCTATTATCT	3780
CGACTCTATC GTTATCAAGA TAGTCAGGGA ATTAGCATTG ATGATGAGTC TAATCCTTGG	3840
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TAGCGATT TT GCTTGGAGGG CAAAGTGGTG CCGGTAAGAC TACAATT CAT CGTATTAAAC	4140
AGAAAGAATT TCAAGGAAAT ATTGTTATCA TAGATGGTGA TAGTTTTCGT TCTCAGCATC	4200
CACACTATTT AGAACTGCAG CAAGAATATG GCAAAGACAG TG TAGAATAT ACCAAAGATT	4260
TTGCAGGAAA AATGGTAGAG TCTTTAGTAA CAAAATTGAG TAGTTTGAGA TACAATCTTT	4320
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ATAAGGGATA TGAAGTACAA TTGGCCTTAA TTGCACAAA GCCTGAATTG TCGTATCTAA	4440
GTACTCTTAT CCGTTATGAA GAACGTGTACA TTATCAATCC AAATCAAGCA CGCGCAACTC	4500
CAAAAGAACA TCATGATTTT ATTGTAAATC ATCTAGTTGA TAACACACGA AAATGGAAG	4560
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GTGCAGCAGA TAAATTGCAT ATTGTATGTA TATATGATTA TGAACAAGAA TCATGGGTTA	5280
ATCAATGGTT AAGTGAAAAT ATTATAAGTG AGAAAGATGG AAGTTATCAA CATTCCTGA	5340
CTATAATGAA GGATTTCAAT AATCAAAAAA TAGTTAACTA TATTGCTCAT TTCAATAGTT	5400
ATGACATTTT GAAAAAAGGT TCTCACTTAT CAGGTGCATA TAAACGAAAA ATTTTTTCTA	5460
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TATTCTCTAT AAAGAAGTTG GTGTATTAAAG TTTGGGACAA AAAGTTGTAG CCATGCTTGA	5580
TTTTTTATTA GCATATAGTG ATTATTCTAA AGACTTCAGA CCATTGATTA TTGATCAGCC	5640

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TGAAGACAAT CTAGACAATC GTTATATTTA CAGGCATTTA GTTCAGCAGT TTAGAGATGT	5700
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GACAGATCAA GTTGTATTAT TGGAGTCAGA TGGAGTTAAC GGATGGATTG AATCACAGGG	5820
ATATGTTAGT GAAAAATATA TAAAAAATCA TATCATCAAT CAATTAGAGG GAGGAAAAGA	5880
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CGTGACGTTT ATGAAGTTTT AATCTTGGCA CAGTCAGAAC GTCAAGTCAC CCAAGAGCAT	7020
GTATCTATTC TCTTAACGTG CGTGCAGGAA TTGATTCAAG AGGTTGCAAA CACCATACCC	7080
CTCAGTAAAG AATTTCTGTA GAAGTACATG AGGTAAGCAC ATGGAACATC GTTACCGAAC	7140
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TCAAAGTGGT TGTAATCCT TTTCTGAATA TGGGAGACGA ACTCTACTCG ATCCTGGTAT	7260
GAATTTTATC ACGATTGACA CAAACGGTTA CCAAGATTTA GTGTTTGAGT TAAAGAGGAT	7320
TGGCAATAAT ATCAACCAGA TTGCTCGAAG TGTTAATCAA TCTCAGTTAA TTTCTGGTGA	7380
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AAATGGTGCA GATGTATCAT GAAAAATTCA TCAGCAACGA TACGCTTTAC GATTTTCGCC	7680
ACGACAGGAT GGAAGAAAAT CAACGAAAAA TACACGCTCA CCACATCATT CAGTCTTTCT	7740
CGCCAGAGGA TCATATCACT CCTGAACAAA TCAATCGGAT AGGTTATGAG ACTGTGAAGG	7800
AATTAAGTGG TGGCAAATTT CGTTTATATCG TTGCGACCCA TGTTGATAAA GACCACCTGC	7860
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TCAAAAAGAA TGCTCCGCTA CTACATGTGG AGATGGATTT CCGTCACAAG CATGCCACCT	8160
TTTTTATTAC GGACTCAACT ATGAAACAGG TGGTGCGTGG CAAGCAACTC AATCGCAAGC	8220
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AAGAGTTCAA GAGTAACAGA GATGCCGTTT ATGAATTTGA GGTGGAGTTG TCACTCAATC	8640
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GCAGAAAAGC GACAGTCGAT ATGATTAAAG AGAAGATTGC GGAAGTGGAT GCTTTGATTG	8940
AACTGGAAGT AGAAAATCAA TCTTATGTCA CGATTAAAGA TGAGTTAGTG CATGAAGTAG	9000
CAGCGTCTGA ATTGAGAATC AATGAGTTGC AAGAACGAAT GTCACCTTG AATCAAGTAG	9060
CAGAATATCT ACTGGCTTCA GTTGAAAGTA AGCAAGAAAT GAAATTAAAT CTTTCAAAAC	9120
TGAATATAAC TGAGAATATC AGTGCTAATA TTGTTGAGAA AAAATTGAAG AGCCTGGGGA	9180

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ATCAACTGGA ATTGGAAAGG GGCAGGTATG AAAAGATGGT AGT

9223

(2) INFORMATION FOR SEQ ID NO: 60:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 6827 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 60:

TCTGCTGGCT ACCATCATCT GACTTGGGCA AGACCAAAGT CTTAGTTACA ACTGTATTCT	60
TCTCAGCATT TTCAATAACT GGCAATGCCG ACTGAAGCGT ATCTTTTCT GTTTTGTAG	120
CTGGTCCAGT TTCTTTTTC TGTCCGCAAC CAACCAGGAC AAAAAGGAAA GCTAGACTAA	180
CAAGAACTAT TTTTTCATT TCTTCTCTCT TTCTTTTGA AATTAAAATA GAATAAGACT	240
GGGAAGTGCT CCCAGCCTTG ATGTTTATAG AGCTGCACGC AAACGTGCTT CTGCATTTT	300
TACATTACGG ACAGAGCGTG GTAGGAAGGC ACGAATATCG TCTTCCTTGT AGCCAACTTG	360
CAGGCGTTTT TCATCTACAA GGATTGGGCT CTTTAAAATT CTCGGTGTTC CCATAATCAG	420
ATTGAGAACT TCATTGACAC TCAAATCTTC AATATCCACT CCAAGGGCTT TGGCATAGCG	480
ATTTTGTAGC GAAACGATGC TGGCTATTCC GTTATCTGTT TTGGTTAGAA TATCCAGTAA	540
TTCTTCTCTC GTAATTCCTT CTTTACCAAG GTTTTGTCT TTATAACTTA ACTGGTGGGC	600
ATTGAGCCAG GTTTTGTCTT TTTTACAGCT AGTACAACCT GAGACTGTAT AAATTTTAAT	660
CATGTACCTA CCCCTTTCGC TACATGTTAC TATCAGTTTA GTCTATTATA CCATAAAAAA	720
CATCCGACTT GCGACCTATT TTTAATTTTT TTGACTTTT TTCGTCAATT TCGTACTTTT	780
TTCTTGACAA ACAACTAAAT GACTATCAAC TCTTTTGGAG CTAGGGTCAA TAATTCACAA	840
CCTGTCTCTG TAATCAGGAT ATCATCCTCG ATACGAACGC CATATTGACC TTCGATATAG	900
ATACCTGGTT CATCGGTCAA GGCCATACCT GTCTTAATAG TTTCTGTAGA AGTCTGACTA	960
AAGTAGGGTT CCTCATGGAT ATCCAGACCA ATACCGTGGC CAATGCCGTG ACTAAAGTAG	1020
TCACCATAAC CTGCCTCAAT GATAATATCA CGAGGGATTI TGTCAAAGTC ACGGAAACCT	1080
AAGCCTGCCT TAGCTTGGTC AATCAAGGCT TGGTTAGCTT TTAGAACCGT ATTGTAAATC	1140
TCTGCCTGCT CATCGCTAAC ATGCCCTAGA TAGATAGTCC GGGTCATATC ACTGACATAG	1200
TGGTCATAGA GACAGCCGAA GTCCATGGTG ATGGCTTCTC CCAACTCCAC TGGTTTGTGC	1260
ATTGGATGGG CATGGGGTTT AGAAGAATTG ATACCGCTAG CTAGGATCGT ATCAAAAGAT	1320
AAGCCAGATG CTCCCAACTC ACGCATGCGG AAATCAAGGA AGTTGGCAAT CTCAATTTC	1380

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GTTCCTCCTG GTTGATAAA GTCAAGCGCA TCGCGGAAAG CTTGGTCTGA GATAGAACAA	1440
GCCTTGCGAA TCGCTGCAAT CTCTGCCTCA TCCTTAATCA TACGAAGACC TTCCACAAAC	1500
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ACTGAAATCT CATCTTCAAA ACCGATACGA GTCAAGCCCA TGTCTTAAC AATTCCTGCA	1620
ATGACAGCCA ATTCATCAGC ATCAGCCACA ATCTCAAAAC CACTGGTTTC TTGCTTAGCT	1680
GCGATGATAT AGCGAGAGTC TGTCATAAG ACCTGACGGT CACGACTGAT AAAGACTGTT	1740
CCGTTTGAGC CCCAAAAACC AGTCAAATAA TAGACGTTTT TAAGATTGTT GATGATGATA	1800
CCATCTAGTT CTTTTCTTG CATTTTAGCT AGAAATGCTT GTACGCGTTT ATTCATGATG	1860
TAACTTTCCT TTCAAATAGT GTCCGTGATA GCTGGCTTCG TTGGCAGCTA CTTCCTCTGG	1920
AGTTCCTGTT ACGATGATGG TTCCACCACC GACACCGCCC TCAGGTCCCA AGTCAATGAT	1980
ATGGTCTGCC GTCTTGATAA CATCCAGATT GTGCTCGATG ACGAGGACTG TATTGCCATC	2040
GTCTACAAAG CGAGCTAAAA CCTTGAGCAG GCGAGCAATG TCCTCTGTAT GAAGCCCTGT	2100
CGTCGGCTCA TCCAGAATGT AGAAAGATTT TCCTGTCGAT CGTTTGTTGA GTTCGCTAGC	2160
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GTAGTGAAT TCTAGGGTTT CACTGTTATA GCGGGTTCG TGGCAAACTT CACAAGCCAC	2400
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ACAGCGACCT CCCTTGACGT TGAAACTGAA GCGCCCTTC TTGTAGCCTC GAATCTTGGC	2520
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GTTAGACCTC GCGTCCGTC CGATAGGGCT CTGGTCAATA TCAATCAAAAC GGTGACATG	2640
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CTTAGGTGTA CCTGCTGCAA CAATCTCACC ACCAAAAACA CCGGCACCAG GACCAACGTC	3000
AATCAGATAA TCAGCCTCAC GCATGGTATC TTCGTCGTGT TCCACCACGA TAAGAGTATT	3060
GCCCAAGTCA CGCATCTTTT TCAGACTGGC AATCAGGCGA TCATTGTCCC TCTGGTGAAG	3120

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ACCGATTGAC GGCTCGTCTA GGATATAGAG GACACCTGAT AGGTTGGAAC CAATCTGGGT	3180
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TAGATAGTTA AGACCCACAT TATTAAGGAA GGTCAAACGA TCCTTGATTT CCTTGAGAAT	3300
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GACAGACAAG GCCTGGTCAT TGAGACGATA GCCTTGACAG GTTCCGCAGG TCAGCTCATT	3480
CATGTAGAGA CGCATCTGAG TCGAGTGTA ATCGCTATTG GTTTCATGGT AACGACGTTT	3540
GATATTATTG ATAACCTCCCT CAAACGGAAT GTCGATATCG CGCACGCCAC CAAATTCATT	3600
CTCATAGTGG AAATGGAATT CCTTACCATC TGACCCATAG AGAATCAAGT TCTTATCTTC	3660
TTCTGACAGG TCCTCAAAAG GCTTATCCAT AGCCACTCCA AAGACTTTCA TGGCCTGCTC	3720
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GCCGTCACAC TCACTACAAG AGCCAAAAGG AGCATTGAAA GAAAAGAGAC GAGGCTCTAA	3900
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GGCGGACAAA CTCTCTACAT AGCGACGTTG TCCTCCGCA TAGAGAGTAT CAAAGCCAG	4560
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GGATAAGGGA TATGAAACAA GTTTTTCTCT CTACAACAAC TGAATTTAAA GAGATCGATA	4860
CGCTTGAAAC GGGTACTTGG ATCAATCTCG TCAATCCGAC TCAAAATGAA TCACTCGAAA	4920



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AGGAAAGAAA	TAACCGCACC	TACTACGTAA	CCATCCCGCT	TGGTATTATC	ATCACTGAGG	5100
AAACCATTAT	CACTACGTGT	TTGGAACCAC	TACCTGTCCT	TGATGCTTTT	ATCAACCGTC	5160
GATTGCGTAA	TTTCTATACC	TTCATGCGTT	CACGTTTTAT	CTTCAAATT	CTTTATCGCA	5220
ATGCAGAGCT	TTACCTAACA	GCCCTTCGTT	CAATCGACCG	CAAGAGTGAA	CAAATCGAAA	5280
GTCAACTGCA	TCAATCAACT	CGTAATGAAG	AATTGATTGA	GCTCATGGAA	TTGGAAGAAA	5340
CTATCGTCTA	TTTCAAGGCC	TCCCTCAAAA	CAAATGAGCG	CGTGATTAAAG	AAATTGACCA	5400
GTTCAACCAG	CAATATCAAG	AAATACCTTG	AGGACGAAGA	CCTGCTTGAA	GACACCCTGA	5460
TTGAAACCCA	ACAGGCCATC	GAGATGGCAG	ATATTTATGG	AAACGTCTTG	CATTCTATGA	5520
CAGAGACCTT	TGCCTCTATC	ATTTCTAACA	ACCAGAACAA	CATCATGAAA	ACCTTGCCCC	5580
TTGTGACCAT	CGTCATGTCC	ATCCCAACCA	TGGTCTTTTC	TGCCTACGGG	ATGAACTTTA	5640
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CCTTTGCTAT	GAGTGTCTCG	CTCACTCTCT	ATCTCATCCA	TAAAAAATGG	TTCTAAGAGG	5760
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ATACGGCGCA	CCAACTCATT	GGGCTCATAG	CTTCACTGTC	AAAGAGCAGT	ACGAAAAAGA	6000
GCATCCAAAA	GAAAATGATG	ACCCAAAAC T	GATGATTATG	GACTCAGCTC	TTTTCATCAC	6060
TAGCCTCTTT	GCCCTTGTC A	GCGCCCTCAC	AACCTTCTTT	GCGGCAGACC	AAGCTTTCGG	6120
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GTACTACTTT	GTTTACCAAT	ACTATGGACC	AGATATGGAT	CGCAGTCAAC	GTCCACCTTT	6240
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AACAAGCTTC	CTACCAGCTA	GCCTTAACCC	AGTACTGGAT	CCATTGCCAC	TAGCTATTAT	6360
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AAGTGCAGGA	CCAACACGCT	ATCAAGAATA	AGAAAACGAT	AAAAGCAACT	GCAGGTGCGG	6480
TTGCTTTTTC	ACTTACTTTT	TTGAGTTATA	TTCAATGAAA	ATCAAAGAGC	AAACTAGGAA	6540
GCTAGCTGCA	GGTTGCTCAA	AGCACAGCTT	TGAGGTTGCA	GATAAAACTG	ACGTGGTTTG	6600
AAGAGATTTT	CGAAGAGTAT	TAAAAGTATT	CTTCTGAAAT	CCCACATAGC	TTTCTCTTAT	6660

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ATTTTGTGAT AAAATAGGCT CAATCTATTT CTAGGAGGAT GAGATATGGT TTCTACTATT 6720  
GGTATTGTTA GTTTATCTAG TGGCATTATC GGAGAGGATT TTGTCAAACA CGAAGTGGAC 6780  
TTGGGTATCC AACGTCTCAA GGATCTGGGA CTCATCCCA TCTTTTTT 6827

(2) INFORMATION FOR SEQ ID NO: 61:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 11864 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 61:

CTGGCTAGTT GCATAGAGCA AAGTTGCTTC TTCATCAACA AAACCGTTCA TTTCAAAATA 60  
GGAAAGCAGC TCATCAGGAC TCTCCAAACG AATCCCTTTG TAATCCAGCT CAACTGCCAC 120  
CTCTTTCAAG GCTGCAAGAA GAAGTGTTC CAGGCCCTGT CTCTGATGGT CAAACTCGAT 180  
GACTAAAGAA TGTACTTTTA GACATTGCGG ATTGTCTGAC TGGGGACTTG ATAAATATA 240  
GCCTAAAAGT TGATTTTCAT CCCTAGCTAG AAGAAAGGTA TCCGCACACT TACGGATACT 300  
TTCTTCTAAA ATATGGGAAA GTTGCTGCTT TTCAGCTGGA AAAGACGAGG TCTGAAGTGC 360  
CCCTATCTCA GGCAAATCAG ACTTGCTTGC CTGAATGATC TTAATTGGAA TTTCCATGGG 420  
AACATCCTAT TGAACATTGC TTGTCAAGTT AGACAAGAGA CGCTCAAATG AGTATTCATA 480  
GGTTTGGATG TCTCTGCTC CCATAAAGAC GTAACAGCA TTGTCATGGT CTAGGAGTGG 540  
AGAAACATTT TCAACAGTAA TCACTTGGTG TTTTGTGTG ATTTTGTGG CTAGGTCTTC 600  
TACCTTAACG TCACCATGAT TACTTTCAG AGCCGAGCCA TAAATTGCG CTAGATAAAC 660  
AGCATCTGCT TGGTTTAAAG CATGGGCAAA GTCGTCCAAC AAGGCAATGG TTCITGTAAA 720  
GGTATGCGGT TGAAAGACTG CTACAATTC CTTGCTTGGG TATTTCTGAC GAGCCGCATC 780  
CAAGGTCGCA ATAATTTCTG TTGGATGGTG GGCAAAGTCA TCGATAATCA CTGTATCATT 840  
GACAATTTTC TCAGTGAAAC GACGTTTAA ACCGGCAAAT GTTTTCAAGT GCTCACGCAC 900  
CAAGTTCAAA TCAAATCCTG CTGTGTAAAG AAGACCAATA ACGGCTGTCG CATTATGAT 960  
ATTGTGACGA CCAAAGGTTG GAATGTGGAA TTGCCCCAAG TTTGTCCAC GGAAATGAAC 1020  
GGTGAAGGTT GAACCAGTTA TTGAACGAAG AAGATCACTA GCTACAAAGT CATTGCCTTC 1080  
AGCTTCAAAA CCATAATAAT AAATTGGTGC ATCAGACGTA ATCTTACGCA ATTCAGCATC 1140  
TTCACCATAG AAAAAAGAC CCTTGGTGAT TTGTTTGGCA TAGTCGTTAA AGGCATTAAA 1200  
AACATCCTCG AGACTTGTGA AATAATCTGG ATGGTCAAAG TCAATGTTGG TGATAATAGA 1260

525

GTATTCCTGGG TGGTAAGGCA TGAAGTGACG CTCATATTCG TCAGATTCAA AGACAAAATA	1320
TTTGCCATTG GCCGAACCAC GACCTGTCCC ATCTCCAATC AAGAAGCTGG TATCTGTAAT	1380
GTGAGACAAG ACATGAGACA ACATACCTGT CGTTGAAGTT TTTCCATGTG CTCCTGCTAC	1440
TCCCATGCTA ACAAAGTCAC GCATAAAGCT ACCTAGAAAC TCATGGTAAC GTTGTAGCT	1500
GATACCATTT TGGTCCGCAT AGGCAATTTT GACGTTGTTA TCTGGACGAA AGGCATTTCC	1560
AGCGATAATT TCCATATCAC CGTCTAGATT TTTTTCATCA AAAGGAAGAA TGGTAATTCC	1620
TGCCTGCTCA AGACCGCGTT GGGTAAAGTA GTACTTTTCA ACATCTGATC CCTGAACCTT	1680
GTGCCCCATC TGGTGCAACA TCAAGGCCAA GGCACATC CCTGATCCCT TAATCCGAT	1740
AAAATGATAT GTCTTTGACA TGTTTTCTCC CCTATTCTGT CATTCTGGTC AGATTCAACT	1800
CTTGGGCAAC CCGACGTTCT TGTCTGTTT GTTTACTTTT TTTATTGTAG ATTGGCTCT	1860
TCTTTAGAAA ATCATAATTG TTTTCTTTG GAGCAGGTGC TGACACTTCT TCATTCTTGG	1920
TAGGGATAGA ATGAACCTCT TCCGCCAAGA TATAATGAGA CTGGGTCAAT TTTTGGCTAT	1980
ATTTGACAAA TTCACCAGGA TTTTCCTTTT GGAAAGGAGC TGTCGGTTGA TTGCCCTGTC	2040
TAACTAGACT GGGCTGAGAA TGACGTCTCG CAAGGCTGAA ATCCTGAGTT AGGTAGTTAG	2100
CAGAGCGTTT CTTTTTCAAG TCCGCACGCG CTTCTTCACG CGCCACCTCC GCATAGCTCT	2160
TTCCCTCTTT TTTAACCCCT AAAGGAGCCT TTTTAGGTTT TPCGACTTGC TTTTCAATCG	2220
GTTTTACTGG TTTTCTTCA GCAATAGGAG CCCATTCTAA ATAATTTTTA TCTCGATACT	2280
CACCCCTGAT ATTACTGATC AGATCAGACT CATCATAGAG ATTCATGACT GGCATTTTCA	2340
TCAACATGAC CTCGTCATCT GACACCAATG GAAATCGTTC TTGTTTCATT TTCTATTTCC	2400
TTTCAACACT TCATTATAGC GTATTGTCTT GATTTTTCAA GTGCTGGCTT CAGAAATTCC	2460
CAAAATTTCT CTAATTTCTG CTAGGGTCAG ACTACCACGT GACTCTGTGC CGTCCAATAC	2520
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CTTGGTCACC AAGCGATAGA CCTCAACCGT TTCTTCCTGA CCCATCCGAT GGGCACGGCC	2640
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ACCTGTCAGG TTCAGACCGA CCCACCAGC CTTGAGGGAA ATCAGAAAGG CATCTCTTTC	2760
TCCTTGGTTA AAGGCTTGG TCATGTCTTG TCTTTCCTTG GCTGGGGTTG AACCCGTAAT	2820
TTTAAAGGAA GTCAGGCCCA AGTCTGGCAG TTCTTGTTC AATTTTTC AATTCCTT	2880
GAACTGAGAG AAAATCAAGA CACGGTGTCC GCCGTCTGCC ACCTGTACCA GTAGTCTCG	2940
GAGACTATCT AGTTTGGCCG TGGCTCCCTG ATAATCTTCC ATAAACAGGG CAGGAGTGTC	3000

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ACATATTTGA CGCAAGCGCA TCAAACCAGA TAAAAATTTCC ACACGACTTC GCTGAAATTC	3060
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CTTTTGCTGG TCTTCCAGTT CATTTTATA AACCACCTCA ATCAAGTCTG GCAATTCAGT	3180
CAGAACTTCT TCTTTCTTGC GTCGCATCAC GAAAGGCTTG ATAACTGAG CCACTCGCTC	3240
TGCTGGCAAT TTCATAAAT CTTTCTTGCT TGGCAAAAGT CCAGGCATGA CGATTGGAA	3300
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TGCTTTTCAA CCATGAACAA CAGTCACATC CAACTGTGGA GCAAATTTCT GAAACTCATC	3600
TGCCCAGTTG TAAATCAAAC CCGACGGAGC GAGAATCAAA ACCCGACTTT CTTTGTGTCAC	3660
TTGACTAGTC AAAAAGCAA TGGTCTGAAG GGTTTTCCCA AGTCCCATAT CATCAGCCAA	3720
AATCCCACCA AAACCATAAT GATGGAGCAT CTGCAACCAG CCAATTCCTT TTTCCTGATA	3780
ATCTCGCAAG TCAGCCTTGA CCTGAGTTGC TTGCAAAGGA AAGTCCTCTG GATGCGTCAA	3840
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GATTTCTCCTC TGGACAATAT TTTGAAAATC AAAGTGGATT TCCAAGAGAC CTCCCTTGA	4140
GGCAATCTGC ACCTGAGGAC TCGCTAGGCT ATAAAGCTCT TCTAGTTTAT CTGATAGGTC	4200
AACATGCCCC AGTTTTTCAA AGACTGGAAT GATATCATGA AAAAAATGAT AGACAGACTC	4260
CGCTTTTAAG GCCTGACGCC AAGATTGAAA ATCGGCCTCA AAGCCCGCAG CCAAACAGAC	4320
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TTCTTCCCTG TCAAAGTAAA AAGAGGGCGC AAAAGTTTGT ATTTGTAGAC GTTCTGGAGC	4500
TGAAACGGTG CCCATCTGGA TAAAAAGAGT CAGACAGGAG GCCAATTTGT CTCGATCACT	4560
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GAGAAGACGC ATCTGCTGGT CTGTTAAAAA ATAAACCTGA CCTTTATGGA AAAGTACTGC	4680
TCCCTGATAA AAGACATTGA CCCTAGGACT CTCACTGATT TCCATTTCAA AATAATCCGA	4740
GTATTCTGTT ACTGTAAAGG CAAATAGATT GGCATCAGCA TGCATATCCT GAAAAAGCAG	4800

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GGTTTGGTAG CTATCCACTT GATGGTCAAA TTGAAAATGG GGCAAGGCCA TCAGTAAATT	4860
CACACCCTGC TCAAAAAAGG TCAGAGGGAA AAAGAGGTGC CGACCTTGGT TTTGGAAAAA	4920
GAGGTCTGGA ACCAGCCCTT CCTCCGTTAG TCCGTGCAAG AAAGTCAAAA GTTCTTGGCT	4980
GGCATCATCA AAGGCTTCCC AAGAAAGAGA CTCCTCATAA ATCTTGCCAA TCATATACGA	5040
CTTTCTCTGC TCGACAATCC TTAAAAAAG TGGAATATCC CGAATGACAT AGTATTTTGT	5100
GCTATTGATT TGGCCGATTC TCAGAGTCCA CAAGATATGA TTGGTTCCTG CTTCCACCTG	5160
ACCCACAGCT GATAACTCAT AGGCGCATTC TGATTTTGGG GATAAAATTC GATCCAAAAA	5220
CTTGCCACCC AAGGTCACCT TGGTTTCAAC AGCCTCTTTT TCTTCATGAC CTTCTTCCAG	5280
ACTCCACAAG ATTTCTGAC CACGCTCATC ATTTTTCAGA AAATGCTCTA GCGCTGCCAA	5340
ATGCACACAG TAGCCCCCTT TTTGAAAAA ATCAGAGGCA CAAAAACCA AATCATCCTC	5400
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AAATCTTGGT GAATCTCATC CGAAACTAAC AAAACACCGT GTTTTGGCA GAGTTGGCCA	6240
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TTGTCAAAGT TGTAACCGTA TTGTGTAGCT TCCCACCTTTT GAACTTCCTT AATTAAGTCT	6600
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TCTAGCATCC TCAATCCCAA TAGACAAACG CAAGAGGTCA TCTGTCAAAC CATAAGAATG	6900
GCGTACCTCT GCTGGAATAT CAGCATGAGT TTGAGTCGTT GGATAAGTAA TAAGACTTTC	6960
CACTCCACCC AAACITTCG CAAAAGAGAA GACCTTGAGA CTGTTCAAAA TATGAGGAAT	7020
GCGTGTTFCA TCGGCTACTT TAAAGGAAAT CATGCCTCCA CGACCAGTGT AGAGAACTTC	7080
CTTAACTGCT GGAGAATCCT TCAAAAAGGC AACCCTTCT TGGCGCTAG CTGTTGAGCG	7140
CTCCATACGA AGAGACAAGG TCTTGAGACC ACGAAGCAAC TGGTAGCTGT CAAATGGAGA	7200
CAAGACTGCC CCTGTTGTAT TAAGATTGTA AAAAAGCTTC TCGTATAGTT CTAACTATT	7260
GGTCACAACC ACTCCAGCCA AGACATCATT GTGGCCTGCT AGATACTGG TTGCTGAATG	7320
GAGAACGATA TCTGCTCCAT CTTCAATCGG ACGTTGGTAG ATAGGGCTAT AGAAGGTATT	7380
GTCCACCACC ACTTTGGCAC CCTTAGCATG AGCCAATTTT GCTAGTTTTT CGATATCAAA	7440
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CTCGGCAATC AACTCTTCTT CTGTATTGGC ATAGGTAAAA TGGAAATGAC CTTCTGCTC	7560
CACTTGGTTA AACCAGCGAA AAGAACCACC GTAAAGATCA CGCACTGCCA AGACCTTACT	7620
TCCTACTGGA AAGACGCTAA AGGCCAGTAC AATAGCTGAC ATCCCTGAGC TAGTCGCTAG	7680
GGCATAGTCT GCTGACTCAA TAGCCGCCAA GACTTCTCA GCCTTACTAC GAGTTGGATT	7740
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TGCTAAAAAT GTGTTAATGT GTAATTCCTT GCTCATACAA TTCCTCCAA TCTATAGTAA	7920
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CAAACTATAT AAAAAGGGAG TTTTCTCTGC TCCCTTTAAT AGACTATAAA ATGGTGAATC	8040
TCAAAGACA CCTTCACTCT ATCATTTGCT CCTGCACAAA ACGAGCATAA CGCTCATGAT	8100
TTTCCAGTAG TTCCTTATGA GTTCTGAGC CAGTGATTTT CCCCTCCTCT AAGAAGAAAA	8160
TACAATCCAC ATCTTTTACC GTTGACAAAC GATGCGCTAT AATCACAACC GTCTTCTCCT	8220
TTAGTACAGA ATAGAGGCTA CTGATAATCG CATACTCAGA ATCCGCATCA AGATTAGCAG	8280
TGGCTTCATC AAATATAAGA ATTTCAAGCAT CTTTAAAGTA GGCTCTAGCT ATTTGAAGTC	8340

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TTTCGTTCCG	CCCCCTGACA	AGAGTCGTCC	GCGTTCACCA	ACTTCAGTAT	CTAGTCCCTC	8400
TTTCATGGAG	CGAATCTCAT	CACCTAGTGA	TACTAAGTCT	AGCACTTTCA	TCAATTTCATC	8460
ATCAGTTACT	AAGCGATTCA	AACCGAGACA	AAGATTGTCA	CGAATACTGC	CAGATAAGAC	8520
TGCATTATTT	TGTGAAACCC	AAGCGATTTT	ACTTCTCCAT	TCTTTTAAGT	TAAAATCATA	8580
TATACTTGAT	TGCTCCATTA	GAATATCTCC	TGAAAGCGGT	TTATAAAACC	GCTCTAACAA	8640
ACGCACAATC	GTTGATTTTC	CTGATCCAGA	TGGTCCAACA	AAAGCAATTT	TTTGCCCTTT	8700
GAAAATTGAA	CAAGTAATAT	CCTTTAAGAC	AGGTCGATTT	TCATCATAAC	CAAAATAGAC	8760
ATGGTTAAAA	TTCAACCTC	GTCTGATAC	CGATTTTCCT	CCCTCAAATT	TTTCTTTAGG	8820
AACTGCAAGC	AAGTCTCCA	GTGCAACTGA	AGATCCCTTG	CTCCTAGAAT	AAACAGTTAC	8880
AAAATTAGCT	ATATTACTAA	TAGGATTAAG	TAATTGAAAG	AGGTAAATCA	AAAACGAAAC	8940
CAAGGTTCCC	ACAGATATAT	ATCCTGCGCT	GACCCGATAA	CCCCCATAGG	TTAGCATCAC	9000
AGCTATAGTC	GCAAAGATAA	ATAAGAGAGC	AAACGGGGTC	TCAAAAGAAG	TAACCTATC	9060
TGATTTCACT	GAATTGTTTT	GTACCCCTTC	AATACAATTA	TCCAAAACAT	CCTGTACACT	9120
TTTCTCTGCT	TGGTTAGTCT	TAATTAATTC	ATGTTCTTGA	ATCTTTTCAG	TCAATTGCCC	9180
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ATAATAAACA	TCATACAAGG	AAGAGTGATG	AATAAAAAGTA	GAGAAAGATT	CCAATCAAGA	9300
CTAAATAAGA	CTACAATGGA	ACCAAGTACC	ATAACTAAAC	TCAGAATAAT	ATTTGGGAAA	9360
GTGTAATTA	AAACTCACG	AATGACACTC	GTGTCATTGA	CAATGGCAGA	AGTCAACTCC	9420
CCACTTTGGC	TCTTATCAAA	GAAGGATTTT	TCTACATAAA	TCAACCCCTC	TATCACTTTT	9480
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TCAATAGAAC	TCCCATCTAT	TAAATCCTTT	AAGATAAGGG	GAAGCAACAA	AGCAAGTAGA	9660
CTAGACAGAA	CAAGTAAGAA	ACTCCCCATA	ATCACCTTAG	TATCTACTCT	TAATAATTTT	9720
AATTTCATAA	ATACTCCTTA	TAATATTTCA	ACGGATAAAG	TCGGGAATAA	CTCAATTTGA	9780
GGATAAAATC	TAATAAATCT	TCCTATAACA	AAACGCATAA	CATCTAGGAT	TTTATATACC	9840
TGATATTATG	CGTTTTTAAG	CACAAAGACT	TCTTACACAA	ACTTATCTAC	AATTAGATTT	9900
TATTTGACAT	GTTTTGCCAA	TTCTTCTTGG	GCTTTTTTAT	TGGATTCTTC	TTTTCTTTTC	9960
AACCATTTTT	CTCTGGCTTT	TGCATATTCG	TCTGTTGTGA	CAATCTTATC	TTGTACTTTG	10020
AGGTATTTAT	ATGATTCAAC	CCCTTTTGTA	CCGGTTAAAC	CATAGGCAGC	AGCAAATGGT	10080

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ACGGTTCTTC TCAATGATGG TGTTCCTCCCA CGCGAAACAC TTGGAAGAAC TAAAGAACTA	10140
TCAATCAACC AAGCTTGAAT ATCAGCATAT TTCTCATAAC GTTTGGCCGG ATCTTGCTCT	10200
TTATTAGCTT CTTCACAT TTGAGTATAG ACATCCAGTC CAACTGCCTT AGCCTTGTC	10260
TTGGCCTCAC CAGGCTCTAG TCCAAGATT TGCAGAAATC CTCCACTATT AGTATTAAAA	10320
ATATCGAGAT AGGTTGACGG GTCTTGATAA TCAGGTCCCC AACCGCCATG ATATAAATCA	10380
TAATCTTTCT GAGCAGCTGT TTGAGCAAAG TAGCCTGAAC TGTCAAATC ATCTGATGTT	10440
AATTGCTGAA TGTCAATCAC TACATTATCA GAACCTAAAA CAGATTCAAT TGATTGTTTG	10500
ATAGAACTAA CTCCTTGAT GCCTACTTTA TCTGTTACTT CCACAGTCTT ATCCAAGTGG	10560
ATTGGGAATT GAACACCTT TGTCTCGAGT TCTTTCTTAG CTTCGCCAAA CTAGCCTTG	10620
GCTTTCTCAG GATTGTAGTA AGGGCTTGA CCATCCGCAA AGTTGATACC TTGCCATTCC	10680
TTACCATAGT TGACCATCTT AGAGGCTACA ACTTCACCAA AGTCTTTTCC CTGATACTG	10740
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GACTGAGCCC CATAAGATGT TCTGTCAAAA GCAAAATTGA TAGCCTGACG GAAGTTTSTA	10860
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TAAGACTTCC TATCTAGGTT AAAATTAAAG AAATATGAAG TTGAATTTTG CATACTATAG	10980
ATGATATTGT TTTTGTATTT TTCTTAAATC CCTTCATAGC TGGAGCTGT AGGAAAAAGA	11040
CGAGCCGTAG TATAAGCACC AGCTGTAAAA TTACGTTCCA GTGATTCTTG GTCGCTACCA	11100
TCATAGTAGG TCAATTTAC ATCGTCTACA AAGCATTTCT TAGCATCCCA GTAATTAGGG	11160
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ACCAAAGTAT ATTGAACCGT TTGGTCATCA AGTGCCTTGA CACCGACAGT TGAAAAGTCG	11400
CTTGTTTAC CAGTGATATA GTCATCCAAA CCAGCAACAG AGTCCTGCAC TAGATACAAG	11460
GCTTCTGATT TTTTATCAGC TGCATATTGC AAACCTGTCA CAAAATCCTG GGCAGTTACA	11520
GGCGCATATT CTTCTCCCTC AGAAGTAAAC CACTTGGCAT CCTTACGAAG TTTGTAGGTA	11580
TAGGTCAAAC CGTCTGAGA AACAGTCCAA TCCTCTGCTA ATGATGGAAT AATATTCCCA	11640
TATTGGTCAT TTTCTAATAA CCCGTCTACC AAATTGCAA CAATATCGGA TGTGCTGCG	11700
CGGTTTCTG CTAGATAGTT CAAGCTAGAT GGATCACTTG AATAAACATA GTTGAGGTT	11760
TTTGACGCG TGCTAGAATT TCCACACGCG CTCATAAAA CTCCTGTACC CAGGACAAGA	11820
CCTGCCAAGG TTAGATATTT GCTCTTAGAC TTTTTCATTT CCGG	11864



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## (2) INFORMATION FOR SEQ ID NO: 62:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 2412 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 62:

TAAGTGCCT AAACATAATA TAAGGAGAGA AAATGTCTGC AATAGAACGT ATTACAAAAG	60
CTGCTCACTT AATTGATATG AACGATATTA TCCGTGAAGG GAATCCTACT CTACGCGCGA	120
TTGCTGAGGA AGTCACTTTC CCCCTATCTG ACCAGGAAAT CATCCTAGGC GAAAAGATGA	180
TGCAATTCCT TAAACATTCC CAAGATCCTG TCATGGCTGA AAAAATGGGA CTCCGCGGTG	240
GTGTTGGACT GGCTGCTCCC CAGTTAGATA TCTCAAAACG CATTATCGCT GTTTTGGTAC	300
CTAATATTGT TGAAGAAGGC GAAACTCCAC AGGAAGCCTA CGATTTGAA GCCATTATGT	360
ACAATCCAAA AATCGTCTCT CACTCTGTTT AAGATGCTGC TCTTGGCGAA GGAGAAGGTT	420
GCCTGTCTGT TGACCGTAAC GTGCCTGGCT ATGTTGTTTG CCATGCCCCG GTTACTGTTG	480
ACTACTTTGA CAAAGATGGA GAAAAACACC GTATCAAACT CAAAGGCTAC AACTCCATTG	540
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AAGACCCATT TGCAAGTAAA GATGGTTTAC TGATTCTTGA ATAAAGAAAA TCCCGTTGCA	660
AGACGGGGTT TTGTGTTATA ATAGAGGCAT GAAAACAAAT GATATTGTCT ATGGTGTCCA	720
CGCCGTTACC GAAGCCCTCC TTGCAAATAC AGGAAACAAA CTCTACCTCC AAGAAGATCT	780
CCGAGGTAAG AATGTTGAGA AAGTCAAGGA ACTAGCTACA GAAAAGAAGG TGTCCATTTT	840
TTGGACATCA AAAAAATCTC TCTCTGAGAT TACTGAAGGT GCTGTTTCATC AAGGTTTGT	900
TCTACGAGTG TCTGAATTTG CCTATAGCGA GCTAGATTAC ATCCTTGCAA AAACACGCCA	960
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TGTCGGAGTA ACTCCTGTCT TTGCCAAAAC AGCCACAGGT GCTATTGAAC ACGTCCCAAT	1140
TGCCCCGAGT ACCAACCTCA GTCAAACTT AGGATAAACT TAAGGATGAA GTTTCTTGGA	1200
CCTTTGGAAC GGATATGAAC GGTACTCCTT GCCACAAGTG GAATACAAA GGGAAAATCG	1260
CCCTCATCAT TGGAATGAA GGAAAAGGTA TCTCTAGCAA CATCAAAAA CAGGTCGATG	1320
AAATGATTAC CATTCCGATG AATGGACATG TTCAAAGCCT TAATGCCAGT GTTGCTGCGG	1380

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CCATTCTCAT GTACGAAGTT TTCCGAAATA GACTATAAAA AAGTTTCCAG TCATCTGATT	1440
GGAAACTTTT TTATGATTAA CTATGTTCTG TAATGAATTT ATAGGCTTCT TGACCAGCGA	1500
TAGCTCCATC TCCAACCGCT GTTGTACTT GCGAAGGTC TTTCAAGCGA ACATCTCCAA	1560
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AGACACCACC GAAGGCTTGT TCTGTCACTT GACCTGTTT CACATTTTCA AATACGACTG	1740
ATTCTACTCG GTTTTCACCC TTGATTTCCC TTACTACAGA ATCCCAGATA AAGCTGATT	1800
TTTCATTTCG AAAGGCGCGA TCTTGTAATA CCTTTTGGG ACGAAGTTGG TCACGACGGT	1860
GAACAATGGT AACAGTCTTA GCAAACGAG TCAAGAAGAG GGCTTCTTCA ACAGCTGAAT	1920
CTCCACCACC AACTACCAAT AAATCTTGGT CACGGAAGAA AGCACCATCA CACACAGCAC	1980
AGTAAGAAAC ACCACGACTG TTCAGTTCTT CTCTCCAGG CACTCCAAA GGACGGTGT	2040
TAGAACCAGT TGCTACGATA ACTGTACGTG TTTCATATGT TTGGTCATCA GTCATCACTT	2100
TCTTAAATC ACCATGGCTT CGACATTTT AACATAACCA TAAATGTGCT CAACACCAAG	2160
ATTTTCAAGT GGTTCAAACA TCTTTTCAGC CAATTCAGGT CCACTAATAT TAGCGTATCC	2220
TGGGTAATTT TCGATATCAG ATGTATTAT CATCTGACCA CCTGGCAGAC CACCTTCAAT	2280
CAAAGCTACT TTTAGATTGC TTCGAGCAGC ATACAAGGCC GCAGTCATCC CTGCAGGTCC	2340
AGCACCGATA ATAATAGTAT CGTACATATA GATTCCTTCT TTCTTGGTGT AACTATCTTT	2400
ATTCTAACTC TG	2412

(2) INFORMATION FOR SEQ ID NO: 63:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 7760 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 63:

CCGATTTGGT GGAATTTTGT TCTCATCATT TAGAAGGTGT TGCAAGAGCA GAGTTTACCT	60
TGGTGCTTCA TACCAAATG GGAGAAGCCT CTGTTTGGC AAATATTGTA GATGTAAACA	120
AGGATGAATG GATTTTAGGA ACAGTTGCTG GTGCCAATAC CTTATTGGTT ATTTGTCGAG	180
ATCAGCACGT TGCCAACTC ATGGAAGATC GTTGCTAGA TTTGATGAAA GATAAGTAAG	240
GTCTTGGGAG TTGCTCTCAA GACTTATTTT TGAAAAGGAG AGACAGAAAA TGGCGATAGA	300
AAAGTTATCA CCCGGCATGC AACAGTATGT GGATATTAAA AAGCAATATC CAGATGCTTT	360

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TTTGCTCTTT CGGATGGGTG ATTTTATGA ATTATTTTAT GAGGATGCGG TCAATGCTGC	420
GCAGATTCTG GAAATTTCCCT TAACGAGTCG CAACAAGAAT GCCGACAATC CGATCCCTAT	480
GGCGGGTGTT CCCTATCATT CTGCCCAACA GTATATCGAT GTCTTGATTG AGCAGGGTTA	540
TAAGGTGGCT ATCCGAGAGC AGATGGAAGA TCCTAAACAA GCAGTTGGGG TTGTTAAACG	600
AGAGGTTGTT CAGGTCAITTA CGCCAGGGAC AGTGGTCGAT AGCAGTAAGC CGGACAGTCA	660
GAATAATTTT TTGGTTTCCA TAGACCGCGA AGGCAATCAA TTTGGCCTAG CTTATATGGA	720
TTTGGTGACG GGTGACTTTT ATGTGACAGG TCTTTTGGAT TTCACGCTGG TTTGTGGGGA	780
AATCGTAAC CTCAAGGCTC GAGAAGTGGT GTTGGGTTAT GACTTGTCTG AGGAAGAAGA	840
ACAAATCCTC AGCCGCCAGA TGAATCTGGT ACTCTCTTAT GAAAAAGAAA GCTTTGAAGA	900
CCTTCATTTA TTGGATTGTC GATTGGCAAC GGTGGAGCAA ACGGCATCTA GTAAGCTGCT	960
CCAGTATGTT CATCGGACTC AGATGAGGGA ATTGAACCAC CTCAAACCTG TTATCCGCTA	1020
CGAATTAAG GATTCTTGC AGATGGATTA TGCGACCAAG GCTAGTCTGG ATTTGGTTGA	1080
GAATGCTCGC TCAGGTAAGA AACAAAGGAG TCTTTTCTGG CTTTGGGATG AAACCAAAAC	1140
GGCTATGGGG ATGCGTCTCT TGCGTTCTTG GATTCATCGC CCCTTGATTG ATAAGGAACG	1200
AATCGTCCAA CGTCAAGAAG TAGTGCAGGT CTTTCTCGAC CATTTCTTTG AGCGTAGTGA	1260
CTTGACAGAC AGTCTCAAGG GTGTTTATGA CATTGAGCGC TTGGCTAGTC GTGTTTCTTT	1320
TGGCAAAACC AATCCAAAGG ATCTCTTGCA GTTGGCGACT ACCTTGCTTA GTGTGCCACG	1380
GATTCGTGCG ATTTTAGAAG GGATGGAGCA ACCTACTCTA GCCTATCTCA TCGCACAACT	1440
GGATGCAATC CCTGAGTTGG AGAGTTTGAT TAGCGCAGCG ATTGCTCCTG AAGCTCCTCA	1500
TGTGATTACA GATGGGGGAA TTATCCGGAC TGGATTTGAT GAGACTTTAG ACAAGTATCG	1560
TTGCGTTCTC AGAGAAGGGA CTAGCTGGAT TGCTGAGATT GAGGCTAAGG AGCGAGAAAA	1620
CTCTGGTATC AGCACGCTCA AGATTGACTA CAATAAAAAG GATGGCTACT ATTTTCATGT	1680
GACCAATTCG CAACTAGGAA ATGTGCCAGC TCACTTTTTC CGCAAGGCGA CGCTGAAAAA	1740
CTCAGAACGC TTTGGAACCG AAGAATTAGC CCGTATCGAG GGAGATATGC TTGAGGCGCG	1800
TGAGAAGTCA GCCAACCTCG AATACGAAAT ATTTATGCGC ATTCGTGAAG AGGTCGGCAA	1860
GTACATCCAG CGTTTACAAG CTCTAGCCCA AGGAATTGCG ACGGTTGATG TCTTACAGAG	1920
TCTGGCGGTT GTGGCTGAAA CCCAGCATTT GATTCGACCT GAGTTTGGTG ACGATTACCA	1980
AATTGATATC CGGAAAGGGC GCCATGCTGT CGTTGAAAAG GTTATGGGGG CTCAGACCTA	2040
TATTCAAAT ACGATTGAGA TGGCAGAAGA TACCAGTATT CAACTGGTTA CAGGGCCAAA	2100

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CATGAGTGGG AAGTCTACCT ATATGCGTCA GTTAGCCATG ACGGCGGTTA TGGCCCAGCT	2160
GGGTTCCCTAT GTTCCTGCTG AAAGCGCCCA TTTACCGATT TTTGATGCGA TTTTACCCG	2220
TATCGGAGCA GCAGATGACT TGGTTTCGGG TCAGTCAACC TTTATGGTGG AGATGATGGA	2280
GGCCAATAAT GCCATTTCGC ATGCGACCAA GAACTCTCTC ATTCTCTTTG ATGAATTGGG	2340
ACGTGGAAC TCAACTTATG ACGGGATGGC TCTTGCTCAG TCCATCATCG AATATATCCA	2400
TGAGCACATC GGAGCTAAGA CCCTCTTTGC GACCCACTAC CATGAGTTGA CTAGTCTGGA	2460
GTCTAGTTTA CAACACTTGG TCAATGTCCA CGTGGCAACT TTGGAGCAGG ATGGGCAGGT	2520
CACCTTCCTT CACAAGATTG AACCGGGACC AGCTGATAAA TCTACGGTAT CCATGTTGCC	2580
AAGATTGCTG GCTTGCCAGC AGACCTTTTA GCAAGGCGG ATAAGATTTT GACTCAGCTA	2640
GAGAATCAAG GAACAGAGAG TCCTCCTCCC ATGAGACAAA CTAGTGCTGT CACTGAACAG	2700
ATTTCACTCT TTGATAGGGC AGAAGAGCAT CCTATCCTAG CAGAATTAGC TAAACTGGAT	2760
GTGTATAATA TGACACCTAT GCAGGTTATG AATGTCCTAG TAGAGTTAAA ACAGAACTA	2820
TAAACCAAG ACTCACTAGT TAATCTAGCT GTATCAAGGA GACTTCTTTG ACAATTCTCC	2880
ACTTTTTCG TAGAATAACA TCACACAAAC AGAATGAAAA GGAGCTGACG CATTGTCGCT	2940
CCCTTTTGTC TATTTTTTAA GGAGAAAGTA TGCTGATTCA GAAAATAAAA ACCTACAAGT	3000
GGCAGGCCCT GGCCTCGCTC CTGATGACAG GCTTGATGGT TGCTAGTTCA CTTCTGCAAC	3060
CGCGTTATCT GCAGGAAGTC TTAGGCGCCC TCCTTACTGG GAAATATGAA GCTATTTATA	3120
GTATCGGGC TTGGTTGATT GGTGTGGCCG TAGTCGGTCT AGTTGCTGGT GGACTCAATG	3180
TTGTCTCGC AGCCTATATT GCCCAAGGAG TTTTCATCCGA CCTTCGGGAG GATGCCTTCC	3240
GTAAAATTCA AACCTTTTCT TATGCTGATA TTGAACAATT TAATGCGGGA AATCTAGTCG	3300
TTCGAATGAC AAATGATATC AACCAGATTG AGAACGTTGT CATGATGACC TTCCAAATTC	3360
TTTTCAGACT TCCCCTCTTG TTCATCGGTT CGTTTATCCT AGCGGTTCAA ACCTTACCTT	3420
CTCTGTGGTG GGTGATTGTT CTCATGGTAG TCTTGATTTT TGGTTTGACT GCTGTCATGA	3480
TGGGAATGAT GGGGCCTCGT TTGCGCAAGT TTCAAACCTT TCTTGAGCGC ATCAATGCCA	3540
TTGCCAAGGA AAATTTACGT GCGGTTCTGT TGGTCAAGTC CTTTGTCCAA GAAAAAGAGC	3600
AAATTGCTAA GTTTACAGAG GTCTCAGACG AGCTTCTTGG TCAAAACCTT TACATTGGTT	3660
ATGCCPTTTC AGTAGTGGA CCCTTTATGA TGTTGGTTGG TTACGGGGCG GTCTTCCTCT	3720
CTATTTGGCT GGTGCGGGA ATGGTTCAGT CGGATCCGTC TGTTGTGGT TCCATCGCTT	3780
CTTTGTGTTA TTACCTAAGC CAGATTATCT TTACCATTGT TATGGTTGGA TTTTGGGAA	3840
ATTCTGTCAG CCGTGCCATG ATTTCCATGC GTCGTATTCG AGAAATCTT GACGCAGAGC	3900

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CAGCTATGAC CTTCAAGGAT ATCCCAGATG AAGAGTTGGT TGGAAGTCTT AGCTTTGAAA	3960
ATGTGACCTT TACCTATCCA ATGGACAAGG AACCGATGCT GAAAGATGTG AGCTTTACTA	4020
TTGAACCTGG TCAAATGGTT GGTGTAGTTG GAGCGACTGG TGCAGGAAAG TCAACCTTGG	4080
CTCAATTGAT TCCACGTCTC TTTGATCCAC AGGACGGGGC CATTAAAAATC GGTGGCAAAG	4140
ATATTCGAGA AGTGAGTGAA GGAACCTGTC GTAAACAGT TTCCATCGTT CTCCAACGTG	4200
CCATTCCTTT TAGTGAACG ATTGCAGATA ACTTGAGACA GGGGAAGGGG AATGCTACTC	4260
TATTTGAAAT GGAGCGCGCA GCCAATATG CCCAGGCTAG TGAATTCATT CATCGTATGG	4320
AGAAAACCTT TGAAAGTCCA GTTGAAGAAC GGGGAACCAA TTTCTCTGGT GGACAAAAAC	4380
AAAGGATGTC GATTGCGCGT GGGATTGTCA GCAATCCACG TATTCGTATT TTTGATGATT	4440
CGACCTCAGC CTTGGATGCC AAATCAGAGC GCTTGGTGCA AGAAGCTTTG AATAAGGACT	4500
TGAAGGGGAC GACAACCATT ATTATTGCTC AAAAAATTAG CTCGGTTGTC CATGCAGACA	4560
AGATCTTGGT TCTAAATCAA GGACGATTGA TTGGTCAAGG TACGCATGCA GACTTGGTTG	4620
CCAAACAATGC CGTTTACCGT GAAATCTATG AAACACAGAA ATGAAAGACA AACTATAAGA	4680
AAAGTCAATA GTTTTATCTA AACTATTCTT TATTTCAATT TGATGATTTG GCGATGATTT	4740
TAGAGCACGG CAAAAAGCCC TTGAAAAAGT CCATTTTTC AAAGGTAATC CTGTGTTAAT	4800
TTCAGAAATT ACATCACTTT TTGTTCTGTA AATGGCAGCT CTTTTTTTAG GATATAAAAC	4860
AGGGTTCGGA TAAGTTTTTT TGCAAGGTGG ATGATGGCTA CATTGTAATG TTTTCCTTGT	4920
TCTAATTTAG TCTTAAGATA GGCCTTAAAA GCAGGCGAAA AGCGAGGGCA TGCTTTGGCA	4980
GCTTGATGTA GTACCTACCG CAGATGAGGG GAACTCCGTT TGACCATTCCT TCCTGCTAAA	5040
TCAATCTGAT CTGACTGATA AATAGAAGAA TCCAGTCCAG CGAAAGCTTG TAATTGAGCA	5100
GGATTATCAA AGGCATGAAT ATTTCTGAATC TCAGCTAAAA TGACCGCCCC TAAACGATCC	5160
CCAATCCCAG TAACCGTCGT GATGACCGAG TTGAACTCAG CCATCAAGTC ATTGACACAT	5220
GTTCCCGCCT TGTCATGAG CCTCTTGTA TGTTTGATGT TTTCATTACA CGAGATAAAA	5280
CGTCTATGCG TTATCAAACT CATTACCAAT TAAACAAAA AGCTGTGGTT AGATCCTTTC	5340
GGAAATTGTC AAGCGATTGG AGGAAATGAA CTAATCCACA GCGGCTTATT CCAAGTATAC	5400
CACCTGGGCT TTGGCAGTAG CTAAGTGGC TAAATATAAT ATAAGGAGGA GTAAATGAA	5460
GACAGTTCAA TTTTTTTGGC ATTATTTTAA GGTCTACAAG TTCTCATTTG TAGTTGTCAT	5520
CCTGATGATT GTTCTGGCGA CTTTGGCCCA AGCCCTCTTT CCAGTCTTTT CTGGACAAGC	5580
GGTGACGCAG CTAGCCAATT TAGTTCAAGC TTATCAAAAT GGCAATCCAG AACTTGTATG	5640

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GCAAAGCCTA TCAGGAATCA TGGTCAATCT TGGCCTGCTG GTTTTGGTTC TATTTATCTC	5700
TAGTGTAATA TACATGTGTC TCATGACGCG CGTGATTGCA GAATCGACCA ACGAGATGCG	5760
CAAAGGCCTC TTTGGTAAGC TTGCTCAGTT GACGGTTTCT TTCTTTGACC GTCGACAAGA	5820
TGGCGATATC CTGTCTCATT TTACCAGTGA TTTGGATAAT ATCCTCCAAG CCTTTAACGA	5880
AAGCTTGATT CAGGTCATGA GCAATATTGT TTTATACATT GGTCTGATTC TTGTCATGTT	5940
TTGAGAAAT GTGACGCTGG CTCTCATCAC CATTGCCAGC ACCCCATTGG CTTTCCTTAT	6000
GCTGATTTTC ATCGTGAAA TGGCACGCAA ATACACCAAC CTCCAGCAGA AAGAGGTAGG	6060
GAAGCTCAAC GCCTATATGG ATGAGAGCAT CTCAGGCCAA AAAGCCGTGA TTGTGCAAGG	6120
AATTCAAGAG GATATGATGG CAGGATTTCT TGAACAAAAT GAGCGCGTGC GCAAGGCAAC	6180
CTTTAAAGGA AGAATGTTCT CAGGAATTCT TTTCCCTGTC ATGAATGGGA TGAGCCTGAT	6240
TAATACAGCC ATCGTCATCT TTGCTGGTTC GGCTGTACTT TTGAATGATA AGTCTATTGA	6300
AACAAGTACA GCCCTAGGTT TGATTGTTAT GTTTGCACAA TTTTCACAGC AGTACTACCA	6360
GCCTATTATC CAAGTTGCAG CGAGTTGGGG AAGCCTTCAG TTGGCCTTTA CTGGAGCTGA	6420
ACGAATTCAG GAAATGTTTG ATGCAGAGGA GGAAATCCGA CCTGAAAAGG CTCCAACCTT	6480
CACTAAGTTG CAAGAAAGTG TTGAAATCAG TCATATCGTT TTTTCATACT TGCCTGATAA	6540
ACCTATTTTG AAAGATGTCA GCATTTCTGC CCCTAAAGGC CAGATGACAG CAGTTGTTGG	6600
GCCGACAGGT TCAGGAAAAA CGACTATTAT GAACCTCATC AATCGCTTTT ATGATGTGTA	6660
TGCTGGTGGT ATTTATTTTG ATGGTAAAGA CATTCGTGGC TATGACTTAG ATAGTCTTAG	6720
AAGCAAGGTG GGAATTGTAT TGCAAGATTC GGTCTTGTTT AGCGGAACGA TTAGAGACAA	6780
TATCCGATTT GGTGTGCCAG ATGCTAGTCA GGAAATGCTT GAGGTAGCAG CAAAAGCAAC	6840
CCACATTCAC GACTATATCG AAAGTTTGCC TGATAAGTAC GATACTCTTA TTGATGATGA	6900
CCAGAGCATC TTTTCAACAG GGCAGAAGCA ATTGATTTC AATCGCTCGAA CCCTGATGAC	6960
AGATCCAGAA GTTCTCATTC TCGATGAAGC AACTTCAAAC GTAGATACGG TGACAGAAAG	7020
CAAGATTCAG CATGCCATGG AGGTGGTTGT AGCAGGTAGA ACTAGTTTCG TCATTGCCCA	7080
CCGCTTGAAA ACCATTCTCA ATGCAGATCA GATTATTGTC CTTAAAGATG GAGAAGTCAT	7140
TGAACGTGGT AACCACCATG AACTTTTGAA GCTAGGTGGC TTTTATTTCAG AACTCTATCA	7200
CAATCAATTT GTTTTCGAAT AAGAAAGAAG TTGTCTATG TGGGCAGCTT TTTCTGTCC	7260
ATAAAAAATG TTTATCACAG CCTTAAAAA AACATATTAG ACGAAAGTCA TTTTGAGTGA	7320
TATGATAGGA CTATCGTTAG CATTCGAAAG GAGAGGCATC ATGGCTAGAA CGTTGTAGG	7380
AGTTGCTGCA AATCTATGTC CCGTAGACGC AGAAGGCAAA ATCATTCAAT CATCTGTATC	7440

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TTGTAGATTC GCAGAGATCA TTCGTCAAGT CGGTGGTCTC CCTTTAGTCA TTCTGTGG	7500
TGATGAGTCA GTTGTACGTG ATTATGTGGA AATGATTGAC AAACCTATTT TGACAGGAGG	7560
CCAAAAATGTT CATCCTCAGT TTTATGGAGA GAAAAAGACC GTCGAGAGCG ATGATTACAA	7620
TCTGGTCCGT GACGAATTTG AATTGGCACT CTTGAAGGAA GCGCTTCGTC AGAATAAACC	7680
AATTATGGCA ATCTGTCGCG GTGTCCAAC TGTCAATGTT GCCTTTGGTG GAACCCCTCA	7740
TCAAGAAATC GAAGGTCAGG	7760

(2) INFORMATION FOR SEQ ID NO: 64:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 2723 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 64:

GAGGTTTTAA TTCACTTACC TCTSCCGTAT CTTTATTTAA AATGAATTCT TTTACGGTTG	60
TATTTCCTGC AAAATCTTTT ACAACAATCT TAATGTTTAG TGTCTTGTCT ATTATTTGTT	120
TAATATCATT AAATGATGTA TATTCTTTTC CATTATATA AATATGTTGT TCTTGAATCT	180
CACCATCGAA TCCATTATTT CTTTATCAT TGATGTTAAA GACTACAGAT TTTCCATCAG	240
CATATTCGAT ACTAGTATTT CCCTTAGGAT CAATGTTTAC TTCGGGTTTA ACATTATCAT	300
ATAAAAACTG ATAGTGGACT CCAACTGCTT TAGCATTCAA ATCGCTATAG CCAGTTTGAA	360
GATAAACATT TCCATCCATA TCTGTTACCT TATCTGGAAA TCCGTTTGCT TTATAGTCTT	420
TCATTCCCCA GTCCATGATG TCACCGTCTT TAACATTCAG CTTAATATTA AAATCTCTAG	480
TGTTATCAAT GTGTAAATCT CCGTAGATTA AATAATTATC TACAACCGAT TCATTAACTC	540
TCAATTCCCA GTTAAACCA CCCTTATCAG AAATCTTACC TCTTAAATAA AATTCTGGAT	600
TTCTGACATA AATTTTATTA GATTAGATG GATTAAAGTA GTTCTTATCC ATTGAAAGGT	660
TTACTGGTTT GGTATCAATA AATAACATGG AGCCATCTTC TTTTATAGCT TCTACATTGA	720
ACTTATCCTC TCCAGTGTAT TCTTTATCAT CCTTACCAA TAATACAAGT TTAGAAGAAT	780
CTGTACAAG ATTTCCGTCT TTATCGATAG CTTCCCTTT ATCGTTCATT TTAAATGTAA	840
ACACTTGATA CCTTATAATG TTAAAGCCGT CCAAAGCCGA CATTAAATACA GATTGGGTAC	900
TTCTTCCATC TTCAACATTT CTACTATCAG CATAAATTGT TGTCTCTGAA AGGGCTCTTA	960
GATTAGGATT GGCCTTTTGT ATTTTGTGCTA TATCTTCCTT GCTATAGACT CCATTTCTCT	1020

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CTAACATATC CGTTTTTCCA GGATTATAGG TAGTCACTTT TAGTGCATAG CCTTTTCTTA	1080
GAATGATATT ATCCTTTAAC AGATATTGTT GTTTTCTGA ATCAGAATAG ATTTTACCAG	1140
ATTCCATTTT AGTTAAATG TCTGGTTGT TTTTGAAAG ATCTCCTTCC CCTAATTCTA	1200
TGACATTCCC ATAAC TTGAT ACATAGGGAT ATTCTGATTT AGTTTCCTTA ATTTTTCAG	1260
GCATTCTAAT TTAAATTTCA GCTTTTTTCT GATCATTATC TTAAACAAAT AATCTCATAT	1320
CTCCTGCAAA AGCTAATCCA TCCACAATAT CATTAATATT AGCGTATAGA TCAAATGTCA	1380
TCGTTTTTGA GTGGAAATCA TACTTGGTCG CTTTGATTTC TATAGATTTA TAGTTATTCC	1440
CATAATATAC CTTGGCATT TTAGAACAT TACTTATCTT TCCAAGAATT TCAAAGTCTC	1500
CATCTTTAGA CGGACTTAGA ACACCATAAA TTTTGTGATT GATTTCGTCA AGTTTCTCAG	1560
TTTCATATTC TAGATCAGTC CCATCATCGT AGGCTATTAT ATTTCTTTTA TCATCGTATT	1620
TATAATCGTA TTCCCTCCATT CTCTTACCAG TTCACTTGT AAAATCATCA ACTTCTCTAA	1680
ATTTCTTTTT AATGAGTTTC TTAAAGTCTT TATTTTCAAA GTCTCTAATT GTTGAAATAT	1740
TTCTATCAAT AGTAAACTA GATTTTCTT TAATAGACTC TTCATTTTCT TGATGATGAT	1800
GTCTACCCC AGTTGTATCT TTTTGTAGAC TACCCTCTTT TCCATTTCTT AAATTTTAA	1860
ATTTAGATTC TGCAATCTCG CCAAGCTTTT GATATTTAGA TGAATCTTGA TCAGGATCTA	1920
CTAGATAATA GGAAATCATC CCCTTTTCAT CAGCCTGATT AGCAAATTTA ATCTATGAA	1980
TCTTTGTGAA ATTGCTAGAA CCATCTAATG CAATGACTTC AATGATTTT CCCCTTAAAT	2040
CTCCCGCACC TTAAATTTCA TAAATGGTAT TTCCGTCTTT ATCAAGTTTT CTATTTCTTC	2100
CTTGACCCTC ACCTGCGTAA GTTACTTCAA GATTTTTTTC AACCTCTCCA TCTTCATTAA	2160
CAAGAGCGGC GCCAGCATAC CAACTTCGT TCGCAATCTC GTCAAATTTT TCAGGATGTT	2220
CTTTTGTATC TCTCGCAAAT AGCGTTTCAT TCTTATACTG ATCTTTTACC TTATGATAAG	2280
TATCCTTTGT AATCAACTTA ATTTTTCAG GATTGAAAA ATCAACCGAA ACAATCTTAG	2340
GGCGGTGTT ATCAATTTTT ACAGGAATAT AGGAAACCTG CCATGGGTAA TCTTTAGTTA	2400
ATCTATATTT AAATTTATAG AAATATTGAC CTTCCGCAAT CGGTTCAAAT TGACCTCTTA	2460
TCTTAGTAGC AGGATCTTGA TTATCCTTAC TTTCTGGTGC ATTTTCTTCT CTACCTCTAG	2520
GATTATAGAT GAGTCCATCC CACTTCAAGT CACCCCAAAC TTTAGTTTA GATGATTGA	2580
TTCCCTTTCG ATCATTGCTT TTAGAATTTA AAATTCCTCT AATAAAGTGT TCTCTCGAAA	2640
TGACTTTTAA GTCTCTTGA TTTCTCCCT CTTATTGTG ATTTACTATT GAAATCAATC	2700
CTTCTTCTGC ACTTCTTAAT ACA	2723

(2) INFORMATION FOR SEQ ID NO: 65:



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## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 11831 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 65:

AAAAAAGTGG GAATGACTCA AATCTTCACT GAAGCTGGCG AATTGATCCC TGTAACAGTT	60
ATTGAAGCAA CTCCAAACGT TGTTCCTCAA GTTAAACTG TTGAACAGA CGGATACAAC	120
GCTATCCAAG TTGGTTTCGA TGACAAACGC GAAGTATTGA GCAACAAACC TGCTAAAGGA	180
CATGTAGCGA AAGCTAACAC GGCTCCTAAG CGCTTCATTC GTGAATTCAA AAACGTTGAA	240
GGCTTGGAAG TTGGTGCTGA AATTACAGTT GAAACATTCG CAGCTGGAGA CGTTGTTGAC	300
GTAACGGGTA CTTCTAAAGG TAAAGGTTTC CAAGGTGTTA TCAAACGCCA CGGACAATCA	360
CGTGGACCAA TGGCTCACGG TTCTCGTTAC CACCGTCGTC CAGGTTCTAT GGGGCCTGTT	420
GCACCTAACC GCGTATTCAA AGGTAAAAAC CTTGCAGGAC GTATGGGTGG CGACCGCGTA	480
ACAATTCAAA ACCTTGAAGT TGTACAAGTT GTTCAGAAA AGAACGTTAT CCTTATCAAA	540
GGTAACGTAC CAGGTGCTAA GAAATCTCTT ATCACTATCA AATCAGCAGT TAAAGCTGGT	600
AAATAATAAA GAAAGGGGAA ATCAGTCACA ATGGCAAACG TAACATTATT TGACCAAACT	660
GGTAAGAAG CTGGCCAAGT TGTTCCTAGC GATGCAGTAT TTGGTATCGA ACCAAATGAA	720
TCAGTTGTGT TTGATGTAAT CATCAGCCAA CGCGCAAGCC TTCGTCAAGG AACACACGCT	780
GTTAAAAACC GCTCTGCAGT ATCAGGTGGT GGACGCAAAC CATGGCGTCA AAAAGGAACT	840
GGACGTGCTC GTCAAGGTTT TATCCGCTCA CCACAATGGC GTGGTGGTGG TGTGTCTTTC	900
GGACCAACTC CACGTTTATA CGGCTACAAA CTTCCACAAA AAGTTCGTCG CCTAGCTCTT	960
AAATCAGTTT ACTCTGAAAA AGTTGCTGAA AACAAATTCT TAGCTGTAGA CGCTCTTTCA	1020
TTTACAGCTC CAAAACTGC TGAATTTGCA AAAGTTCTTG CAGCATTGAG CATCGATTCT	1080
AAAGTTCTTG TTATCCTTGA AGAAGGAAAT GAATTCGCAG CTCTTTCAGC TCGTAACCTT	1140
CCAAACGTGA AAGTTGCAAC TGCTACAACT GCAAGTGTTT TTGACATCGC AAATAGCGAC	1200
AACTTCTTTC TCACACAAGC AGCTATCTCT AAAATCGAGG AGGTTCTTGC ATAATGAATT	1260
TGTATGATGT TATCAAAAAA CCTGTCTATCA CTGAAAGCTC AATGGCTCAA CTGAAGCAG	1320
GAAAAATATG ATTTGAAGTT GACTATCTGT CACACAAACT TTTGATCAAG CAAGCTGTTG	1380
AAGCTGCTTT CGAAGGTGTT AAAGTTGCCA ATGTTAACAC AATCAACGTA AAACCAAAAG	1440

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CTAAACGTGT TGGACGTTAC ACTGGTTTTA CTAACAAAC TAAAAAGCT ATCATCACAC	1500
TTACAGCTGA TTCTAAAGCA ATCGAGTTGT TTGCTGCTGA AGCTGAATAA TCTAAGGAGG	1560
AAATATCGTG GGAATTCGTG TTTATAAACC AACAAACAAAC GGTGCGCCGTG ATATGACTTC	1620
TTTGGATTTC GCTGAAATCA CAACAAGCAC TCCTGAAAAA TCATTGCTTG TTGCATTGAA	1680
GAGCAAGGCT GGTGCGTAACA ACAACGGTCG TATCACAGTT CGTCACCAAG GTGGTGGACA	1740
CAAACGTTTC TACCGTTTGG TTGACTTCAA ACGTAATAAA GACAACGTTG AAGCAGTTGT	1800
TAAAAAATC GAGTACGATC CAAACCGTTC TGCAACATC GCTCTGTAC ACTACACTGA	1860
CGGTGTGAAA GCATACATCA TCGCTCCAAA AGGTCTTGAA GTAGGTCAAC GTATCGTTTC	1920
AGGTCCAGAA GCAGATATCA AAGTCGGAAA CGCTCTTCCA CTTGCTAACA TCCCAGTTGG	1980
TACTTTGATT CACAACATCG AGTTGAAACC AGGTCGTGGT GGTGAATTGG TACGTGCTGC	2040
TGGTGCACTT GCTCAAGTAT TGGGTCTGA AGGTAAATAT GTTCTTGTTT GTCTTCAATC	2100
AGGTGAAGTT CGTATGATTC TTGGAACCTG CCGTGCTACA GTTGGTGTGG TCGGAAACGA	2160
ACAACATGGA CTTGTAAACC TTGGTAAAGC AGGACGTAGC CGTTGGAAAG GTATCCGCCC	2220
AACAGTTCGT GGTTCGTGTA TGAACCCTAA CGATCACCCA CACGGTGGTG GTGAAGGTAA	2280
AGCACCAAGT GGTGCTAAAG CACCATCTAC TCCATGGGGC AAACCTGCTC TTGGTCTTAA	2340
AACTCGTAAC AAGAAAGCGA AATCTGACAA ACTTATCGTT CGTCGTGCGA ACGAGAAATA	2400
ATATTAACT AGTCGCTTAA GCAACTAGTA AATCCGCCAG CTCGGTAGCG CTCATAGGA	2460
GTGCAAGCCG CTGTGGTACA ACATTTAAAG GAGAAAAATAT AAAAATGGGA CGCAGTCTTA	2520
AAAAAGGACC TTTGCTCGAT GAGCATTGTA TGAAAAAAGT TGAAGCTCAA GCTAACGACG	2580
AAAAGAAAAA AGTTATTAAA ACTTGGTCAC GTCGTTCAAC GATCTTCCCA AGTTTCATTG	2640
GTTACACTAT TGCAAGTTAT GACGGACGTA AACACGTACC TGTTTACATC CAAGAAGACA	2700
TGGTAGGCCA CAAACTTGGT GAATTTGCAC CAACTCGTAC TTACAAAGGT CACGCTGCAG	2760
ACGACAAGAA AACACGTAGA AAATAAGGAG AACATAAATG GCAGAAATTA CTTACAGCTAA	2820
AGCAATGGCT CGTACAGTAC GTGTTTCACC TCGTAAATCA CGTCTTGTTT TTGATAACAT	2880
CCGTGGTAAA AGCGTAGCCG ATGCAATCGC AATCTTGACA TTCACTCCAA ACAAAGCTGC	2940
TGAAATCATC TTGAAAGTTT TGAACCTAGC TGTAGCTAAC GCTGAAAACA ACTTTGGTTT	3000
GGATAAGCT AACTTGGTAG TATCTGAAGC ATTCGCAAAC GAAGGACCAA CTATGAAACG	3060
TTTCCGTCCA CGTGCAGAAAG GTTCAGCTTC ACCAATCAAC AAACGTACAG CTCACATCAC	3120
TGTAGCTGTT GCAGAAAAAT AAGGAGGTAA AATCGTGGGT CAAAAAGTAC ATCCAATTGG	3180
TATGCGTGTC GGCATCATCC GTGATTGGGA TGCCAAATGG TATGCTGAAA AAGAATACGC	3240

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GGATTACCTT CATGAAGATC TTGCAATCCG TAAATTCGTT CAAAAAGAAC TTGCTGACGC	3300
AGCAGTTTCA ACTATTGAAA TCGAACGCGC AGTAAACAAA GTTAACGTTT CACTTCACAC	3360
TGCTAAACCA GGTATGGTTA TCGGTAAAGG TGGTGCTAAC GTTGATGCAC TCCGTGCAAA	3420
ACTTAACAAA TTGACTGGAA AACAAGTACA CATCAACATC ATCGAAATCA AACAACTGA	3480
TTTGGATGCT CACCTTGTAG GTGAAGGAAT TGCTCGTCAA TTGGAGCAAC GTGTGCTTT	3540
CCGTCGTGCA CAAAAACAAG CAATCCAACG TGCAATGCGT GCTGGAGCTA AAGGAATCAA	3600
AACTCAAGTA TCAGGTGCTT TGAACGGTGC AGATATCGCC CGTGCTGAAG GATACTCTGA	3660
AGGAACTGTT CCGCTTCACA CACTTCGTGC AGATATCGAT TACGCTTGGG AAGAAGCAGA	3720
TACTACATAC GGTAACTTG GTGTAAAGT ATGGATCTAC CGTGGTGAAG TTCTTCCAGC	3780
TCGTAAAAAC ACTAAAGGAG GTAAATAACC AATGTTAGTA CCTAAACGTG TTAACACCG	3840
TCGTGAGTTC CGTGGAAAA TGCGCGGTGA AGCAAAAGGT GGAAAAGAAG TAGCATTCCG	3900
TGAATACGGT CTTCAAGCTA CAACTAGCCA CTGGATCACT AACCGCCAAA TCGAAGCTGC	3960
TCGTATCGCC ATGACTCGT ACATGAAACG TGGTGGTAAA GTTTGGATTA AAATCTTCCC	4020
ACACAAATCA TACTGTCTA AAGCTATCGG TGTGCGTATG GGATCTGGTA AAGGGGCACC	4080
TGAAGGTGG GTAGCACCAG TTAACGTGG TAAAGTGATG TTCGAAATCG CTGGTGATC	4140
TGAAGAGATT GCACGTGAAG CGCTTCGACT TGCTAGCCAC AAATTGCCAG TTAATGTAA	4200
ATTCGTAATA CGTGAAGCAG AATAAGGAGA AGGCATGAAA CTTAATGAAG TAAAGAATT	4260
TGTTAAAGAA CTTCTGGTC TTTCTCAAGA AGAACTCGCG AAGCGCGAAA ACGAATTGAA	4320
AAAAGAATTG TTTGAATTC GTTTCCAAGC TGCTACTGGT CAATTGGAAC AAACAGCTCG	4380
CTTGAAAGAA GTTAAAAAC AAATCGCTCG CATCAAAACA GTTCAATCTG AAGCGAAATA	4440
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CCCAGTCTAT GGTAAACGTA TTAATACTC TAAAAATAC AAAGCTCATG ATGAAAACAA	4620
TGTTGCCAAA GAAGGCGATA TCGTACGTAT CATGGAAACT CGCCCGCTTT CAGCTACAAA	4680
ACGTTTCCGT CTTGTAGAAG TTGTTGAAGA AGCGGTCATC ATCTAATCAA ACCTGAAAGG	4740
AGAAAATGA AATGATTCAA ACAGAACTC GTTTGAAAGT CGCAGACAAC AGCGGTGCTC	4800
GCGAAATCTT GACTATCAAA GTTCTTGGTG GTTCAGGACG TAAATTGCA AACATCGGTG	4860
ATGTTATCGT GGCATCTGTA AAACAAGCTA CTCCTGGTGG TCGGGTTAAA AAAGGTGACG	4920
TTGTTAAAGC AGTTATCGT CTTACTAAAT CAGGTGCTCG TCGTGCTGAT GGTTCATACA	4980

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TCAAATTTGA CGAAAACGCA GCAGTTATCA TCCGTGAAGA CAAAACTCCT CGCGGAACAC	5040
GTATCTTTGG CCCAGTTGCA CGTGAATTGC GTGAAGGTGG CTTTCATGAAG ATCGTGTAC	5100
TTGCTCCAGA AGTACTTTAA TTTTATAGGAA CAACTAGTC CCCTAGCTTC AAGCTAGGGT	5160
GCCCTTATGG GCGTAAGAAA AATCAAGGAG AAACCTAATG TTTGTAAAAA AAGGCGACAA	5220
AGTTCGCGTA ATCGCTGGTA AAGATAAGGG AACAGAAGCT GTTGTCCCTTA CTGCCCTTCC	5280
AAAAGTAAAC AAAGTTATCG TTGAAGGTGT TAACATTGTT AAGAAACACC AACGTCCAAC	5340
TAACGAGCTT CCTCAAGGTG GTATCATCGA GAAAGAAGCA GCTATCCACG TATCAAACGT	5400
TCAAGTTTGG GACAAAAATG GTGTAGCTGG TCGTGTGGA TACAAATTTG TAGACGGTAA	5460
AAAAGTTCGC TACAACAAAA AATCAGGCGA AGTGCTTGAT TAATCACGAA GAAAGGAGA	5520
AGTATAATGG CAAATCGTTT AAAAGAAAAA TATCTTAATG AAGTAGTTCC TGCTTTGACA	5580
GAACAATTCA ACTACTCATC AGTGATGGCT GTGCCTAAAG TAGATAAGAT TGTTTTGAAC	5640
ATGGGTGTTG GTGAAGCTGT ATCAAACGCT AAAAGCCTG AAAAGCTGC TGAAGAATTG	5700
GCACTTATCT CAGGTCAAAA ACCACTTATC ACTAAAGCTA AAAATCAAT CGCCGGCTTC	5760
CGTCTTCGTG AAGGTGTTGC GATCGGTGCA AAAGTTACCC TTCGTGGTGA ACGTATGTAC	5820
GAATCTTGG ATAAATTTGG ATCAGTTTCA CTTCCACGTG TACGTGACTT CCACGGTGTC	5880
CCAACAAAAT CATTTGATGG ACGCGGGAAC TACACACTTG GTGTGAAAGA ACAATTAATC	5940
TTCCCAGAAA TCAACTTCGA TGACGTTGAC AAAACTCGTG GTCTTGACAT CGTTATCGTA	6000
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GCAAAATAAT ATAGGAGGTA AATCTAATGG CTAATAAATC AATGGTAGCT AGAGAGGCTA	6120
AACGCCAAAA AATTGTTGAC CGTTATGCTG AAAAACGTGC TGCATTAAAG GCGGCAGGGG	6180
ACTACGAAGG TTTATCTAAA TTACCTCGCA ACGCCTCACC GACTCGTTTA CATAATCGTT	6240
GTAGGGTTAC GGGGCGCCCA CATTCAAGTT ACCGCAAAAT TGGTCTGAGT CGTATCGCTT	6300
TTTCGGAAGT TCGGCATAAA GGTCAAATC CTGGTGTAAC AAAAGCATCT TGCTAATTTA	6360
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TTTGAACACG AGCTACAGCT TTGGCAAAAA AGACCAATTT GCTTTGGAGC ATTGCTTCTG	6540
CATTAAATTG TCTATTTTGG CTCGTGCTGT TACGCTCTTT GTATCATGTA TTAAGTAGCA	6600
AGTGCAACTT GCAAACTACT AGTAAGAGGA GAAAAACAAA ATGGTTATGA CTGACCCAAT	6660
CGCAGACTTC CTAAGTCGTA TTCGTAATGC TAACCAAGCT AAACACGAAG TACTTGAAGT	6720
ACCTGCATCA AACATCAAAA AAGGGATTGC TGAAATCCTT AAACGCGAAG GTTTTGTAAG	6780

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AAACGTTGAA ATCATGGAAG ATGACAAACA AGGCGTCATC CGTGTATTTC TTAAATACGG	6840
ACCAAATGGT GAGAAAGTTA TCACTAACTT GAAACGTGTT TCTAAACCAG GACTTCGTGT	6900
CTACAAAAAA CGTGAAGACC TTCCAAAAGT TCTTAACGGA CTGGAATTG CCATCCTTTC	6960
AACTTCTGAA GTTTGGCTTA CTGATAAGA AGCACGCCAA AAGAATGTTG GTGGTGAGGT	7020
TATCGCTTAC GTTTGGTAAA ATCAAGATAC AAAGCTCGTA AAGAACAAG CAAAATTAGG	7080
AAGTTGGAGA AGTTTGTTTA CAAACAAGCC AACTTATCTA TTTTGCACAG TTCTTAGAGC	7140
GTGTTCAAGT CAGCTCTTGA ACTAATAAG TATCTGAACC CCGTGAAAAC TGGCCGTTCT	7200
GGCCTGACAA TTAAACAGGA GAAAATAAAC ATGTCACGTA TTGGTAATAA AGTTATCGTG	7260
TTGCCTGCTG GTGTTGAACT CGCTAACAAAT GACAACGTTG TAACTGTAAA AGGATCTAAA	7320
GGAGAACTTA CTCGTGAGTT CTCAAAGAT ATTGAAATCC GTGTGGAAGG TACTGAAATA	7380
ACTCTTCACC GTCCAAACGA TTCAAAGAA ATGAAAACTA TCCACGGAAC TACTCGTGCC	7440
CTTTGAACA ACATGGTTCT TGGTGATCA GAAGGATTCA AGAAAGAACT TGAAATGCGT	7500
GGGGTTGGTT ACCGTGCACA GCTTCAAGGA TCTAAACTTG TTTTGGCTGT TGGTAAATCT	7560
CATCCAGACG AAGTTGAAGC TCCAGAAGGA ATTACTTTTG AACTTCCAAA CCCAACAACA	7620
ATCGTTGTTA GCGGAATTTT AAAAGAAGTA GTTGGTCAAA CAGCTGCTTA CGTACGTAGC	7680
CTTCGTTTAC CAGAACATA TAAAGGTAAA GGTATCCGTT ACGTTGGTGA ATTCGTTTCG	7740
CGTAAAGAAG GTAAACAGG TAAATAATGT TGAGTGGTTG ATCATCAACC ACCAACCTAT	7800
TTTCCAACIT TGTGCATAGC ACACGATTTA AAATAAAGA GGTGAAAAC GTGATTTCAA	7860
AACCAGATAA AAACAAACTC CGCCAAAAC GCCACCGTCG CGTTCGCGGA AAATCTCTG	7920
GAACGTCTGA TCGCCACGT TTGAACGTAT TCCGTTCTAA TACAGGCATC TACGCTCAAG	7980
TGATTGATGA CGTAGCGGT GTAACGCTCG CAAGTGCTTC AACTCTTGAT AAAGAAGTTT	8040
CAAAGGAAC TAAACTGAA CAAGCCGTTG CTGTCGGTAA ACTCGTTGCA GAACGTGCAA	8100
ACGCTAAAGG TATTTAGAA GTGGTGTTTC ACCGCGGTGG ATATCTATAT CACGGACGTG	8160
TGAAAGCTTT GGCTGATGCA GCTCGTGAAC ACGGATTGAA ATTCTAATAG GAGGACACTA	8220
GAAAATGGCA TTAAAGACA ATGCAGTTGA ATTAGAAGAA CGCGTAGTTG CTGTCAACCG	8280
TGTTACAAAA GTTGTTAAAG GTGGACGTCG TCTTCGTTTC GCAGCTCTTG TTGTTGTTGG	8340
TGACCACAAT GGTCGCGTAG GATTGGTAC TGGTAAAGCT CAAGAAGTTC CAGAAGCAAT	8400
CCGTAAAGCA GTAGATGATG CTAAGAAAA CTTGATCGAA GTTCCTATGG TTGGAACAAC	8460
AATCCACAC GAAGTTCCTT CAGAATTCGG TGGAGCTAAA GTATTGTTGA AACCTGCTGT	8520

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AGAAGGTTCT GGAGTTGCCG CTGGTGGTGC AGTTCGTGCC GTTGTGGAAT TGGCAGGTGT	8580
GGCAGATATT ACATCTAAAT CACTTGGTTC TAACACTCCA ATCAACATTG TTCGTGCAAC	8640
TGTTGAAGGT TTGAAACAAT TGAAACGCGC TGAAGAAATT GCTGCCCTTC GTGGTATTTT	8700
AGTTTCTGAT TTGGCATAAG AAAGGGGATA AAATGGCTCA AATTAAAAAT ACTTTGACTA	8760
AGTCTCCAAT CGGACGCATT CCATCACAAC GTAAAACTGT TGTAGCACTT GGAATTGGCA	8820
AATTGAACAG CTCTGTTATT AAAGAAGATA ACGCTGCTAT CCGTGGTATG ATCACAGCAG	8880
TATCTCACTT AGTAACAGT GAAGAAGTAA ACTAATGAAG TTTTAGGGGA TGTGCACTGT	8940
ACCATCCCCT AAAACTAGAT ATAGTCATCT ATGATGACAT CGTATAGGCG AGTTGATGGG	9000
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TGAAACTTCA TGAATTGAAA CCTGCAGAAG GTTCTCGTAA AGTACGTAAC CGCGTTGGTC	9120
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TTGTTAAAGC TGAAAAGTCA GGTATTAAAA TTCTTGGTAA CGGTGAGTTG ACTAAGAAAT	9420
TGACTGTGAA AGCAGCTAAA TTCTCTAAAT CAGCTGAAGA AGCTATCACT GCTAAAGGTG	9480
GTTCAGTAGA AGTCATCTAA GAGAGGTGAC CTATGTTTTT TAAATTATTA AGAGAAGCTC	9540
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GTATCGGAAC TAGCATTACA GTTCCTGGTG TGAATGCCAA TAGCTTGAAT GCTTTAAGTG	9660
GATTATCCTT CTTAAACATG TTGAGCTTGG TGTCGGGGAA TGCCCTAAAA AACCTTTCGA	9720
TTTTTGCCCT AGGAGTTAGT CCTATATCA CCGCTTCTAT TGTTGTCCAA CTCTTGCAAA	9780
TGATATTTTT ACCCAAGTTT GTAGAGTGGG GTAAACAAGG GGAAGTAGGT CGAAGAAAAT	9840
TGAATCAAGC TACTCGTTAT ATTGCTCTAG TTCTCGCTTT TGTGCAATCT ATCGGGATTA	9900
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TTTTTCTGAC GATTGGTATC ATCTTAACAG CTGGTAGTAT GATTGTCACT TGGTTGGGTG	10020
AGCAAATTAC AGATAAGGGA TACGGAACG GTGTTTCCAT GATTATCTTT GCCGGGATTG	10080
TTTCCTCAAT TCCAGAGATG ATTCAGGCA TCTATGTGGA CTACTTTGTG AACGTCCCAA	10140
GTAGCCGTAT CACTTCATCT ATCATTTTCG TAATCATTTT GATTATTACT GTATTGTTGA	10200
TTATTACTT TACAACCTAT GTTCAACAAG CAGAATACAA AATTCCAATC CAATATACTA	10260
AGGTTGCACA AGGTGCTCCA TCTAGCTCTT ACCTTCCGTT AAAAGTAAAC CCTGCTGGAG	10320

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TTATCCCTGT TATCTTTGCC AGTTCGATTA CTGCAGCCTG CGGCTATTCT TCAGTTTMTG	10380
AGTGCCACAG GTCATGATTG GGCTTGGGTA AGGGTAGCAC AAGAGATGTT GGCAACTACT	10440
TCTCCAACCTG GTATTGCCAT GTATGCTTTG TTGATTATTC TCTTTACATT CTTCTATACG	10500
TTTGATACAGA TTAATCCTGA AAAAGCAGCA GAGAKCCTAC AAAAGAGTGG TGCCTATATC	10560
CATGGAGTTC GTCCTGGTAA AGGTACAGAA GAATATATGT CTAAACTTCT TCGTCGTCTT	10620
GCAACTGTTG GTTCCCTCTT CCTTGGTGTG ATTTCCATT TACCGATTGC AGCTAAAGAT	10680
GTATTTGGTC TTTCTGATGT TGTGCTTTT GGTGGAACAA GTCTCTTGAT CATTATCTCT	10740
ACAGGTATCG AAGGAATCAA GCAATTGGAA GGTACCTAT TGAAACGTAA GTATGTTGGT	10800
TTCATGGACA GAACAGAATA AAAGTATTTA CTGAATCAGT AAATACTGAG GGAGTGGAGG	10860
TTTAAACTCT GACATTTGTA AGAGTTGGAT CTCCTCTCTT CTATTTTGT TTTAAATCGG	10920
GGTGAAAAGA CTTTGTGCTT CTATTTAAAA ATAAAATAAG GAGATCAAAT CATGAATCTT	10980
TTGATTATGG GCTTACCTGG TGCAGGTAAG GGAACCTAAG CAGCAAAAAA CGTAGAACAA	11040
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GAAATGGGTG TTCTTGCTAA GTCATATATT GACAAGGGTG AATTGGTTCC TGACGAAGTT	11160
ACAAATGGAA TCGTAAAAGA ACGCCTTTCA CAAGATGATA TTAAAGAAAC AGGATTCTTA	11220
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CTTGGCATTG AACTAGAAGG TGTATCAAT ATTGAAGTA ACCCTGACAG CCTTTTGGAA	11340
CGTTTGAGTG GCGTATCAT CCACCGCGTA ACTGGAGAAA CTTTCCACAA GGTCTTTAAC	11400
CCACCAGTTG ACTATAAGA AGAAGATTAC TACCAACGTG AAGATGATA GCCTGAGACA	11460
GTAAAACGTC GTTTGGATGT TAATATTGCT CAAGGAGAAC CAATCATTCG TCACTACCGT	11520
GCCAAAGGTT TGGTTCATGA CATCGAAGGT AATCAAGATA TCAATGATGT CTTCTCAGAT	11580
ATTGAAAAAG TATTGACAAA TTGAAATAA AGCGTTTTC AACTTGCAA AAATCCGCTA	11640
CAATGTTAT ACTGAGATAG TCTGACTTAT AATTGTTGTC TCTGTGTCTA GAGGCATCGA	11700
ATCGAAATTT ATGGAGGTGC TTTGCGTGG CAAAAGACGA TGTGATTGAA GTTGAAGGCA	11760
AAGTAGTTGA TACAATGCCG AATGCAATGT TTACGGTTGA ACTTGAAAAA GGACATCAGA	11820
TTTtagcagg G	11831

(2) INFORMATION FOR SEQ ID NO: 66:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 10726 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 66:

CCCGGCATTT GAAAGCTATT CGTGAAGGAT TTATGATGGC AATGCCTTTG ATTTTAGTCG	60
GCTCTTTATT TCTTATTCTA ATCAGTTGGC CTCAAGAGGC TTTTACAAAT TGGCTGAATA	120
GTGTGGGATT GCTAAGTATC TTGACAACTA TGAATCAGTC AACAGTAGCG ATTATCTCCT	180
TGGTCGCTTG TTTCCGTATT GCCTACAGGT TGTCGGAAGG ATATGGTACA GATGGTCCGT	240
CGGCAGGGAT CATAGCCTTA TCCAGTTTGG TATGATGGC ACCTCGTTTT TCGAGTATGG	300
TTTATGATAA AAATGGGGAG CAGGTCAAGC AGTTATTTGG CGGCGCAATA CCATTTTCTA	360
GCCTGAATGC ATCTTCTTTG TTTATGGCGA TTACTATTGG ATTGGTTACA GCAGAGATTT	420
ATCGTATGTT TATCCAGCGC GGAATTACGA TAAAAATGCC AAGTGGTGTC CCAGATGTAG	480
TAAGTAAATC ATTTTCAGCT CTMTTATCTG GTTTTACTAC TTTTGTTTTG TGGGCTTTGG	540
TCTTAAAAGG TCTTGAAGCG GCAGGAGTTG CAGGAGGTCT CAACGGACTC CTAGGTGCAA	600
TTGTGGGAAC ACCGCTTAAG TTAATTGCAG GAACGCTTCC AGGTATGATT CTATGTGTTA	660
TTGTAAACTC ATTCTTTTGG TTCTGTGGAG TTAATGGGGG ACAAGTTTTA AATGCTTTTG	720
TAGACCCAGT TTGGTTACAA TTTACTACAG AAAACCAAGA AGCTGTGGCT GCAGGACAAA	780
CACTCCAACA CATTATTACA TTACCGTTTA AAGATTTATT TGTATTTATT GGTGGCGGTG	840
GAGCGACTAT TGGTCTTGGC ATTTGTCTCT TCCTATTTAG TAAGAGTCGT GCGAATAAAA	900
CATTAGGTAA GCTAGCTATT ATACCGTCTA TTTTAAATAT CAATACAGCT ATTCTATTTA	960
CGTTTCCAAC AGTTTTAAAT CCGATTATGC TGATTCCGTT TATTGCTACT CCTACAATCA	1020
ATGCCTTGAT TACCTATGTA TCAATGGCTG TAGGATTAGT ACCCTATACA ACAGGTGTAA	1080
TCCTTCCGTG GACAATGCCA CCGATTATAG GAGGCTTCCT TGCAACAGGG GCTAGTTGGC	1140
GAGGAGCTCT ATTACAAGTT GTTTTGATTT TGGTTTCTGT AGCAATTTAT TATCCATTCT	1200
TCAAAATGTC AGATAAACGC AATCTTGAAA AAGAAAAAGC TACTGTTGGA GGGAAATAAG	1260
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TACCGAATGT TTCATGAATT TGGGGTTGTG TATACTAGAC CAGGGCGCAG ACATGACTTT	1560
GTCCAGAGT TACGATTGTA AGATTTTTTA GATAAACAGC TATCTATAGA TGAACAGCC	1620



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AGTTACTATC ATAGGGGAGT ATGTATAGAG GGAGCGGATT CATTTGAAAA TATACTAGAT	1680
TTCATTGATT GGCTACCTAA GATTGGGATG AACAGTTTTT TCATCCAGTT TGAAAATCCT	1740
TACTCTTTTT TGAAACGTTG GTATGAACAT GAATTTAATC CATATCTAAA TAAAGAACAA	1800
TTTTCAAATG AATTAGTACA AGAATTGAGT GATAGGTTGG ATAAAGAATT GCAAAAAAGA	1860
GGTCTTATTC ATCATCGTGT TGGTCATGGA TGGACAGGTG AAGTTTTAGG TTACTCTTCA	1920
AAATTTGGCT GGAATCAGG TCTTAGTATT TCAGAGGAGA AGAAACCCTA TGTCGCTGAA	1980
ATAAACGGGA AACGAGAATT GTTTAATACG GCTCCGATTT TAACCAGCCT GGATTTTTCA	2040
AATCCAGATG TAGCTGATAA GATGGTAGAA ATTATCAAGG ATTATGCCAA GAAAAGACCT	2100
GATGTTAACT ACTTACATGT ATGGTTGTCG GATGCTCGTA ATAATATTTG TGAATGCGAA	2160
AACTGTAGAC AAGAATTGGT TTCGGATCAG TATATTCGTA TTCTCAATCA ATTGGATAGG	2220
GCTTTAACGA GTGAGGGATT AGATACAAAG ATTTGTTTTT TGCTTTATCA TGAGTTGTTA	2280
TGGGCACCTC AGAAAGAAAA ATTAGATAAT CCTGAACGCT TTACCATGAT GTTTGCACCG	2340
ATTACAAGAA CATTTGAAAT GAGTTATGCA GATGTAGATT TTGACAATTC CATACCTACG	2400
CCTAAACCTT ATATGCGTAA TAAATTTATA CTTCCGAATT CTCTTGAGGA AAATTTATCT	2460
TATCTTTTTG AGTGGCAAAA AGCATTTAAA GGAGATAGTT TCGTATATGA CTATCCTTTA	2520
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AATTTTTTAC CAATTATTGA GGAAAATATT TCTAAGTTAT TAAATAGTCA AAAGGATGAA	2940
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CAAGCAACTG GAAAAACAAG GCAAGCTCAA GATGAATGGA GAAATGTGTT GAATTATATC	3060
CGTGGGCACG AATTGCTATT TCAATCTAAT TTGGATGTTT ATCGTGTAAT TGAAGTAGCA	3120
AAAAATTACG CTGGTTTCCA CTTATAAATC ATAAGTATAG AAAATGAACT AAGGTATTCA	3180
GAGAAGATTG ATCCTAAATA TTATGAAATT TAAGGATTTT TAAGATATTT AGGGTCAACT	3240
TTCTATTTAT ATCGTAGCGA AGTCATTTTA ATAATGATGT GTAAAAGATG GATCAAGATT	3300
GAGGAGGAAG AAAGATGAAA TCAAAAGAAG AAATAAATAT GCTTGGTTTT ACAATTGTCG	3360

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CTTACGCAGG AGATGCAAGG TCAGATTTGA TGGATGCTTT GGCCTTTGCG AGAGATGGAT	3420
ATTTTGAACA GGCAAGAGAA TTGGTTGAGT CTGCAAACGA CTCATAGTG TCTGCCCATC	3480
GAGAACAGAC TAATTTATTA GCGGAGGAGG CATATGGAGA TAATTTTGAA GTGAGCTTTA	3540
TTATGATTCA TGGTCAAGAT ACTTTGATGA CAACGATGCT ATTGTATGAT CAGGTAAAGT	3600
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GATTAGTCAT GGAAAAATTA CAGGTTAAAG CCTTACCGAA GGAGTTTTTA TTAGGAACTG	3720
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ATCGTTACGA AGAGGATATA GCTTTGGCGG CAGAACATGG TTTGCAGGCT TTGCGTTTAT	3900
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ATTATTACCA TAGAGTTTTT CAGTCTTGCT TAAAACATAA TGTGATTCCG TTGTTTCTT	4020
TACATCATTT TGATTCGCCT CAGAAAATGT TAGAAACAGG GGATTGGTTG AACAGAGAGA	4080
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ATTGGTTTAC AATCAATGAA CTGATGTCTC TTGCTGCAGG TCAATATATA GGAGGTCAGT	4200
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TGGCGCATGC TCTGCGAGT CTGCAATTC ATCAATTAGG GATTGAGGGA AAGGTAGGTT	4320
GTATTCATGC TTTAAAGCCA GGCTATCCTA TTGATGGGCA AAAAGAAAAT ATTTTGGCAG	4380
CTAAACGSTA TGATGTTTAT AATAATAAAT TTCTATTAGA TGGAACTTTT TTGGGCTACT	4440
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TTATTGAAGA TGGTGATTTA GAAATTATGA AGAGAGCTGC ACCTCTTAAT ACGATGTTTG	4560
GGATGAATTA TTATCGTTCA GAATTTATTC GTGAATACAA AGGTGAAAAT AGACAAGAAT	4620
TTAATTC AACGGAATAAAA GGACAGTCTT CTTTTAAAT AAATGCTCTA GGTGAATTTG	4680
TAAAAAACC TGGTATTCCT ACAACAGATT GGGATTGGAA TATTTATCCT CAAGGTTAT	4740
TTGATATGTT GCTTCGTATC AAAGAAGAAT ATCCTCAACA TCCGGTCATT TATTTAACTG	4800
AAAATGGTAC AGCCCTTAAA GAAGTTAAGC CAGAGGCGA GAATGATATT ATTGATGACA	4860
GTAAGAGAAT CCGTTATATT GAGCAACATT TACACAAAGT TTTAGAGGCT CGAGATAGAG	4920
GAGTCAATAT TCAAGCTAT TTTATATGGT CTTTGCAAGA TCAATTTTCT TGGGCGAATG	4980
GCTACAATAA GCGATATGGT CTTTCTTTG TTGATTATGA AACACAGAAG AGATATATTA	5040
AGAAAAGTGC TCTTTGGSTA AAAGGGCTAA AACGGAATTA AGGTTAGCGA TTTGACTGAT	5100
GTTTAATATG TTTTAAATAT GAGGTTGAAT TTTTATAGG AGGAGTTTTA TGGATAAGCT	5160

AGTCGCTGCC ATTGAAAAGC AACAAAGGAA ATTTGAAAAA ATTTCTACTA ATAACTATAT 5220  
GATGGCTATT AAAGATGGAT TCATTGCTAC TATGCCTTTA ATTATGTTTT CAAGCTTTTT 5280  
GATGATTATT ATTATGATTC CTA AAAATTT CGGAGTAGAG TTACCGAGTC CAGCTATTGT 5340  
CTGGATGAGA AAAGTGTATA TGTTAACCAT GGGAGTTTTG GGTATTATTG TTTCAGGGAC 5400  
TGTTGGAAAG TCATTAGTTG GAAATGTTAA CAGAAAAATG CCTCACGGAA AGTAATAAA 5460  
TGATATTTCT GCAATGTTGG CAGCCATATG TAGTTATCTG GTATTAACTG TAACGCTTGT 5520  
AGTTGATGAG AAGACGGGAT CTACAAGTTT GTCGACAAAC TATTTAGGAT CTC AAGGATT 5580  
GATAACTTCG TTTGTCAGTG CCTTTATTAC TGTA AATGTT TACCGATTCT GTATT AAGCG 5640  
AGACATTACT ATTCATTAC CTAAGGAAGT TCCTGGGGCT ATATCACAAG CTTTTAGAGA 5700  
TATTTTCCCT TTTTCTTTTG TTTTACTTAT TAGTGGTTTG TTAGATATTG TATCTCGGT 5760  
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GGCAGAATCA TATCCTGCTA TGATGTTGAT TTGGTTTATG TGTGCTTTC TTTGGTTTGT 5880  
TGGAATTCAT GGACCATCTA TTGTCTTACC TGCTGTTACA GCTTTGCAAC TGAGCAATAT 5940  
GGAAGAGAAT GCTCAACTTC TTGCA AATGG GCAGTCCCT TATCATTCCT TAACACCTAA 6000  
TTTCGGGAAT TATATCGCTG CTATTGGAGG AACGGGGGCT ACCTTTGTTG TACCATTAT 6060  
TTTGATTTTC TTTATCGGT CTAACAATT AAAATCGTA GGTA AAGCTA CAATTACTCC 6120  
TGTTTTATTT GCGGTAAATG AACCTCTTCT ATTTGGTATG CCTGTTATTT TGAATCCCTA 6180  
TCTTTTGTG CTTTTTTGA TGA CTCCACC AGTGAATGTA TTTCTAGGAA AGGTCTTTAT 6240  
TGATTTCTTT GGAATGAATG GATTTTATAT CCAGTTACCT TGGACCTTTC CTGGTCCCTT 6300  
GGGATGTTA ATTGGAACGA ATTTTCACT TATCTCCTTT GTATTTTAT CTTTGATTTT 6360  
AGTTGTCGAC ATATTGATTT ATTTGCCATT CTGTAGAGCG TATGATAGAC AGTTACTGGT 6420  
GAAAGAAGAT ATTGCAAGCT CAAATGATAT TATTTTAGAG GAGGATACAA GTGAAATAAT 6480  
TCCTGGTGAG ATAGATGAAA TAAAAAGTAA GGAGTTGAAA GTACTGGTTC TTTGTGCAGG 6540  
GTCTGGAACA AGTGCGCAAT TAGCCAATGC AATTAACGAG GGGGCTAACT TAACAGAGT 6600  
TAGAGTGATT GCGAATTCAG GAGCGTACGG AGCTCATTAT GATATTATGG GTGTTTATGA 6660  
TTTAATTATT CTGGCCCCAC AAGTTCGGAG TTATTATAGA GAGATGAAGG TGGATGCAGA 6720  
AAGATTAGGT ATTCAGATAG TTGCTACCAG AGGAATGGAA TATATTCATT TAACAAAGAG 6780  
TCCAAGTAAA GCCTTACAAT TTGTATTGGA GCATTACCAA GCTGTGTAGT AAGTTTTTCC 6840  
ATCTTTTATT TGAGTAAAGA TTTTGTTTAC AGATAGGCTT GGATTTAAAA ACGTTCCCCC 6900

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TTTTTTAATA TAAGAATCCC TCTTTCACAA TTGTAAAAAG AGGGATTTTG TATTTTATCT	6960
CTTAGACCAA GTTCTCTTCA TAAAGAGAAG GAGGATTGGG TAAATCTCCA AGCGCCCTGC	7020
AATCATTGCA AAGGATAGGA GAATTTTGA GATGGGACTA AAGATTGAGA AACTAGAAGT	7080
GGTTCCTAGA ATAGGCCCGA TATTATTGAA ACAGCTAAAG ACAGCGCTGG TCACGACCAG	7140
AAAATCATTG CTATCTAGGC TGACAATAAA GATAAGCGCT AGCAAAATCA TAGCATAGAT	7200
GACAAAGTAC TTGAGAATCT TATGCTGGGT ATCTTTGTCA ATCACCCTTT TATTAACATG	7260
GAGGGTCAAA ACACGGTGGG GCGATAGGAT TGACAAAATT TGGTTTGTGG CAATTTTGA	7320
AAGGATGAGG CCTCGAATAA TCTTGAGTCC ACCTGCAGTT GATCCAGCAG AGCCACCGAT	7380
TGCCATGAGG AAAAGGAGGA TAACTGGGA GAAGAGGGGC CAGTTGGTAA TATCTCCATA	7440
TCCAAAACCA GTTGTGTAA TGATGTTGGA AACCTGGAAG AAGGTCATTT CAAAGCTCTT	7500
TGAAAACCTT GGGTAGAGGT AGAGGGTGT GAGGCTAATC AAGCCTGTAG AAACCAGTAC	7560
AATGACCAAG TAAGCCCTAA GCTCTTCATC TCCAAGAAG GCCTTGATGC GACGGAGCAT	7620
GAGGTAGTAG TAGAGGTGA AATTTACTCC AAAAACCAGA ACTCCGATAC TGACCAGATA	7680
GGTAATCAGT GAGCTGCCAT AGTGGGCAAT TCCGTCGTTA TAGACGGTAA AGCCTCCAGT	7740
TCCCGCTGTC CCCATAGCAA TAACAAAAC ATCGTAGAGA GGCATACCGG CTAGATAATA	7800
GATGATGACA AAGAGGGAGA AGAGAGCTAG ATAAAGGAGA TAGAGAATCT GGGCAGTGTT	7860
TTTAGTTTG GATACAACCT TGCCAAAAC AGGACCTGGA ACCTCAGCCT TCATCACCTC	7920
TAGGTGGCTA TTTTGGCAT TGTCCATAAT AGCAAGTGCA AAAACAAGCA CTCCCATCCC	7980
TCCAATCAAG TGGGTAAAAC TTCGCCAGAA GAGGAGGGA CGGCTGAGAA CCGAAACGTC	8040
GTTCAAAATA CTGTCTCCAG TAGTTGTAAA TCCAGAACTA ATTTCAAAAA AGGCATCAAT	8100
AAGGCTGGGG ATTTGCCAG AAAAGACAAA GGGGAGACCA CCAAAGAAAG ACCAAAGGAT	8160
CCAACAGAGG GCAACGATCA AGACTCCCTC CTTGGCATAA ATCCGTTGAT TTTTGGCTT	8220
CTGTAACTC CCTGAACCGC CTAACAATAC GAGAATCCCT ATGGTCGAAA AGAGGGCTGT	8280
AAAGACTTGG CTCGATTAC GGTAAATAGAC AGCAATCGCA ACAGGAACCA AAAGAAGAAC	8340
AGCTTCAATC AAAAGTAATT TTGAAAGGAG GTAACGAATC ATACTTTTAT TCATTCTTA	8400
CCTCGCATC AAGTCATAAA TCTTGGTGAT GTTTGGCAAC AAGGTTGTTA CTAGGAGCTT	8460
GTCTCCAAC TCCAACATAT CCTCCCCAGT TGGGAAAATA GTCTTGCCCT TTCGAATAAT	8520
GGCTGCAATA AGAACCCCTT TTTTCAATTT CAGTTGAGAA AGAGGTTTGG CAGTCATTTT	8580
ATTGGCTTCC TTGATATGGA ATTGCAGGT TTCGATTGG CCATTGGCTA GATGGTGCAT	8640
AGCTTGAAGG TCTGAATACT GGGCATTAA TCGACCACGA ATAAAGTGCA TAATCGTATC	8700

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TACAGCGATG CTTTTAGGTG TGATGATACT TGAAAAATCA GGCGCATTGA TAATCTCGAG	8760
GAGACTGGTA CGATTGACCT TAGTAATATT TTTCTGTACA CCTACCCTGT CAAGGAACAT	8820
AGATGTAATC AGATTTTCCT CATCGACTCC TGTTAGAGTC GCAACGGCAT CATAGTGTG	8880
AGCACTTTCT TCCAGCAGGA TATCTTTTGC GGTTCATCT CCTTGAACGA TGTAGAGATT	8940
TGGGAATTC TCGCTAAAGA AGCTGGCGAT TTCAGGATTG ATTTCAATGA CTTTGTATC	9000
GATACGACTA TCTTTGAGAA TACCAAGTAG ATAATAGGCA ATTCTACCTG CCCCAACGAT	9060
GAGAAGGCTC TTCACGGCGC GTGATTTAAA ATAATTATGG AAGAGTATCA TATCGACACG	9120
GTTACCAGTG ACAAAGATTC TATCTTTATC CTGTACAGTC ATGTCACCGC TTGGAATGAT	9180
AATTTGATGA TCCCTCTCTA TCGCACAGAC AATGACATTA CCAAATTTTT TACGAAAATC	9240
AGAAATGGGC ATTTGGCAAA GACCGCTGGT GGAATTGACG ACAAATTTCCA TGAGGCTAAC	9300
GCGTCCACCA GCAAAGCGTT CGACAGACAG GGCCTTGGGG AAGTCAATGA TATTCGCGAT	9360
AGCGCGGGCA GCCAAGAGCT CAGGATTAAC GATAAGAGAA AAACCGAGAA TATTCTTTTC	9420
CTTGAAATAA GAGTTAGAAT ATTCAGGGTT CCGCACCCGA ACGATAGTTT CTTAGCTCC	9480
CATTTTCTTG GCTAGAAGCT CTGCAATCAT GTTGACTTCA TCGTGCTCAG TCAGGGCGAT	9540
AAAGATATCA CAATCTTGA CGCTGGCTTG CTCAAGAATG GCAAATTCGG CCCCGTTACC	9600
AAGGATACCA ATGATATCAA AGCGACTGAC AATATGATTG AGAACAGCTT CGTCTTGCTC	9660
AATCAGCAAA ACATCATGCT TTTCTGCAAC CAAGGAGCGA CAGAGGGCAA AACCAACTTT	9720
TCCCCCTCCG ACAAGGATAA TTTTCATAAT AAAACCTACT TTTTCATGAT GTAACATCA	9780
TACCCTTTTT CAAGAAAAAA TGCACCTACT AGCTAATAAC AAGAGTTTTT AGTGAAAATT	9840
CGCTATAAGG TAAAACTATA CCCTAACCAA TTGAAATAGC TATTAGCGAC TTTCTCTGAA	9900
ATATGGTATG ATAAAGGATA TACAAGGAGA TAAATGAAT AATAATTAC TGGTATTACA	9960
ATCAGACTTT GGTCTGGTTG ATGGTGCGGT ATCGGCTATG ATTGGAGTGG CTTTGAAGA	10020
GTCTCCAACC TTAATAATAC ATCACTTGAC GCACGATATC ACGCCTTATA ATATTTTGA	10080
GGGGAGCTAT CGTCTCTTC AGACGGTGA TTAAGGCTT GAGGGAACGA CGTTGTATC	10140
GGTTGTGAT CCAGGTGTCG GTTCGAAACG TAAGAGTGTG GTTGCCAAGA CTGCAAAAAA	10200
TCAATACATT GTCACGCCAG ATAATGGGAC GCTTTCCTTT ATCAAGAAAC AGTTGGCAT	10260
TGTAGCCATT CGTGAGATT CTGAGGTGGC CAATAGGCGT CAAAACACAG AGCATTCTTA	10320
TACCTTCCAC GGTCTGATG TCTATGCCTA TACTGGTGCT AAAGTGGCCA GTGGTCACAT	10380
TACTTTTGAG GAAGTAGGGC CAGAGCTCAG TGTGGAACAG ATTGTAGAGC TTCCAGTCGT	10440

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AGCGACCATC ATAGAAGATC ATCTGGTGAA GGGAGCCATT GATATTCTGG ATGTGCGTTT	10500
CGGTTTCGCTT TGGACCTCTA TCACACGGGA AGAATTTTAC AAGCTGGAAC CAGAATTTGG	10560
TGATCGTTTT GAAGTGACCA TCTATCATGC TGATATGCTG GTCTATCAAA ATCAGGTTGT	10620
CTATGGCAAA TCATTTGCAG ATGTGAGAAT TGGGCAACCS ATcTTTACrc TCAGCaTCTt	10680
CGATTAGCTG GGCAATTCGT TCTAGTTGGA TTTGCTCAAT CAAGGT	10726

(2) INFORMATION FOR SEQ ID NO: 67:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 7163 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 67:

TTATCTTTAA CGATATCAAT CAAGATCTGG TCAATAAAGG GATTGGGGCT TATCGTGAAG	60
TTGGCATCCA AGCCCATGGA TATGTCTGTG ACGTGACAGA CGAGGACGGT ATCCAAGCCA	120
TGGTCAAGCA AATCGAACA GAGGTTGGTG TCATTGACAT CCTCGTTAAT AACGCTGGTA	180
TTATCCGCCG AGTTCCAATG TCGGAAATGA GCGCCGCTGA TTTCCGTAAG GTCATCGATA	240
TTGACTTAA CGCACCATTT ATCGTTTCAA AGGCAGTTAT TCCTTCTATG ATAAAGAAAG	300
GGCATGGAAA GATTATCAAT ATTTGTTGCA TGATGAGCGA ACTGGGACGT GAAACAGTTA	360
GCGCTTATGC TGCTGCTAAA GGGGGCTTGA AAATGTTGAC CCGCAACATT GCGTCTGAAT	420
ACGGTGGAGC CAATATCCAA TGTAAACGAA TTGGACCGGG TTATATTGCC ACTCCTCAAA	480
CAGCACCTCT TCGTGAATTG CAAGAAGATG GTTCTCGCCA CCCATTGAC CAGTTCATCA	540
TTGCAAAAAC ACCTGCTGCA CGTTGGGGAA ATACTGAAGA TTTGATGGGC CCTGCTGTCT	600
TTCTCGCTAG TGATGCCAGC AATTTTGTCA ATGGCCACAT CCTATATGTA GATGGCGGTA	660
TCTTAGCCTA CATCGGAAAA CAACCTGAGT AAAAATAGAA AGAAGATCTT ATGAAAATCG	720
CATTAATCAA TGAAAATAGT CAAGCTAGCA AGAATCACAT TATTTACGAT AGTCTAAAAG	780
AAGCGACAGA TAAAAAAGGC TACCAATTAT TTAACATATG TATGCGTGA GAAGAAGGAG	840
AAAGTCAATT AACTTATGTG CAGAACGGAC TAATGGCTGC CATCCTTTTA AATACAAAGG	900
CAGTTGACTT TGTGTGTACC GGCTGTGGTA CGGGTGTAGG GGCTATGCTT GCTTTAAACA	960
GCTTCCTG TGTTGTCTGT GGTCTAGCAG TGGACCCAAC TGACGCTTAC CTTTATTCTC	1020
AAATCAATGG TGGAACGCC TTGTCTATCC CTTATGCCAA AGGATTGGC TGGGGGGCAG	1080
AACTGACCCT CAAATTGATG TTTGAACGCT TATTTGCTGA AGAAATGGGC GGTGGCTACC	1140

CAAGAGAACG TGTAAATCCCT GAACAACGCA ACGCTCGTAT CTTAAACGAG GTGAAACAAA	1200
TCACCCACAA TGATTGTGATG ACCATCCTTA AAATAATCGA CCAAGACTTC CTCAAAGACA	1260
CCATCTCTGG CAAATACTTC CAAGAATACT TCTTTGAAAA CTGCCAAGAT GATGAAGTTG	1320
CTGCTTATTT GAAAGAAGTA TTAGCCAAGT AAAGCTATTC TAAACCAGAA AGGAACTAAT	1380
GGATGACGAA AATATTACTG TTTGGCGAAC CATTAAATTCG AATTTACCA TTAGATGCCA	1440
CCAGTATCGG CGATCATGTT GCCAGTTCGA CTTATTTTGG CGGATCAGAA ATTAACATCG	1500
CTTGTAATTT GCAAGCCCTG GGTATCTCAA CGAAAGTTT TACCGCACTC CCTGCCAACG	1560
AGATTGGAGA TCGTTTCTC ACATTCTTGA AACAGCACCA AATCGATACC AGTTCAATCT	1620
GTGGGCTTGG CGATCGAATC GGCCTCTACT ATTTGGAGAA CGGCTTTGGT TGTGTCAAA	1680
GTGAAGTTT CTACGATCGT AAGCATACGA GTATCAGCCA GATTCGGCCA AACATGCTAG	1740
ATATGGATTC TCTCTTTCAG GGGATTAGCC ATTTTCATTT TAGTGGAAATC ACCGTAGCTA	1800
TCGGTCAAGA GGTCCGTGCG ATCCTTCTCC TACTCTTGA AGAAGCCAAG CGCCGAGGAA	1860
TTGTCGTTTC AATGGATCTC AATCTGAGAA CAAAGATGAT TTCAGTCCCTA GAAGCCAAGT	1920
ATGAATTTTC TAAGTTTGCA CGTTTACTG ACTATTGCTT CGGTATTGAT CCTCTCATGA	1980
TTGATGACCA AAATCTAGAG ATGTTTCCAA GAGACAGTGC TAGCCTAGAA GAGGTGAAA	2040
ATCGCATGCG ACTTTTAAAA GAAGCCTATG GTTCAAGGC CATTTTCCAT ACCCTCCGCT	2100
CTAGTGATGA GCAAGACAAA AATGTCTATC AAGCCTATGC TCTAGAAGAA CTATTTGAAG	2160
AGTCTGTCCA ACTAAAACT GCAGTCTATC AACGAATTGG TAGCGGGGAT GCCTTTATAT	2220
CTGGTGCCCT TTACCAACTA CTCCATCATT CCTCCCTAAA AACTACCATT GACTTTGCAG	2280
TTGCGAGCGC AACTCTCAA TGCACCTTC CAGGAGACCA TCTCTCCACT TCCTCAACTA	2340
GTATTGAAAA TTTACTGGCA AATGCACAAG ATATCATTCG TTAGGAGAAT TACATGACCA	2400
AATCAGATAC GATTATTGAA CTAAAAAAC AAAAAATTGT CGCTGTTATT CGAGGAAATA	2460
CAAAGGAAGA AGGACTACAA GCCTCGATTG CTTGTATCAA GGGCGGTATC AAAGCTATTG	2520
AAATCGCCTA TACCAATCAG TATGCAGGAC AAATCATCAA GGAACCTGTA GACTTGTATC	2580
AGGACGATCA GAGTGTGTTG ATCGGTGCAG GTACTGTGCT TGATGCCGTA ACTGCTAGAG	2640
ATGCCATTCT AGCTGGAGCA AATTACGTTG TTTCTCCATC TTTCCATGCT GAAACTGCCA	2700
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CGACTGCACT TGAAGCCGGT AGTGAAATCA TCAAACCTT CCCAGGTAGT ACTCTCAGTC	2820
CAGCATATAT CTCTGCAGTC AAGGCACCGA TCCACAAGT TTCCGTAATG GTAACCGGAG	2880

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GAGTCGGCCT AAACAACATC CCTCAATGGT TCGCTGCTGG TGCAGATGCC GTTGGAAATTG	2940
GTGGCGAACT CAATAAACTC GCTTCCCAAG GCAACTTTGA CCGCATCAGC GAGATTGCCC	3000
AACAGTATAT TACACTCAGA TAAAATCATA ACTACCCGTC TAACGGGTGG TTTATCTCAG	3060
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CTTATTGCTC TTGACTCGTC ACTTGCCCTCT TTAAGAGACT TTGGTATTAC TTACCACTAT	3180
CCCTAAAGGG ATCCTCATAT TCTTTTACAC TCAATTTATC TAGTGCTATA GTAGATTGAA	3240
ACTGGAATAG TACACCTCTG CTTCTAAAAC ATTGTTAAAA ATCGATTTGA CTGTCCTGAT	3300
CGATTTTGTC CTGTTCTTAT TTCATTTTAC TATATATCAT ACTTTACTCG TTCTCAAATT	3360
TTCATACTCA TGAAGAAATC ATCCACTCGA TAATTTCTTT AATCTTGACT ATATTTCTTA	3420
ATTGTGGCTT CATTAAGCCC TACTGGACTT ACATAATAAC CTTCCCTCCA GAAATGCCGA	3480
TTCCCAAAT TGTACTTGAG ATTGGCGTGT TTGTCAAACA TCATGAGTGC ACTTTTGCCT	3540
TTTAAATACC CCATAAACT TGAAACACTT AGCCTCGACG GAATACTGAC TAACATGTGT	3600
ACATGGTCTG GCATTAAGTG ACCCTCGATC ATTTCAACAC CTTTATAACT ACACAAGCGA	3660
TGAAATATTT CGTCTAACT ACTTCTATAT TGATTATAGA TGACTTTTCG TCTATACTTA	3720
GGGGTGAACA CAATATGATA GAACACCTCC ACTTTGTGTA TGATAAACTA TGAGTCTTTT	3780
GTGCCATATT TTTTCTCCTT TCGCTTTACA ATTGGATTGA ACACCTTTAT TGTATCGCGT	3840
TTGGAGTTTT TTTGGTATAA CCTTCGACGC GCACCCGTAT AGCGGGTGGT TGTTTTGTCT	3900
CGCACCTCAC GGAGCGAGAC GGAATAATAT AGTGGAGTGA AATAGGATAC GAACAAATTG	3960
ATTAGGAAAA TCAAATGAAT TTATAGAAAT CTTTTCAGC TTATAACGTT CTATTCAGT	4020
TTCAAAACGC TATAGTCACA TAATAATGAA GTAAAAAAGG ATAAGTATCA ACTTATCCTT	4080
TTTTAAAAGA AAAATCCGAA GATATTTGGC CTTCTTCGGA TTTTTCCTAT TTTCCACAGT	4140
TTTATGTAAT TCATCTAGAT GATGAACAAA TTAGTTGTTC TTTCTCTAC GGAATAGATA	4200
AAATGCCCCA AGTAGCAAGA ACCCTAGACT TGCCAAGATT GACTGACCTT CTCCTGTCTG	4260
AGGGAGATTC TTTTGATCCG AATGGTTCTT TTCCTCTTCA GATTTTTCCT TTTCTTTTGA	4320
ATTCTGTAAT TGTGGCTGAG CTGCTTGCTC TAGCTTTTTA AAGACTTCCT GATCTGGAGC	4380
TGATTCCTGG GTTTCAGGAT TATAGTAGGC AATCTTATAT TCATCCCTT CTTTTCGAAT	4440
GGTATAGACT CCACGTTTCA AAACCTGGAA TTGGTTGGAA ATAGTAGAGA CAGAATCATC	4500
ATATTTTACA ATGCCCCAAA CTCCTTGTTT AGCATCATAA ACAGACTGAA GGGTTTCGTT	4560
ATTTTCGATG AGGCTACTTT CTAACCTTTT TATCATTTGA TTGAAGGTGG CACGATCCAC	4620
GTTAGGAATG AGCATATAGC CATAAGAATC TCTATTTTGC TTATGAGCCT GACTAATCGT	4680



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AAGAAATTCA TTTTCAACTT CCTGTCTGA CTGTCCTTCA TTGATATCCT TCCAGGCTCC	4740
CTTTTGCAAA GCCTTACTCA TACTGATTGA ACTCTTCTTA AAGAAAAAGT AACCAATATT	4800
CTTTTTCGAA TCGAACGATT CTAAAAAGAC ACTTTGGGTT TCAGGATAAT CCTTTTCTTG	4860
TTCTGTAAGG GAGGCTTCTT TATCATTGAC ATAGACTTTA TATGGATTAC CTGATTCCAG	4920
TTTTCTCTGG TCAATTGTAG TTGCAGCAGT ATCTGTTGAA GTGTTTGGGA TATTGCTTCC	4980
TAAAAAGGCG ATCTTATCCT TTAGCATAAA CCAGCTCTTA TGAGCAGTCA ATGTTTGATT	5040
CCAGTTGGTG AAATCCATGG TTGCTGTGCG ATTGGCATCA TCTAGTTTGC TCGTTCCAAC	5100
GAAAGCAGAC GGTAAACTT TACCTGTATC GCTATCCGCT CTCTTAGCAT CCGTCTCTGT	5160
TGTACCAGGC ATCTTATATG GATTAACTGT TGGCCAGTAG CCATCGCTAT AGTGACTCAA	5220
ATCGCCATTG TAAAGATAGA ACATCCCATC ACTCGTATAC CAACCACGTT TATTTTCCTT	5280
GTTCATGTGT TCGTAATTCA AGGTACGACT GGAAAAGAGT GACAAGCCAA ATCCAAACCC	5340
TTTCTCTGCA TTGTACATGG CTGTTTTATC CATCTTGTTA AAGGCAGATA GGTAACCTGG	5400
TCTTGGAACA CTTGCGACTC CTGCATCACT TAACAAGGAT TGCATCAAAC TGATATCCTT	5460
ATAAGTCTTC AAATCTTAA AGACATCATA ATAACATATC GATTGAACAA TGSTCTTAC	5520
AAGACTCTGC AAACATTGTT TGGTTTCTCC TTCAGACATA TCCGCTATTC GGTGAATCCC	5580
TCTTAGTACT TCTACTGCGG CCACGTGCCC CTCGCTATTT GCACGACTGA TCGAGCGTCC	5640
ACGACTCATA TCCATCAACT CTCCATTAC CAGCAAAGGA GCAAACGATT TATCAATCCA	5700
GTGTACATG GTTTGCATTT TATCTTTATC GATTGGATTG TTGGTCTTTT GAATGACTGG	5760
CAACAGTTGA GACAGGCCAT CAATCAAAAC ATTCCCATAA GCACCCGTAT AGGCAACATT	5820
GGTGTGGTCG ATATAGGATC CATCTTGATA AAAACCTTCA CCTTGGTCTA CCAACTTGAA	5880
CACTTGCTCA ATCGAGCGAA TGGTAGAAGA AATTTCTTGA TCATCCTTAC GCAGTAAACC	5940
AGCTATTACT TTTACCCTTC CCATATCAAC TAAGTTTCCA CCTAGAGCCT TGAATGGGT	6000
ATCAGTCGTC TTTCGGAAAT GTTCGGGATC TGGTACAAAT TTTTCAATCA CATCTGTATA	6060
TTTTTTAATT TCCTCATCAG AGAAGTATTC TTTCATCAGA GACAAGGTAT TGTGATGGC	6120
ACGAGGTGTA CCGATTTTCA TATCCCAACA GTTCCCAACA ATGCTCTTTT CACTATTGTA	6180
GACATGTTTA TGATCCATT CCATGGAATC CTGACTGTT CGAACGACAG TTTCATCTTG	6240
ATAATAACGA GAAGAAGGAT TGGTCACTTG CTTGGCCATC TCCTCCAATT TCCGATAAGT	6300
GGCAGTCAGA TTTGCAGACG TTTTATAATT TGAAAAATTT TCCCACAAAT AGGTGCGGTC	6360
CGCCTGACTT GAAATACTGG ATAGGCTATC AGCTACCTTT CCTTCCAATT CCTGGTTTAA	6420

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TTTGGCCATC TGTTTCATTT TAGAATCATA GTATTGATTG CCAGCGATGA TGCCATTCCA	6480
GTCAATCCAAA CGGTCTGTGT ATGCATCCTT AACAGAGGCC AGAATCTTCA AAGGAATCTT	6540
TTTCACTTCC TTGCCATCTT TACTGACAAT GACATTGGTT GTCCCTTCCT TAAGAGGTTT	6600
TAAAATTCCA TTTTGGACTG AAGCAACGTC AGGATTTTCT ACCTTATAAG TATAGTCCGC	6660
AAGAGAAAAA ACATGTTTTT TTCCAATTGG TAAATCAATC TTTTCCTCAA GCTGTTTATC	6720
TGTTTGAGAA TCCTCAGAAA GCTGGTCTGC TACCTCTACC AGCTCAATAT CCTTAAAGGA	6780
AACAGTCCCA GTTCCTGTTT CATAGAATAA CTCCAGCTTG ATTTTATCAA CATCTAAAGT	6840
CGGGCTATAG TCTGCTTCAA TGGTCTGCCA GTCCTTGTG CCTGACGTCG TTGCAGAATT	6900
CCACAATCGC TTGTCCTTAC CACTTTCCTC AATGATACGA ACTTTGGCAA TCCCATTGTT	6960
ATTATCTGTT TTAATCTTGA AACGCAGTTT ATACTTTTTC TTAGCTTCAA TAGGAACCAT	7020
ACGGTGAAGC GCTGCCCTTA ATTTCTCATG GCTTGAGATA GTGATAGCCC CATCCTTAGC	7080
CTCAATGACT CGAGTTGAGG CATCTGCACT ATTCTTCTGG TCTACCCAAG CTGACCACCC	7140
CCTGAGCTTT GCTTCTGTG CCG	7163

## (2) INFORMATION FOR SEQ ID NO: 68:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 9244 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 68:

CGTTATAACA TACATGTAAG CGGTACCCAA AATGGTGCCA AGTCAAAATT TTAAAGGAGG	60
AAAATACATG TCTTCACATC CAATTCAGGT CTTCTCAGAA ATTGGGAAAC TGAAAAAAGT	120
TATGTTGCAC CGTCCAGGCA AGGAGTTAGA AAACCTGTTG CCGGACTATC TTGAAAGGCT	180
TCTTTTGGAT GATATTCCTT TCTTGGAAGA TGCTCAAAAA GAACATGATG CATTTGCCCA	240
AGCTCTTCGC GATGAAGGAA TTGAGGTTCT CTACCTAGAA CAACTCGCTG CTGAATCATT	300
GACCTCTCCA GAAATCCGCG ATCAATTTAT CGAGGAATAC TTAGACGAAG CCAACATCCG	360
TGATCGTCAA ACCAAGGTTG CTATTCGTGA ATTGCTTCAC GGCATCAAGG ACAACCAAGA	420
ATTGGTTGAA AAAACAATGG CTGGGATTCA AAAAGTTGAA TTGCCAGAAA TTCCTGACGA	480
AGCTAAAGAT CTAATGACT TAGTTGAATC AGAGTATCCA TTTGCAATTG ACCCGATGCC	540
AAACCTCTAT TTCACTCGCG ACCCATTTGC AACAAATTGGA AACGCCGTAT CGCTTAACCA	600
CATGTTTGCA GACACTCGTA ACCGTGAAAC ACTCTACGGT AAGTATATCT TCAAATACCA	660

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CCCAATCTAT GCGGAAAAG TGGATTGGT CTACAACCGT GAAGAAGATA CGCGTATCGA	720
AGGTGGAGAC GAGTTAGTTC TTTCTAAAGA CGTCCTTGCA GTAGGTATCT CTCAACGTAC	780
AGACGCAGCT TCTATCGAAA AACTTTTGGT CAACATCTTC AAGAAAAATG TTGGCTTCAA	840
GAAAGTTTTC GCCTTTGAAT TTGCTAACAA CCGTAAATTC ATGCACTTGG ATACTGTCTT	900
CACTATGGTA GACTATGACA AGTTCACAT TCACCCAGAA ATCGAAGGCG ACCTTCACGT	960
TTACTCAGTT ACTTACGAAA ACGAAAACT TAAAATCGTT GAAGAGAAAG GTGACTTAGC	1020
TGAACCTCTT GCTCAAAACC TTGGTGTAGA AAAAGTTCAT TTGATTCGTT GCGGTGGTGG	1080
CAATATCGTA GCAGCTGCGC GTGAACAATG GAACGACCGT TCTAACACTT TGACCATCGC	1140
ACCTGGTGTG GTAGTTGTTT ATGACCGCAA TACCGTGACC AATAAGATTT TGGAAGAATA	1200
CGGGCTTCGC TTGATTAAGA TTCGCGAAG TGAATTGGTT CGGGCCCGTG GTGGACCTCG	1260
TTGTATGTCT ATGCCATTTG AACGTGAAGA AGTGTAATCG CTGTTGATA TTCGTCAATA	1320
GAAAATGTAA AAAATAGAAA GAGGAAATAA TAAAATGACA AATTCAGTAT TCCAAGGACG	1380
CAGCTTCTTA GCAGAAAAAG ACTTTACCCG TGCAGAGTTA GAATACCTTA TTGCTCTTTC	1440
AGCTCACTTG AAAGATTGA AAAAACGCAA TATTCAACAC CACTACCTTG CTGGCAAGAA	1500
TATCGCTCTC CTATTTGAAA AAACATCTAC TCGTACTCGT GCAGCCTTTA CAACTGCGGC	1560
TATCGACCTT GGTGCTCACC CAGAATACCT CGGAGCAAAT GATATTCACT TGGGTAAAAA	1620
AGAATCTACT GAAGATACTG CTAAAGTATT GGGACGTATG TTTGACGGGA TTGAATCCG	1680
CGGATTCAGC CAACGTATGG TTGAAGAATT GGCAGAATC TCAGGCGTTC CAGTATGGAA	1740
CGGTCTAACT GACGAATGGC ACCCAACTCA AATGCTCGCT GACTACTTGA CTGTTCAAGA	1800
AAACTTCGGT CGCTTGAAG GCTTGACATT GGTATACTGT GGTGATGGAC GTAACAACGT	1860
TGCCAACAGC TTGCTCGTAA CAGGTGCTAT CCTTGGTGTG AATGTTTACA TCTTCTCACC	1920
AAAAGAACTC TTCCCAGAAA AAGAAATCGT TGAATTGGCA GAAGGATTTG CTAAAGAAAG	1980
TGGCGCATAT GTTCTCATCA CTGAAGATGC TGATGAAGCA GTTAAAGATG CAGACGTTCT	2040
TTACACAGAC GTTTGGGTAT CAATGGGTGA AGAAGACAAA TTCGCAGAAC GTGTAGCTCT	2100
TCTTAAACCT TACCAAGTCA ATATGGACTT AGTTAAAAA GCAGGCAATG AAAACTTGAT	2160
CTTCCTACAC TGCTTGCCAG CATTCCACGA TACTCACACT GTTTATGGTA AAGACGTTGC	2220
TGAAAAATTT GGTGTAGAAG AAATGGAAGT AACAGACGAA GTCTTCGCA GCAAGTACGC	2280
TGCCCCTTC GATCAAGCAG AAAACCGTAT GCACACTATC AAAGCTGTTA TGGCTGCTAC	2340
ACTTGGAAC CTTTATATTC CTAAAGTATA ATTTTAGATA ATAAACCGTC TACCAACAGC	2400

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TATGAGGGCT GCGACTAATA GCTTTAGTCC GGTCTCTCTT TATGTAATGG TAATCTATTA	2460
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GATAAAGGAG AATTATGGC AAATCGTAAA ATTGTAGTAG CTTTGGGAGG AAATGCGATT	2580
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CTTGTAATAA TGATTAAAA TGGAGATGAT CTGATTATCA CTCACGGTAA TGGACCTCAA	2700
GTTGGGAATC TCTTGCTCCA ACATTTGGCA TCAGACTCTG AAAAGAACCC TGCCTTCCCA	2760
CTCGACTCAC TTGTCGCTAT GACAGAAGGT AGCATCGGTT TCTGGTTGAA AAATGCTTTG	2820
CAAAATGCTC TCTTGGATGA AGGCATCGAA AAAAATGTTG CCTCTGTTGT AACGCAAGTT	2880
GTCGTAGATA AAAATGATCC AGCTTTTGT AACTTGAGTA AACCAATCGG TCCTTTCTAT	2940
TCAGAAGAAG AAGCAAAAGC AGAAGCCGAA AAAAGCGGAG CGACTTTCAA GGAAGATGCT	3000
GGCCGTGGCT GCGTAAGGT CGTTGCCTCA CAAAACCTG TTGACATCAA AGAAATTGAA	3060
ACCATCCGTA CTCTTTTAAA TAATGGTCAA GTCGTCGTAG CTGCAGGTGG TGGCGGTATT	3120
CCCCGCTCA AAGAAAACAA TGGACATTG ACTGGTGTG AAGCGGTTAT TGATAAAGAC	3180
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GTAGATTATG TATTGTGTA CTACAACAAG CCAAAACCAGG AAAAATTGGA ACATGTGAAT	3300
GTTGCCCCAGC TGGAAGAATA TATCAACAA GATCAGTTTG CACCAGGTAG CATGCTTCCA	3360
AAAGTAGAAG CAGCTATCGC TTTTGTCAAT GGTGCTCCAG AAGGAAAAGC AGTTATTACT	3420
TCCCTTGAAA ATCTAGGCGC CTTGATTGAA TCTGAAAGCG GAACAATTAT TGAAAAAGGA	3480
TAAGTTGTTT TACTAATAAG ATGTATTCTA TTTCTAGTAT CTTTATATCA AATTAGAAAT	3540
TATTCCTGAA AACATGTACA ATATTTCAA AGATACTAGT TTTAGACTTT AATATGGTAA	3600
AACAAATATA AATAGAAAGC GTTTTCTTGA ATGTTTATTT AAGAAAGTAG TTGGTTTTTT	3660
ACACTTTGTT AGACATCAGG AGGAAAAACA AATGAGTGAA AAAGCTAAAA AAGGGTTTAA	3720
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AGGTTGCTC ATTAAGAAA CGAGCGCAGC GATTGATGTA GCCTTCTTCA TCCTTATGGT	3960
TGGTGGTTTC CTTGGCATG TCAACAAAAC TGGTGCTCTT GACGTAGGGA TTGCCTCTAT	4020
CGTGAAGAAG TATAAGGGCC GCGAAAAAT GTTAATTTTG TACTGATGC CTTGTTTGC	4080
CCTCGGTGGT ACAACTTATG GTATGGGTGA AGAAACAAT GCCTTCTATC CACTCCTTGT	4140
GCCAGTTATG ATGGCCGTTG GTTTTGATAG CCTGACTGGT GTTGCAATTA TTTGCTCGG	4200

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TTCTCAAATC GGCTGTTTGG CATCTACTCT GAATCCATTT GCGACAGGTA TTGCTTCAGC	4260
GA CTGCGGGA GTTGGTACAG GGGACGGTAT CGTACTTCGT CTGATCTTCT GG GTTACCTT	4320
GA CTGCTCTT AGTACTTGGT TTGTTTACCG TTATGCGGAT AAGATTCAAA AAGATCCGAC	4380
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TTCATCTGTA GAATCTACAC TTAGCAGCAA ACAAAAATCA GTTCTCTTCT TATTTGTGTT	4500
GACATTCATC TTGATGGTAT TGAGCTTCAT TCCATGGACA GACCTTGGCG TTACCATTTT	4560
TGATGACTTT AATACTTGGT TGACTGGTCT TCCAGTTATT GGTAAATATTG TCGGTCATC	4620
TACTTCTGCA CTAGGTACTT GGTACTTCCC AGAAGGCGCA ATGCTCTTTG CCTTTATGGG	4680
TATCCTGATT GGTGTTATTT ATGGTCTTAA AGAAGATAAG ATTATCTCTT CCTTCATGAA	4740
TGGTGCTGCT GACTTGCTCA GTGTGCGCTT GATCGTAGCG ATGCTCGTG GTATTCAAGT	4800
TATCATGAAC GACGGTATGA TTACCGATAC AATCCTCAAC TGGGGTAAAG AAGGCTTGAG	4860
CGGTCTATCT TCACAAGTCT TTATCGTTGT AACTTATATC TTCTATCTAC CTATGTCATT	4920
CTTGATCCCA TCTTCATCTG GTCTTGCCAG CGCAACTATG GGTATCATGG CTCCACTTGG	4980
AGAATTTGTA AATGTCCGTC CTAGCTTGAT TATCACTGCT TACCAATCTG CTTCAGGTGT	5040
CTTGAAC TTG ATGACACCAA CATCTGGTAT TGTGATGGGA GCTCTTGAC TTGGACGTAT	5100
CAACATTGGT ACTTGGTGGA AATTCATGGG CAAACTCGTA GTCGCTATTA TTGTAGTGAC	5160
CATCGCCCTT CTCTCTCTTG GAACCTTCCT TCCATTCCCTA TAAAATAGTG AGTGAGGTGA	5220
TTCCATGAAA ATAGATATAA CAAATCAAGT TAAAGATGAA TTTCTTATAT CATTA AAAAC	5280
CTTGATTTCC TATCCTTCAG TACTCAATGA AGGAGAAAAT GGAACACCTT TTGGACAAGC	5340
AATCCAAGAT GTCCTAGAAA AAAC TTTAGA GATTTGTCGA GACATAGGTT TCACTACCTA	5400
TCTTGACCTT AAAGGTTATT ACGGATATGC AGAAATCGGT CAGGGAGCAG AGCTTCTGGC	5460
CATTCTCTGT CATTTGGATG TTGTTCCATC AGGTGATGAA GCAGATTGGC AGACACCGCC	5520
ATTTGAAGCA ACTATCAAAG ACGGCTGGGT ATTCCGACGT GGTGTCCAAG ATGATAAAGG	5580
CCCTTCGCTC GCAGCTCTCT ATGCAGTAAA AAGCTTGCTG GACCAAGGTA TTCAGTTCAA	5640
AAAGCGCGTA CGCTTTATCT TTGGTACCGA TGAGGAAACC CTCTGGCGCT GCATGGCAGC	5700
CTACAATACC ATCGAAGAAC AGGCCAGTAT GGGCTTTGCA CCTGACTCAT CTTTCTCTCT	5760
GACCTATGCT GAAAAAGGGC TTCTACAGGT CAAACTTCAT GGCCCTGGAT CGGATCAACT	5820
AGAGCTTGAA GTAGGAGGCG CCTTTAACGT TGTACCAGAC AAGGCCAACT ACCAAGGTCT	5880
CCTCTATGAA CAGGTTTGTA ACGGTCTCAA AGAAGCTGGT TATGATTACC AAACCACTGA	5940

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ACAAACCGTA ACGGTTCCTG GAGTGCCAAA GCATGCTAAG GATGCTAGTC AAGGTATCAA	6000
TGCTGTCAATC CGACTAGCTA CCATTCTTGC TCCTCTCCAA GAACACCCCTG CTCTCAGTTT	6060
TCTTGCAACA CAAGCAGGTC AAGACGGCAC AGGAAGACAA ATCTTTGGTG ATATAGCAGA	6120
TGAACCTTCT GGTCACTAT CCTTTAATGT CGCAGGTCCT ATGATCAATC ATGAACGTTT	6180
TGAAATCCGT ATTGACATTC GGACTCCTGT CTTAGCTGAC AAGGAAGAAC TAGTAGAGTT	6240
GCTTACAAGA TGTGCACAAA ACTACCAACT CCGCTACGAA GAGTTTGACT ATCTAGCGCC	6300
TCTATACGTC GCAGAAGACA GTAAACTCGT TAGCACACTG ATGCAAATCT ACCAAGAAAA	6360
GACTGGCGAT AACAGTCCCTG CTATTTTCATC CGGTGGTGCC ACTTTTGCTC GCACCATGCC	6420
AAATGTGTGA GCCTTCGGCG CCTTATTTCC AGGAGCGAAG CAGACAGAAC ATCAGGCAAA	6480
TGAATGTGCC GTTCTAGAAG ATTTGTACCG TGCTATGGAT ATTTATGCCG AAGCCGTCTA	6540
TCGACTTGCA ACTTAATCAG GCAACTGTTT CTACCAAAAA AAATCGACCG ATTAATGAAC	6600
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CTTTATAAAT CGCTTTTTC AGTTTGTGCA CTGGTGTTC GATAAACTCA AACTTTTTCAG	6840
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AACATTTTGA GAAATCGATT TGACTGTCCT GATCGATTG TCCTGTTCTT ATTTTCATTT	6960
ACTATATTTG AGCCACTTCG TCTTTAACGG CTTTATTCAT AAGCTCTTGT AATTTTCTT	7020
TACTATCAAT TACTTCTGAT TTTCCGTTGT AATTATTTGT AATAGGTTT AACTTACCTA	7080
ATTTCTCGAC ACGCTCATTA ATTTGATCTT TTTTGAAGGC TGCTTATGTT TTTCTAAGA	7140
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ATTAATTTGA AACATAAGGA ACAAATCCTT CATAGTAACC TAATGCTCCC ATAAGTTCAA	7260
AAGCTGTGTT TCTAATTCAA ACCATTGCAA CTCAGATTTC AGCTTTTCAG ATAAATCCTG	7320
CTCATCCAAA TAATGACTTG AAATTAGTGC TGAACCTCGT TCTGTATCCT GTACAGGCTG	7380
AGCACCCATA CCAGCAAAAA ATAACTCGT TCCTAGCAAG ACCGAACAAG CTCCTATTCG	7440
ATATGGCCTC AAAGAAAAAC GCTGCTTTCT CTCAAATTGA AATCTTTTCA TCCCATCTCC	7500
CATCATTCAT TATTACTGTA TATTTGTAT ATCAGAAATA GTTTGTATTC ACAAATCTTT	7560
CTAGTTATTC CCTTATCATT CCTAATTAAAG GGAGATAACA TACAATAATT TTTAGTTAAA	7620
TGTATATCGA TGTTTTTTGT TTTCTTAAT AAACGCAATA CAAAAAGAGC CTGTTACCAA	7680
GCTCTTTGTA CTCAATGAAA ATCAAAGAGC AAATTAGGAA ACTAGCCACA GGTGCTCAA	7740

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AACACCGTTT TGAGGTGCA GATAGAACTG ACGAAGTCAG CTCAAAACAC TGTTTTGAGG	7800
TTGCAGATAG AACTGACGAA GTCAGTAACA TCTATACGGC AAGGCGACGC TGACGTGGTT	7860
TGAAGAGATT TTCGAAGAGT ATTAGTCTAT TATTTCTTCT CAGCGCGAAG GGCTGACAAG	7920
ATTTGTGTTT GGATATCATC CACACCATTT GGAGTATTG GTAAAAAGAT AGTTTGATTT	7980
CCTTTAGAGG CAAAGGTATT CAAGGTATCC AAATACTGGT TGGTCAAGAG GATAGACATG	8040
ATTTGTCTTT CTGTTCATGCC AACATTGGCT TCCTTGAGTT CGGTGATAGA CTCTGCCAAT	8100
CCATCCACAA TCGCCTTACG TTGTTGGGCA ATCCCCACAC CATGAAGGCG GTCTTTTCT	8160
GCTTCTGCTT CAGCTGCAGT GACAATTTTA ATCTTGTGAG CTTCGCCAA TTCTTGTCGT	8220
GCGACCCGCT TACGTTGCGC CGCATTGATT TCATTCATGG ATTGCTTAAC TTCTGCATCT	8280
GGTTCGACCT TGGTAATCAA GGTTCACG ATAATGTAGC CGTAAGTGGT CATTTCTTCT	8340
GCTACTTGGT GTTGAACCTC AAGGGCAATC TCATCTTTT TCTCAAACAA TTCATCCAAG	8400
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GCTACATTCA TCATAACGAA CACATTGTCC TTGGTCTTAG TCTCAACCAC AATATCACTT	8580
TGCAACAAGC GCAACTGAAT CCGTGCTGCA ATCGAGTCAA TCCCAAAAGG CAAGCGAATA	8640
TGAATACCGC TATTAGCAAC CTTTGGTAT TTCCCAAAGC GTTCAATAAT CGCCACCGAC	8700
TGCTGACGAA CCACATAAAC TGTACTCAGT GTGACTATCA CCAATAGGAG CACACAAACA	8760
ATCAGAAAAA TCATGAAAAA TATTGCCATA ATGGAACCTC CACAAGTATT TTTCTAGTAT	8820
TATAGCACAT TTAAGAAGG CTGTGCCGTT TTTACTGCGA TTTTTCCTGA AATGTCAATA	8880
ATTAGAGGTG AATTGTCCTA TTGTCGTCCA ATCTCTTGCT AAAATAACTC TTTATAAAAG	8940
GCAATCGTTT CTTCTAAGGT TGGCATAAAT GGATTCCTG GTGCGCAGGC ATCAATCAAG	9000
GCATTCCTAG AAAGGTATTC AAAGTCGAAA TCTTTTCTT CAATACCAAG TTCAGTCAGT	9060
TTCTTAGGAA TACCTACTGT CTCAGAAAGC TTCTCAATCT CAGCAATCGC ATAATCGGCA	9120
CATTCTTGAT CTGATTTACC TTCTACATGA AGTCCCAAGG CTTTGGCAAC ATTGCGGAAA	9180
GCTTCTGGTA CACGTTTAGC ATTTTCACGT TCTATAACTG GTAGCAACAT GGCACAGCAC	9240
ACGG	9244

(2) INFORMATION FOR SEQ ID NO: 69:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 8898 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double

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(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 69:

GATCTGAACT TTATCATCAT AACTTAATTT CATAATAAAA ACACCCCAAA AGTTAGATTT	60
TTTCTGTCTA ACTTTTGGGG TGTAGTTCAG TCATTGGACT GACGTTTTTT TGTATGCTTA	120
TTTTGATTTG ATGTAGTTGA TACCATCTGC TTTTGGTGCG ACTGCTTTTC CAAAGAAGGC	180
TGCTAAGACA AGAATTGTCA AACATAAGG TGCAATTGA AGATAAACCG CTGGCACTCC	240
TTGTAGGAAC GGCAATTGAG AACCGATAAC AGCCAAACTT TGTGAAAGTC CAAAGAAGAG	300
ACTAGAAAGC ATAGCACCGA TTGGATTCCA TTTCCTAAAG ATCATCGCAG CAAGGGCGAT	360
AAATCCAGGT CCAACAATAG TTGTCCTGA GAAGTAACT GAGATTGATT GCGCATAAAT	420
CGCTCCGCCA ATTCCACCTA GAAAACCTGA AATAATAACC CCTAAATATC TCATCTTGTA	480
GACGTTGATT CCCAAGGTAT CCGCTGCTTG AGGATGTTCA CCGACAGAGC GGAGACGAAG	540
ACCAAATTGA GTCTTAAAGA GAATAACCA AGCAAGGAAT GAGAAGGCAA TCGCCAGATA	600
ACCAAGTAGA CTAGTTGACT TGAAGAAGAT ATCACC AATC ACTGGGATAT TTGCCAAGAC	660
TGGGAAATCA AAGCGTCCAA AAGTTTGACT TAGGTTGTCG GTTTGTCCTT TGTATAAAG	720
AACTTTAACT AAGAAAACAG CCAAGGCAGG CGCCATCAAG TTCAATACCG TACCGCTGAC	780
AACATGGTCT GCACGGAAAT GAACCGTCGC TGCTGCCTGG ATGATAGAGA AAACACTACC	840
AACCAATCCT GCTACAAGCA AGGATAGCCA TGGAGTTGCT GCTCCAAAT GTTCTGCAAA	900
TTCAAGGTTA AAGACAACTC CAGAAAAGGC ACCCATAACC ATAATTCCTT CAAGGCCAAC	960
GTTTACCACA CCACCACGTT CAGAGAAAAC ACCACCGATA CTTGTAAAGA TGAGAGGTGC	1020
TGAGTAAATC AGCATAGAAG ACACCAAGAG GGGGAGCAAG GTTATAATAG ACATCTTTAC	1080
TTACCTCCTT TAACTTGTTT TTTCGGTTTG ACAAAGCGTT CGATAAGGTA ATGAACACTG	1140
ACAAAGAAGA TAATAGACGC TGTACAATG CTGACAAGCT CAGATGGTAC CTGCGCCGCA	1200
TTCATACCAG GAGCCCAAC TTGGAGAACG CCAAATAGGA AGGCTGCAAA GAGTATACCA	1260
ATTGGTGAGT TGGCCGCAAG CAAACTAACC GCCATTCCGT TAAATCCGAT AGCTAATGAC	1320
GAACCTTGAA CATAGACGTT CTGGAAGGTT CCCAAACCTT CAACAGCTCC ACCAAGACCT	1380
GCCAAGGCAC CTGAATAAT CATAGATAGG ATAATAGTCC GCTTGGCAGA AATACCAGCA	1440
TATTCTGAAG CATGTGGATT AAGACCAACT GCACGGATTT CAAAACCAAG AGTTGTTTTC	1500
TTGAGCATGA ACCAAATAAC TGCAACGGCA ATGATGGCAA AGAAAATACC AATATTCATC	1560
CGTGAGTTAC CAGTCAACTC AGCCAACCA GGTGTCTGAT AGGTGCAAT AGCCCAACA	1620



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CGAATGGTCG AATCTGTACT TTGCATGAAG TCTTTAGGGA AAGCATGGAT AAAGGCATTC	1680
CCTACATACA AGACAATGTA GTTCATCATG ATGGTTACAA TAACCTCTGA CGTCCCTAGA	1740
TAGGCCCTAA GAATACCTGG AATCGCTCCG ACAATCCCAC CAGCAATCAA GGCAATCACG	1800
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CTGAGAATCC AACCTGCCAA AGCCTGACCA GGAAGTCCGA CGTTAAAGAA ACCAGCTCGA	1920
CTGGCAACGG CAAAACCAAG ACCAATCAAG ACCAGAGGAC CCATAGCACG GAAGATTCT	1980
CCAATCCCAC GCAGACTGCC AAAGGCTGTA TAGAACAATT CTTCGTAGCC CCAAATAGCA	2040
TCATAACCGA AGATCCACAT GACAATGGCT CCGAGTAAAA TTCCTAGGAA TACAGAAATC	2100
AAGGAACCG AAATTGTGTG TAATTTTTTA GACATCACTC TTCTCCTTTC CCAAGTTTCC	2160
ACCAGCCATC AAGACACCAA GTTCTGTGTT ATTGGTTGTT TCTGGTGATA CAATACCTTG	2220
AATCTTACCA TCGTGGATAA CGGCAATACG GTCTGAGACG TTTAAATCT CATCCAATTC	2280
AAAGCTGACA ACAAGGACAG CCTTGCCATT ATCAGCTCT TCAATCAAGC GTTGTGGAT	2340
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ATCTCGATCA ATTTACGAG CAATAATTGC TTTTGTGTA TTTCTCCTG AGAGTGCAGC	2460
TGCAGGAAC TATTCACTGG CAGCGCAAC ATCAAATCT TCCATCAGCT TTTTAGCATA	2520
AGAAGTAATA TTTGAATAAT TCAAAATCC ATTTTACTA TGTGTTCTT TATAGTAGGT	2580
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ACGTCCTACC ATCATTTCCG CCAAATCAGC ATTGGTAGCC CCTGCAATTT CAACGGTTTC	3000
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CAACTCATCA ATTTCTGATG GAGTCAAAAC AGCCGTGGT TCGTCAAAGA TAAGGATATC	3180
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TGCTACCTTG GCAGAAGGT CAACAGCTAA GCCATAACGT TCAGAAAGAG CCTTGATTTT	3300
TTTGCTAGCT CCAGCGATAT CTAGCACACC ATTTTGTAGT AATCACTAC CTAAAATGAT	3360

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GTTTTTCAGCC ACTGTGAAGG CTTCAACCAA CATAAAGTGC TGGTGAACCA TCCCGATTCC	3420
CAAGCTAGCT GCTTTAGATG GGGAGTCGAG ATTGACAACCT TGACCGTTGA CCGCGATTTC	3480
ACCACTAGTT GGTTCAGAA GGCCTGCTAA CATGTTTCATT AGCGTGGACT TACCAGCCCC	3540
ATTTTCTCCT AAAAGTGCAT GAATTTACCC TTTTCGTAGG TGCAAGTTGA TTTTGTCTGT	3600
GGCAACAAAT CCACCAAACA CCTTGGTAAT ATCACGCATC TCAATGACAT TTTCTGTGTC	3660
CATGTGCTCT TCCTTTCAGA GTCTTATTTT ATTTCAATAA AACTTGCTAG TTTGTCTAGT	3720
AGCAAGCTTT ACTTAGACAA AATGACTTTG TCTCAACTCT TAAAAAGCG GCCCTTGGCC	3780
GCTTCCTAAG AAATGACTTC CATCCATTAT TTTTCAGGAA CTTTACGCT TCCATCAAGG	3840
ATTTTAGCTT TTGCATCTTC GACAGCTTTT TTACCTTCTT CTGAAAGGTT TGTACTGTC	3900
AAGTCAACCC CTTTATCCTT CAATGAGTAA ACGATCACTT GACCGCCAGG GAATTCCTCT	3960
CTTTCTGCCT TGTTAGAAAT ATCTTTTACA GTTGTACCAA CTTGTTTCAA AGTAGATACA	4020
AGACAAAGT TTGATTCTTT GCCATCTTTA GAAGTGTATT TAÇCTTCTGC TTCTTGGTCA	4080
CGATCAACAC CGATAACCCA AACTTTTCA TTTTCAGGAC GGCTTTCGTT GAGAGATTTT	4140
GCCTCTGCAA AGACACCTGC ACCTGTACCA CCAGCTACTT GGTAAACAAT ATCTGCACCG	4200
GCTGCGTATT GTGCGGCTGC AATTGTTTCA CCTTTAGCCG CATCACCAA TGAACCAGCG	4260
TAGTCAACTT GGACTTTGAT AGATGGGTCT ACTGACGCAA CACCAGCCTT GAATCCTGCT	4320
TCAAAACGAG AGATAACTTC AGATTCGATA CCACCTACAA AACCAACTTG TTTTGTCTTA	4380
GTGTTTTTGT CTGCAGCCAC ACCTGCAAGG TAACCTGACT CATATCAGC GAAAGTTACG	4440
CTCGCAACAT TCTTTTGGTC TTTAATCACA TCATCAATCA AGACATAGTT CAAGTCAGTG	4500
TGTTCTTTTG CTGCATCTTT AACTGCATTA TTAAGGGCAA AACCAACACC GAAGATTAGG	4560
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ACTGAACCTC CTAATAAGA TGTGCAACGA TGTGCAAGT ATGGATTGGT TGGCCACAAG	4920
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ATTCCCCGAC CGTCATCTCG ACCGTCGATT TATCTTTTGC GACTAAGGTC ACTTTTAGAT	5040
CTTGTTCAAA AAATTCAGCC ATCACTTGGC GACAAGCACC ACATGGCGAG ATCGGTTTTT	5100
CAGTTTGACC ATAGACAATC AATTCTGAAA ATTCTCTTTG GCCTTCAGAT ATAGCCTTAA	5160

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AAATAGCTGT TCTCTCACCG CAATTGGTCA AAGGATAGCT AGCATTTTCA ATATTCACTC	5220
CCGTGTAAAC ACTTCCGTCT TPAGCTACTA AACTGCTCC GATAGGAAAG TGAGAATAGG	5280
GGACATAGGC ATGTTTGCTG GTTTC AATTG CCAGTTCAAT CAACTCAGTA GTCGCCATCT	5340
GCCAAATTCTC CTTTAAAT AGCTACCCCA GCTGACGTTT CGATACGGGT CGCACCTGCT	5400
TCGACAAAGG CAAGAGCATC TGCATAAGAA CGAGCTCCAC CGGCGGCCTT GACACCCATA	5460
TCAGATCCAA CTGTTTCACG CATTAAATGTA ACATCTGCTA TCGTAGCACC ACCAGTTGAA	5520
AAGCCAGTAG ATGTTTGTAC AAAGTCAGCC CCAGCTTTT GGGCCAATTG GCAAACAACA	5580
ACTTTTCTT GGTCTGTGAG AAGGCAAGCT TCAATAATGA CTTTCACTAA CTTATCACCA	5640
CTTGCTTCCA CTAATGCGCG AATATCTGAC TCAACCAAGG CTAAATTACC TGATTGAGA	5700
GCTCCAACAT TGATCACCAT ATCAATCTCA TCTGCACCAT TTTGGATAGC TTCTTTGTG	5760
TCAAATGCTT TCACGGCTGA AGTTGTTGCT CCCAAAGGGA AACCTACTAC TGTGCAAACC	5820
TTAACATCTG TGCCTTCAAG TCCTTTT TTA GCATGTTCAA CCCAGGTCGG ATTAACGCAA	5880
ACACTGGCAA AGTCATACTC TCTAGCCTCA GACAACAAAC TATCAATTG TTTTCTCTT	5940
GCATCTGTT TTAAGCGT ATGATCTATA TATTTATTTA ATTTCAATTC GGTTCCTCT	6000
CCATTAGGA GATGATTCT ACAATTCAC GGATTTT CACTTCATCA CTTATTTTAA	6060
CACATTTTG GAAATCTGTA ACTAGTTGAG GTGGAATTT TTCATTTGTG TATACTTTG	6120
CAACAATTC ACCCTTTGA ACGGAGTCTC CAATCTCTT TTCAAAAACA ATTCCTGTTT	6180
CATAGTCCAA GGCATCAGAC TTAAGTGCAC GACCAGCACC CAGCCTCATG GCATAAAGAC	6240
CAAAGTCCAT AGCTGGAAGA GCTGAAATGA CACCCGTTTC CTGAGCAGGG ATTTCCACCA	6300
CATGAGCTAC ATTTACAGGA CGATAGAGGT CTTCCAAGTC TCCACCTGG GCTTGCACCA	6360
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TATCTGACG TCCTTGACCT TGCAAAATCT CCAATGCTTC AAGGATTTCC AGACGATTC	6540
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CAACCTTACC AAGATCTACC ATAGTTTGAG CCAACTCACG CGCCTCATCA ACCGTCTTCA	6660
TGAAGGCACC CTCACCGACA GTCACGTCTA GCAAATAGC ATCCGCCCCC GCCGCAATTT	6720
TCTTGCTCAT CACCGAACTC GCAATCAAAG GAATCGTGTG GACAGTTGCG GTCACATCAC	6780
GAAGGGCATA GAGAAGCTTA TCTGCTTTGA CCAGCTGGTC TGATTGCCCA ATGACAGATA	6840
CTCCAATATC CTGAACCTGA CGAATAAAAT CCTCTTGACT ACGTTCTACT TGATAGCCCT	6900

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TAATGGACTC CAATTTATCA ATTGTTCCGC CTGTATGGCC AAGACCACGA CCACTCATTT	6960
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CGACACCACC AGTAGAATGC TTGTCAACTT TCACACCATC AATGGCTGAC AGGTCAAAC	7080
CTTGCCCACT CTTAACCATA TTCATCGTTA AATCAGAGAT TTCTCGAGTC GTCATTCCCTT	7140
TAAATAAAC AGCCATAGCA AAGGCAGACA TCTGATAATC AGGAACAGTT CCTGATACAT	7200
AGCCTTCTAT CAGCCATTCA ATTTCACTTG AAGTCAGTTC TTGACCGTCT CGTTTTTTTT	7260
GGATTAAATC AACTGCTCTC ATTCTTTCAC ACTTCTAAGG ATATAGTATC CCTTGTCTTT	7320
TTTAAGGATT TCACAATTGC CAAACACATC TTCCATCTTA GACTTGGCAC TTGGAGCTCC	7380
TTGTTTTTTC TGGATGACGA TGGTCAAATC TCCACCAATT TCCAAGAAAT CTTTACTTTT	7440
CTCGATGATT TCATGAACGA CTGCTTGCC CGCACGGATA GGAGGATTGG AAATGACATG	7500
GTCAAATCGC CCTTGAACTC TTGCATAAAT ATTAGATTGA AATATCGTCG CTTTTCGATT	7560
ATTTTTTTCA GCATTCTCTT GAGCTAAATC CAGGGCACGA GTGTTAATAT CAACCATGGT	7620
CGCCTGAAC CCGTAAACCT TGACCAAGGA CAAACCTAAT GGACCATAAC CACAGCCTAC	7680
ATCTAGGACT GTCTCTCCTT GGTGACATC CAGACACTTG AGCAAGAGTT GACTTCCAAA	7740
GTCAACCATT TTCTTGCTAA AAACACCCGC ATCTGTCAAA AAAGTCATTT TTCTCCCAA	7800
CAAGTCCACT CTCAACTCAT GAATGTCGTG AGCAGCGTCA GGATTTTCTG CATAGTACAT	7860
TTTACTCATG ACACTATTTT ACCATAATTT GACTCAAATT GTAAATCGTT TACAAATTGA	7920
TAATAAAACG AAAAAGACCG AAGAAAGCAA GTCACGAAGC CATTTTCTTC AATCTCTTTC	7980
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ATTATCAACA AAATTCCTAA CAAAATGTTT AGATAAAAGC CCAACTGATA CGTTTATGTC	8160
AGGATTTCOA AACTTGTCOA AAGTCGTATC AAATCTTCTA GTGACATGTG GAAGAAATAA	8220
CCCTCTGTCG CAATCCGTAG GACTAAAAAG CAATAACTAC CCGCAGCAAT CCATTTCTGC	8280
CATCGTTTTT TAGTAAGAAA GCAATTAAGA ACGAACAAAT AAAGACAGCT GTTACAATAG	8340
CATGTTCCAT CAAAAAGTA AAACCGTAAT AGGTTTCCAC AAAGCATCTA CCATTATCTG	8400
CATGGGTTCC TTTTATAAAA GGTAAGCAA AACTTAAAT AAAACAGAGT TCCAATATGT	8460
AACGTTTTAA GATTTTCATA GTACACCTCC TATAAGTTGT GAACTAAAAA GCCCCCTTTA	8520
TAAGCTTATA AATCAGTAGA ATCTATCTCC TATTTTCATCA ATAAATTGAT CACTTATACT	8580
ATATACCATT GACTTACCAC ATTCAAGAAA CCGCTTTATT TTTTTCAGCTT TTTATGGTAT	8640
GATAGACAAA ATATCTAGGG GAAAACAAAT GACCAACGAA TTTTTCATT TTGAAAAAAT	8700

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CAGCCGCCAG ACTTGCAAT CTTACATCG AAAGACAACA CCTCCTTTGA CAGAAGAAGA 8760  
ATTGGAATCT ATCAAGAGTT TTAATGACCA AATCAGTCTC CAAGACGTTA CAGATATCTA 8820  
TCTCCCTTG GCTCATTTGA TTCAGATTTA CAAGCGAACT AAGGAAGATT TAGCCTTTTC 8880  
AAAAGGAATT TTCCTCCA 8898

## (2) INFORMATION FOR SEQ ID NO: 70:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 13188 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 70:

TATCTTAACG aGGATTGGGT TTATCGTCAG TCTTATTGCC CTAATTGTGG GAACAATCCC 60  
TTAAATCATT TTGAAAATAA TCGGCCTGTA GCAGATTTTT ACTGTAATCA TTGTAGTGAG 120  
GAGTTTGAAC TAAAGAGCAA AAAAGGAAAT TTTTCATCAA CAATCAATGA TGGTGCTTAT 180  
GCAACGATGA TGAAGCGTGT GCAGGCAGAT AATAATCCTA ATTTCTTTTT TTTAACTTAC 240  
ACAAAAAATT TTGAGGTAAA TAACTTTCTT GTCCTTCCGA AGCAATTTGT TACACCGAAA 300  
TCGATTATTC AAAGAAAACC ACTTGCACCA ACTGCTAGAC GAGCAGGTG GATTGGTTGT 360  
AACATTGATT TATCACAAGT ACCTTCTAAA GGAAGGATAT TTCTTGTGCA AGATGGACAA 420  
GTTAGAGATC CAGAAAAAGT TACAAAAGAA TTAAAGCAAG GTTTATTTTT AAGGAAGAGC 480  
TCTCTGT CAT CAAGAGGTG GACAATAGAA ATTCTAAATT GTATAGATAA GATAGAGGT 540  
TCAGAATTTA CCCTTGAAGA TATGTATCGT TTTGAAAGTG ACCTAAAAAA TATCTTTGTT 600  
AAGAACAATC ATATCAAAGA AAAGATTAGG CAACAGCTTC AAATATTAAG AGACAAAGAA 660  
ATAATAGAAT TTAAGGTAG AGGAAAGTAT CGGAAATTAT GAAAACGAAA CAACTTGTG 720  
CATCAGAAGA GGTGTATGAT TTCTTAAAAG TCATCTGGCC TGATTATGAA ACTGAAAGCC 780  
GTTACGATAA CCTAAGTTTA ATCGTCTGTA CCTTATCAGA TCCCGATTGT GTGAGATGGT 840  
TATCTGAAAA TATGAAATTT GGTGACGAAA AACAACTAGC TTTGATGAAG GAAAAATATG 900  
GGTGGGAAGT AGGAGATAAA TTGCCAGAGT GGCTACATAG CTCCTATCAT AGATTATTGT 960  
TAATAGGTGA ATTATTGGAA AGCAATCTAA AACTGAAAAA GTATACAGTA GAAATTACAG 1020  
AAACTTTATC ACGTTTAGTA AGTATAGAGG CTGAAAATCC AGATGAAGCC GAACGACTTG 1080  
TAAGAGAAAA GTATAAGAGT TGTGAAATTG TTCTTGATGC AGATGATTTT CAGGACTATG 1140

568

ACACTAGCAT ATATGAATAG GTAGATGTTT TTATTTTGTG AACAAAAAG AGGCTCGCAC	1200
CTCTTTTCT TATTTCTTTT TATGATTAA TACGGCATTG AGGACAATAG CGAGTAGGCT	1260
GGCTACGACG ATTCCGTTG AGAAGAACAT TTGGAAGGCT GTCGGCATGC TGACAAAGAG	1320
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TTCAATTGTTA GCAAAGTCAA CACGGGCGAG GATTTGCATC CCTTGAATTG ATACAAAACC	1440
AAACATTACC AGCATGGCAC CACCGAGGAC GGAGCTTGA ATGATTGGG CAAGGGCGCC	1500
AAACTTAGGA AGCAGTCCA GGAGAACCAG GAAACCAGCT GCGTAGTAGA TTGGCAGGCG	1560
TTTTTTGATG CCTGACAAAT TAACCAAACC AACGTTTTGT GAAATCCGG TGAAGGGAA	1620
GGTGTTAAAG ATTCTCCGA GAAGTACGGC CAAACCTTCT GCGCGGTATC CGTTGCGAAG	1680
GCGCGTGCTG TCGATTGGAT CCTTTGTGAT ATCAGACAAG GCCAGATAAA CACCAGTTGA	1740
CTCAACCATA GACACCGTTG CGATGATACA CATCATGACA ATAGATGAGA TTCAAAGGT	1800
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GAAGTCCACC AAGCCCATAG TAGCAGCAAT GGCAGTTCCA ACAACCAGAC CAATCAAAAT	1920
AGAGATAGAC TTGATAAATC CTTTGGTAAA GATGTTGATC AAGAGGATAA TCAGAACAGT	1980
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AATAGCGACA GGGATCAAGG TTAAACCAAT CGTGTAATA ACAGATCCTG TTACGATAGA	2100
TGGGAAGAGA TTGGCTACTT TTGAGAAGAT GCCTGAAACA AGAACCACGT AAATCCCAGA	2160
TGCGATAAGG GCACCAAACA TAGCGCCACT ACCATGGCTT TGCCCAATCA TAATCAAGGG	2220
AGCGACCGAC TGAATGCAA CTCCAAGAAC GACTGGGAGT CCAATCCCA AGTATTTGTT	2280
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GGTCAACTGC TCAGCTGAAT AGCCAAGGGC TGTGCAATC ATGATGGGAA CCAGGATAGA	2400
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AAACGAGCAA GTGATAGGAC AGGGTAGCCT GCTTTTTCAA GCAAATCAG ACCATCTTGG	2580
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AAAATCATGG GAACGTTTAA GGCTTCAGCT GTAAAAACGG CTGGGGCAAT ACCCGACGCT	2880
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CCTAAAGTCT AAAAGTTAAT TTAATTGTTG TTAAATATT TCTATAGTGA TCCCTTTTGC	3120
TAATACTATA TATTTGATAA AACTATTACG AGCGAAGCGA GTCTTATCAA ATATTTCCCG	3180
TTGTAGTGGT ATCATAGACA ATAATCTTGT TATTGTCTAT GACGGGATTT TTGAGAGTAA	3240
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ACCTTGTA GAACGCTGC CAATTCACGA CATAACAAG TAAACGATA TTCAATTTTA	3540
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AAAACACTGT TTTGAGGTTG TGGATAGAAT TGACAGAGCC AGTATCATAT ACCTACGGTA	3780
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GGACGTTGGT ATTCAATCCT AAAACCCAGT AAACCACAGT AGAAGGACCG GGACTGTTTCG	4260
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AGTCAATTTC CAAGACAATC GGTGTATGGT CTTGGCGAGC ACCTGAGTCA ATCATATCAG	4380
ATTTAGTGAC CTTGTCAGCG ATACGGTTAC TTGTAGCCA GTAGTCGATT CTCCAGCCTG	4440
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CGCCATGAAC ATGGCGGAAG GTGTCTGTAA ATCCAGTTGC CAAAAGGTTG GTAAATCCAG	4560
CACGTTCCCT GTCAGTAAAT CCAGGTGAAC GGCGGTTGCT AGCAGGATTT GCAAGGTCGA	4620
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CAGCCAAATA CTCAGCATAT TTGGCATCCC AGACTTGGCG TTCTTCCAAG CGTTTGAGAC	4740
CGTCACCAGC GTTTGGAGTG TAAACTTGGG TTACGAAAAA TGCATCAAAT TCTAGAGTGA	4800
TGATACGACC TTCCAAGTCC ATGGTAGAAG GGGCACCAGT TTCTGGGAAG CTGATAGTAG	4860
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TCTTTGTAGG TCCTTTGGCA GAAAGCTTGG TTTCTTGGAT AGCAATGATA TCAGCATTTT	5040
CAGCGACCAA GGTTTGTAGG ACTTCTTGGG ACAATTTGGC ACGAGCTGAG TCACTAGTTA	5100
GGGCAGCGTT TAGGGAATCA ATATTCCATG AGATAAGTTT CATAAAGTTA CCTTTTTCAT	5160
TCAGATTATA GATTTTATTA TACCAAAAAA AGATCTATTT CCCCACGTA TGGTTTGAAA	5220
AATTACTCTC TTTCTTTAT AATTAAGAAT GATTTTATGA AAGGGAGTGA AAATACATGA	5280
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AAGTTAGAAA AACGCCGTTA TCTAGTCGGA ATTGTGGCCC TGATCTTGGT TTCCGTCCTC	6480



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TATTTGCGCT ATGTGTGGCG TATGTATATC CTTGGGACCT CTTATTGCTT GGGACAGATC	6660
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CCTACAAACT GTAGTTCAGT ATGTCGGCAA TCTTCTCTTT GCGCGCGTGT CTTACAGTAT	8400
TGTTAGGGAT ATTCGTCGGG ATGCCTTTGC CAATATGGAG AAATGGGCA TGTCTTACTT	8460
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AGGTCGTGTC TTTGCCCTGA TAGACGAGAG GACCTATGAA CCTCTTCAAG AAAATGGGCA	9120
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GAGAAAAAC ATCGGTTTGG TCTTGCAGGA ACCCTTCCTC TATCATGGAA CTATTAAGTC	9420
CAATATCGCC ATGTACCAAG AAACCAGTGA TGAGCAGGTT CAGGCTGCGG CAGCCTTTGT	9480
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CCGCCTTTCT ACTATTCAAG ATGCCAACTG CATCTATGTC TTGGATAAGG GACGCATTAT	9780
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AGCGTGTGAC CCAGTACAAC CGTCGGTTCA AGATTGGA GTTTCGTACC ATGGTGACGG	10320
ATGCGGATAA AAAAGGAAGT CTGGTGACTT CTGCTAACGA TAGCCGCATT ACCAAGGTTG	10380
GAAATTTTCAT CCGACGTGTC CGTTTGACG AACTGCCTCA GTTGGTCAAT GTCTTTAAAG	10440
GTGAGATGTC CTTTGTGGT ACACGACCTG AAGTGCCACG TTATACAGAG CAGTATAGCC	10500
CTGAAATGAT GGCAACCTTG CTCTTGCAAG CAGGGATTAC CTCTCCAGCC AGCATCAACT	10560
ACAAGGATGA GGACACAATT ATCAGTCAAA TGACGGAGAA AGGTCTGTCA GTTGATCAGG	10620
CCTATGTGGA GCATGTTCTT CCTGAAAAGA TGCGCTATAA CCTCGCCTAT CTCCGAGAGT	10680
TTAGTTTCTT TGGGGACATC AAAATCATGT TTCAAACCGT GTTTGAGGTA CTAATAATAA	10740
GTAGTCATAA GAAATGAGT ACAGATAAAA GGAGCAAATC AATGCCAAAT TACAATATTC	10800
CATTTTCACC GCCTGATATC ACAGAAGCAG AAATTACTGA AGTAGTGGAT ACCCTGCGTT	10860
CTGGTTGGAT CACAACAGGT CCTAAAACAA AAGAACTGGA GCGCCGCTTG TCTCTTTACA	10920
CACAGACACC TAAGACTGTT TGTCTCAACT CTGCGACAGC CGCTCTGGAG TTGATTTTAC	10980
GCGTTTGGGA AGTGGGACCT GGTGATGAAG TCATCGTTCC AGCCATGACC TATACGGCTT	11040
CATGTAGTGT CATTACGCAC GTGGGAGCAA CCCCTGTCTAT GGTGGATATC CAAGCAGATA	11100
CGTTTGAGAT GGACTATGAC CTGCTTGAGC AAGCTATCAC TGAGAAAAT AAGGTGATTA	11160
TTCCAGTAGA GCTCGCAGGG ATTGTTTGCG ATTATGACCG TTTGTTCCAA GTCGTGGAGA	11220
AAAAACGTGA CTTCTTTACC GCTTCAAGCA AGTGGCAAAA GGCCTTTAAC CGTATTGTCA	11280
TTGTCTCTGA TAGTGCCAC GCTTTGGGAT CTATTTATAA AGGACAACCT TCTGGTTCTA	11340
TCGCTGACTT TACTTCCTTC TCATTCCATG CAGTTAAGAA CTTTACAACG GCAGAAGGTG	11400
GAAGTGCAC TTGGAAAGCC AATCCAGTGA TTGATGACGA AGAGATGTAC AAGGAATTC	11460
AAATCCTTTC CCTTCACGGG CAACTAAGG ATGCTCTTGC CAAGATGCAA CTGGGGTCAT	11520
GGGAATACGA TATCGTTACA CCAGCCTATA AGTGCAACAT GACCGATATC ATGGCTTCAC	11580
TTGGTTTGGT ACAATTGGAC CGCTATCCAA GTTTGTTGCA ACGCCGTAAG GACATTGTGG	11640
ACCGCTATGA TAGTGGTTTT GCAGGTTCTC GCATCCATCC TTTGGCACAC AAGACTGAAA	11700
CTGTGGAATC TTCACGCCAC CTCTACATCA CCCGTGTAGA AGGAGCAAGC CTAGAAGAAC	11760

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GCAACCTCAT CATCCAAGAA TTGGCTAAAG CAGGAATTGC AAGTAATGTT CACTACAAAC	11820
CGCTTCCTCT CTTGACAGCC TATAAGAATC TTGGATTGTA TATGACGAAC TATCCTAAGG	11880
CCTATGCCTT CTTTGAGAAT GAAATTACCC TCCCTCTTCA TACTAAATTA AGCGATGAAG	11940
AAGTAGACTA TATCATTGAG ACTTTCAAAA CAGTTTCTGA AAAAGTGCTA ACTTTATCAA	12000
AAAAATGACA AACTACAGTC AAGCGAAAGT GATCCTGCCC CTAAAAAGTC TAATTGAGTG	12060
TAAAAACTGT TGTTTTCAAT TGATAATAGT TTACACCTGT AGTTGAGGCC CCTTTCCTCT	12120
CAGAGAGAGA ATTTTATAG GATTTCTCTT TCTTGTGGA GTCCCGTGGT TTGAAATAAG	12180
ATGTGAGCAA TTTAGTGTAG CATTTAGAAT CCTTACTAGA CATCATTTAG AAAATCTAGT	12240
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ATTGTGAAA CTCGCTCTT TTTTGTGTTT CAGAATATG TTCAAAATTT TGTGCCTGTC	12360
TTTCATGTT TAGTCATTCT TTTGCATGAT AGAATTTATA GCATGTTGAT ATTATAATAA	12420
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TGCTTGATG ACAAGGTATT TGTCTTTCA TTTATAATTT ACAACATATC AACAAATTTA	12720
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AAGGCTAAAG AGCAAACTAG GAAGTTGGCC ATAGATAGCT CAAAACCTG CTTTGAGGTT	12840
GTAGATATAG TAAATGAAA TGAGAATAGG ACAAATTGAT CGGGACAGTC AAATCGATTT	12900
CTAACAATGT TTTAGAAGTA GAGGTGTACT ATTTTAGTTT CAGTCTACTA TAGAACTGAC	12960
CAAGTCAGTA ACCTAGACTT AGGGCAAGGC GGCCTGACC TAGTTTGAAG AGATTTCGA	13020
AGAGTATAAA TTTTAATATT TTCTTGTTT ATTCTTGAC AATTCAATTT GGAAAATATA	13080
TGATAAAGAT AATGACAGCG GTGTCATTCT ATCTATTTTA AGAAAAGTAA TAATCAATTG	13140
TTAAAAATAG TAAAAAATT GGAGTTCTG ATGAAATATT TTGTTCCG	13188

(2) INFORMATION FOR SEQ ID NO: 71:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 32768 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 71:

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AACGAGTGCA TCAGTCTCAG CAAGCACCAG TCGTCGGCC TCAGCAAGCA CCAGCGCGTC	60
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AACAAGTGCA TCGGCTTCAG CAAGCACAAG TGCTTCAGCC TCAGCAAGTA TCTCAGCGTC	180
TGAATCCGCA TCAACGAGTG CGTCCGCTTC AGCAAGTACT AGCGCCTCAG CATCAGCGTC	240
AACAAGTGCT TCGGCTTCAG CGTCAACGAG TCGCTCTGAG TCAGCATCAA CGAGTACGTC	300
AGCCTCAGCA AGCACATCAG CTTCTGAATC TGCATCAACC AGTGCCTCAG CCTCAGCATC	360
GACAAGCGCC TCAGCTTCAG CAAGTACCAG TCGCTCAGCC TCAGCAAGTA CCAGTGCTTC	420
AGCCTCAGCG TCGACAAGTG CGTCGGCCTC AACCAGTGCA TCTGAATCGG CATCAACCAG	480
TGCGTCAGCC TCAGCAAGTA CTAGCGCCTC AGCCTCAGCA TCAACGAGTG CGTCCGCTTC	540
AGCAAGTACT AGTGCATCAG CATCAGCATC AACGAGTGCA TCGGCTTCAG CAAGTACCAG	600
CGCCTCAGCT TCAGCAAGCA CCAGTGCGTC AGCCTCAGCA AGTACCAGCG CCTCAGCCTC	660
AGCAAGCACC AGTGCCTCAG CTTCAGCAAG TACCAGTGGC TCAGCCTCAG CGTCGACAAG	720
TGCGTCGGCT TCAGCAAGTA CCTCAGCGTC TGAATCAGCA TCAACGAGTG CATCAGCTTC	780
AGCATCAACA AGTGCTTCAG CTTCAGCAAG TATCTCAGCG TCTGAATCGG CATCAACGAG	840
TGCGTCCGCT TCAGCAAGTA CTAGCGCCTC AGCATCAGCG TCAACAAGTG CTTCCGCTTC	900
AGCGTCAACG AGTGCCTCTG AGTCAGCATC AACGAGTACG TCAGCCTCAG CAAGCACATC	960
AGCTTCTGAA TCTGCATCAA CCAGTGCGTC AGCCTCAGCA TCGACAAGCG CCTCAGCTTC	1020
AGCAAGTACC AGTGCCTCAG CCTCAGCAAG TACCAGTGGT TCAGCCTCAG CGTCGACAAG	1080
TGCGTCGGCC TCAACCAAGTG CATCTGAATC GGCATCAACC AGTGCCTCAG CCTCAGCAAG	1140
TACTAGCGCC TCAGCCTCAG CATCAACGAG TCGTCCGCT TCAGCAAGTA CTAGTGATC	1200
AGCATCAGCA TCAACGAGTG CATCGGCTTC AGCAAGTACC AGCGCCTCAG CTTCAGCAAG	1260
CACCAGTGGC TCAGCTCAG CAAGTACCAG CGCCTCAGCC TCAGCAAGCA CCAGTGCTTC	1320
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TACCTCAGCG TCTGAATCAG CATCAACGAG TGCATCAGCT TCAGCATCAA CAAGTGCTTC	1440
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AACCAGTGCC TCTGAATCAG CATCAACAAG TGCCTCGGCT TCAGCAAGCA CCAGTGCGTC	1560
GGCTTCAGCA AGTACTAGTG CATCGGCTTC AGCATCGACA AGTGCCTCTG AATCGGCATC	1620
AACGAGTGCT TCGGCTTCAG CATCAACGAG TCGCTCAGCC TCAGCAAGCA CATCAGCTTC	1680
TGAATCTGCA TCAACCAAGTG CGTCCGCTTC AGCGTCAACC AGTGCCTCGG CTTCAGCGTC	1740

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GACAAGTGCT TCGGCTTCAG CATCAACGAG TGCCTCGGCC TCAGCAAGCG CAAGTACCTC	1800	
AGCGTCAGct TCCGCCTCAA CCAGTGGGTC GGCTTCAGCA AGCACAAGTG CGTCAGCCTC	1860	
AGCAAGTATC TCAGCGTCTG AATCGGCATC AACGAGTGCG TCTGAGTCAG CATCAACGAG	1920	
TACGTGAGCC TCAGCAAGCA CATCAGCTTC TGAATCTGCA TCAACCAGTG CGTCAGCCTC	1980	
AGCATCGACA AGCGCCTCAG CTTCAGCAAG TACCAGTGCT TCAGCCTCAG CGTCGACAAG	2040	
TGCGTCGGCC TCAACCAGTG CATCTGAATC GGCATCAACC AGTGCCTCAG CCTCAGCAAG	2100	
TACTAGTGCA TCAGCTTCAG CATCAACGAG TGCATCGGCT TCAGCATCAA CCAGTGCCTC	2160	
GGCTTCAGCG TCAACCAGTG CGTCAGCTTC AGCAAGTACC AGTGCTTCAG TCTCAGCATC	2220	
AACAAGTGCT TCAGCCTCAG CATCGACAAG TGCCTCGGCT TCAGCAAGCA CATCAGCATC	2280	
TGAATCAGCG TCAACCAGTG CTTCCGCTTC AGCAAGTACC AGTGCTTCAG CTTCAGCATC	2340	
AACCAGCGCC TCGGCCTCAG CAAGCACCTC AGCTTCTGAA TCGGCCTCAA CCAGCGCCTC	2400	
GGCCTCAGCA AGCACCTCAG CTTCTGAATC GGCCTCAACC AGCGCCTCAG CCTCAGCATC	2460	
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TATCTCAGCG TCTGAATCGG CATCAACGAG TGCCTCTGAG TCAGCATCAA CGAGTACGTC	2640	
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TGCCTCGGCT TCAGCAAGCA CATCAGCATC TGAATCAGCG TCGACAAGCG CCTCAGCTTC	3000	
AGCAAGTACC AGTGCCTCAG CCTCAGCGTC GACAAGTGCG TCAGCCTCAG CAAGTACTAG	3060	
TGCATCAGCT TCAGCATCAA CGAGTGCATC GGCTTCGGCG TCAACCAGTG CATCAGAGTC	3120	
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TGCATCGGCT TCAGCATCAA CGAGTGCCTC CGCTTCAGCA AGTACTAGCG CCTCAGCCTC	3480	
AGCGTCAACA AGTGCATCGG CTTCAGCGTC AACGAGTGCG TCTGAGTCAG CATCAACGAG	3540	

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TGCGTCGGCT TCAGCAAGTA CCAGTGCCTC AGCCTCAGCA AGTACCAGTG CGTCAGCCTC	3720
AGCGTCGACA AGTGCCTCGG CCTCAACCAG TGCATCTGAA TCGGCATCAA CCAGTGCCTC	3780
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AACCAGTGCA TCAGAGTCAG CAAGTACCAG TGCCTCAGCT TCCGCATCAA CAAGTGCCTC	3900
GGCTTCAGCA AGTACTAGCG CCTCAGCCTC AGCGTCAACA AGTGCTTCAG CTTCCGCGTC	3960
AACCAGCGCC TCGGCCTCAG CAAGTATCTC AGCGTCTGAA TCGGCATCAA CAAGTGCCTC	4020
GGCTTCAGCA TCAACGAGTG CATCAGTCTC AGCAAGCACC AGTGCCTCGG CCTCAGCAAG	4080
CACCAGCGCG TCTGAATCCG CATCAACCAG TGCTCAGCT TCAGCAAGTA CCTCAGCATC	4140
TGAATCAGCA TCAACAAGTG CCTCGGCTTC AGCAAGCACA AGTGCTTCAG CCTCAGCAAG	4200
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TGCATCAACC AGTGCCTCAG CTTCCGCATC AACAAGCGCC TCGGCCTCAG CAAGTACAAG	5040
TGCTTCAGCC TCAGCATCAA CCAGTGCATC AGCTTCAGCC TCAACAAGTG CTTTCAGCCTC	5100
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TGCGTCAGCT TCAGCATCAA CCAGTGCTTC GGCTTCGGCA TCAACAAGTG CCTCAGCATC	5220
AGCATCAACG AGTGCCTCAG CCTCAGCAAG TACTAGTGCA TCAGCATCAG CATCAACCAG	5280

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TGCATCAGCC TCAGCAAGTA TCTCAGCGTC TGAATCGGCA TCAACGAGTG CATCAGCATC	5340
AGCATCAACG AGTGATCGG CTTTCAGCGTC AACCAGTGCA TCAGTCTCAG CAAGCACCAG	5400
TGCGTCGGCT TCAGCATCAA CGAGTGCCTC AGCCTCAGCA AGTATCTCAG CGTCTGAATC	5460
GGCATCAACG AGTGCGTCAG CCTCAGCAAG TACTAGTGCA TCGGCTTCAG CAAGCACCAG	5520
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GGCATCAACG AGTGCGTCAG CCTCAGCAAG TACTAGTGCA TCAGCmTCAG CATCAACGAG	5640
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GCTTCAGCTT CAGCATCAAC AAGTGCGTCA GCTTCAGCAA GTACATCAGT TTCAAATTCA	5940
GCAAACCATT CGAACTCACA AGTTGGAAAT ACTTCTGGAT CGACAGGTAA ATCCCAAAAA	6000
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GCTGTTACAG GTATTGGATT GGTTCGAAA CGCCGTAAAC GTGATGAAGA AGAGTAAGAC	6120
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GATGATAAAA TAACAGTCAT TGTACCAGTA TACAATGTGG AAAACTATCT GAGGAAGTGC	6240
CTAGATAGTA TTATTACTCA AACATATAAA AATATTGAGA TTGTTGTCGT TAATGATGGT	6300
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GCTTTGATAT CTGCTTGGGG TAAACTCTAT AAGGCAAGAT TGTTCGAGCA GTTGCCTTT	6720
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AAGGTAATTT ATTTAAATAA AAGTCTTTAT GCTTATCGGA TTAGAAAAGG TAGTTTATCA	6840
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GAAGTCAGTC TCGCCAACGG TCAAGCTAGT GGTTCATCTG ACACAGCAAC GTATAAAGAG	7020
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GCCATTGTCC TCGCAGCAAA CTATGGCTAT GTAGACCAAG TTTTAACGAC AATCAAGTCT	7140
ATTTGTTATC ATAATCGTTC GATTGTTTT TATCTGATTC ATAGCGATTT TCCAAATGAA	7200
TGGATTAAGC AATTAAATAA GCGCTTAGAG AAGTTTGACT CAGAAATTAT TAATTGTCGG	7260
GTAACCTCTG AGCAAATTTC ATGTTATAAA TCGGATATTA GTTACACAGT CTTTTTACGC	7320
TATTTTCATAG CTGATTTTCGT GCAAGAAGAC AAGGCCCTCT ACTTGGA CTG TGATCTAGTT	7380
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TATCCAATA AGGAACCTTT CACTTGCTTA ATCTATACTG CCTCAGACCA TATTGAACAA	7920
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CACTATTGCG TAGATGTCGA TAATGAATTG GTAGAAACCA GTCAAGTACT TTTAGATATT	8100
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ATTGTAGATC ATGTTCTTAA AAAGTTTCAT TTACCGTTAA AGAATTTAAG TTATGCCACT	8820

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GACATCATTG TTACAGGAAG TTTAGACTAT TTATTTGATA TAGAACTAGA TGGTTATGCC	8940
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ACCAATCAAT ATCATGAAAC AGCATATGGA GATCAAGGAA TTTTAAATAT GTTATTCCAT	9120
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CACATAGAAG GAAATCATAA ATGGTATGAG ATTTCTGAGT TGAAAAATGG AGATTTACCT	9240
AGTGTATAC ATTATACTGG GGTAAACCT TGGGAAATAA TTTCCAATAA TCGCTTTAGA	9300
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AAGAAAAGAT AGCTATTTTA GCAAGTTCAG ACTATGACTT GACCAATCAT ATTTTGATTT	10560
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GTTATCTTAG CTCAAAAAG TGTTCAAAAG ATAGCTAGTC AACTGGGATT TAGAGAGGTT	10800
GGTATTTATT TTACACAT TGCTTCAGAT AGTCCTTCTG AAATGAATAA GCGTCTGGAT	10860
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GACTTGGTTC AACATGCCGA GTATGTTTTT AAGGGAAACC TGATTCCGAA GGATTACTTT	25140
TCTTATACGC GTTATTGTAG CGAGTATTTT GCTCCCAAGG ACAATGTTGC AGTCTTATAC	25200
CAACGAAC TT TATAATGA AGACGGGACT CCAGTCTATG ATATCTTGAT GAATCAAGGG	25260
AAGGAAGAAG TTTATCATTT CAAGGATAAG ATTTTCTATG GAAAGCAAGC TTTTGTGCGT	25320
GCCTTTATGA AATCTTTGAA TTTGAATAAG TCTGATTTGG TCAATTCTCGA TAGGGAGACA	25380
GGTATTGGAC AGGTTGTGTT TGAGGAAGCA CAGACAGCAC ATCTAGCGGT AGTTGTTTAT	25440
GCGGAGCATT ATAGTGA AAA TGCTACAAAT GAGGACTATA TCCTTTGGAA TAACTATTAT	25500
GACTATCAGT TTACCAATGC AGATAAGGTT GACTTCTTTA TCGTGTCTAC TGATAGACAA	25560
AATGAAGTTC TACAAGAGCA ATTTGCCAAA TATACTCAGC ATCAGCCAAA GATTGTTACC	25620
ATTCCTGTAG GCAGTATTGA TTCCTTGACA GATTCAAGTC AAGGGCGCAA ACCATTTTCA	25680
TTGATTACGG CTTACGCTCT TGCCAAAGAA AAGCACATTG ATTGCTTGT GAAAGCTGTG	25740
ATTGAAGCTC ATAAGGAGTT ACCGGA ACTA ACCTTTGATA TCTATGGTAG TGGTGGAGAA	25800
GATTCTCTGC TTAGAGAAAT TATTGCAAAT CATCAGGCAG AGGACTATAT CCAACTCAAG	25860
GGGCATGCGG AACTTTTCGA GATTTATAGC CAGTATGAGG TCTACTTAAC GGCTTCTACC	25920
AGCGAAGGAT TTGGTCTGAC CTTGATGGAA GCTATTGGTT CAGGTCTACC TCTAATTGGT	25980
TTTGATGTGC CTTATGGTAA TCAGACCTTT ATAGAGGATG GGCAAAATGG TTATTTGATT	26040
CCAAGTTCAT CTGACCATGT AGAAGACCAA ATCAAGCAAG CTTATGCCGC TAAGATTTGT	26100
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GGCTTCTTGA CCAAGAAAT TTTAGAAAAG TGAAGAAAA CAGTAGAGGA GGTGCTCCAT	26220
GATTGAAC TT TATGATAGTT ACAGTCAAGA AAGTCGAGAT TTACATGAAA GTCTAGGCGC	26280
TACTGGTCTT TCTCAACTTG GAGTGGTCAT CGATGCAGAT GGTTTTCTGC CTGATGGTCT	26340
GCTTCTCCT TTTACCTATT ATCTAGGTTA CGAGGATGGA AAACCTCTCT ATTTTAATCA	26400
AGTTCCCGTT TCAGATTTTT GGGAAATTTT AGGAGATAAT CAGTCTGCTT GTATTGAAGA	26460
TGTGACGCAG GAGAGGGCTG TCATTCAATTA TGCTGATGGA ATGCAGGCTC GCTTGGTTAA	26520

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ACAGGTAGAC TGGAAAGACC TAGAAGGTCG AGTACGTCAG GTTGACCACT ACAATCGCTT	26580
CGGAGCTTGT TTGCTACAA CGACTTATAG CGCAGATAGC GAGCCGATTA TGACAGTTTA	26640
CCAAGATGTC AATGGTCAAC AAGTTTACT GGAAAACCAT GTGACGGGTG ATATCTTATT	26700
GACTTTGCCA GGTCACTCCA TGCCTTACTT TGCAAATAAA GTTGAATTTA TCACCTTCTT	26760
TTTGCAAGAT TTGGAAATAG ATACCAGTCA GCTTATCTTT AATACTCTAG CGACTCCTTT	26820
CTTGGTTTCC TTCCATCATC CAGATAAATC TGGCTCGGAT GTCTTGGTAT GGCAGGAACC	26880
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TAAGAAGATC ATCATTCCAA ATAAGGCGAC TTATGAGCGC GCTTTAGAGT TAACTGACGA	27000
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CCTAAGACGA GATGCCTTAA TCTTGACCAA TTCAGATCAG ATTGAGCAAG TAGAAGCAAT	27120
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CTTGCTTTGA TTGTATTGGT AACTATACAA CCCCCTCAA ATCAACTATT TTCCATGGAT	27840
GCCACTAGTA ATATTGGTAA ACCAAGCTAC TGGCAGAGCA ACACCTTGGT CAAGGTGCTC	27900
ACTTTATTGG TGAGTTTGGC TTTATTTATT CTACTATTAA CCTTTATGGT GATTACTTAT	27960
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TACTCAATGA AATCAAAGA GCAAACAGG AAGCTAGCCG CAGGCTGCTC AAAACACCGT	28080
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AGCTCAAAAC ACCGTTTGA GGTGTGGAT AGAACTGACG AAGTCAGCTC AAAACACCGT	28260
TTTGAGGTTG TGGATAGAAC TGACGAAGTC AGCTCAAAAC ACCGTTTGA GGTGTGGAT	28320

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AGAACTGACG AAGctCAGTA ACATATATAC AGCAAGGCCG CGCTGACGTG GTTTGAAGAG	28380
TATTACTGTC TATATTTTGG GTAAAAATCA ACTTTTACTT GGATGAAGGT TTTGGCTTCA	28440
CGTAGGAGTT GAAGAAGGGT GCGCGGGTT TCAAATTCCT CTCTTGCTTT GGCAGACTG	28500
CGGTTCGGA AGACTTCCAG ATAACGTCA ATTTCATCTA GCAAATCAGA AGCAGGATTG	28560
GTCTGGCTCA GTTGACCTGC AATTTTGTAA AAGAGTTGCG CTAAGATCAG GCTTTCCTG	28620
GCGCAAGGT GACAAGTGT AATCTGTGG GCCATGTTTC TCAGGATACG ACTTTGTGCG	28680
TGTCTCATCT CAAAGTAGTG GATATGGTAG TCTGTCTGGT GAAAGAGGTG GTCAGAGTGA	28740
TCCAAATAGA CCAGTCTGAG GGCTTCTTTC AAAAGCGTGT CTAATTCGTC TACCAGCTGT	28800
GCTCGGTGCG GTCCGTCTCC TCTGGATAAA TAGTATTTGA AGCGCTGGAG GATATCTTTT	28860
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CTCAAGAGAG CGATAATTCC AGCCGAAACT GCTGACGAAA GATTGAGAAA ATAAGCAAGC	29280
AGGCAGGCAA GACAGGTAGC TAAGATGAGC TTGGTCGTAC GTTGGCTAAT AGACATAAGA	29340
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GAGGGAACCT CCGGCAATAC CTGAAGCATC ACAGGATGAG ATAGCTGCTA CCACACTGAG	29640
GACAAAGGCT GTGGCAAAGT CAACAGGAAT TCCAAGAGTG TTAAGTCAG CAAGGGTCAA	29700
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TAGAGGGTAA GGATTGCGTC TCATAAGAA GAAGGCAATC AAAGGGTTGA CCACAGGGGC	29940
AACAAAAAGC ATAGTCGTTA CTAATAGAAC CAATAAAATA CCGTAGTTGG CAAGGCTTCC	30000
GACTCCCTTG TCAGAAATGG TTTTAAAAAC AAGACCAAGG ATTCCAAATG GAGCCAGATT	30060

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ATTTTACTG GCTTCTCTCA TAGCGATTCC AAAAATGACT GCCCAAGATA AGATTCTAAT	30180
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CATAGGATAT ACAAGAAAAC AACAGTTTTT ATATTGCTAT CTTGTCCCTT TTGATGTTGG	30420
GAAAGGGCAT TGGCAACGAG AGCAAAGACT AGGATAGGAG CAACAGCTTT TAGACCTCCA	30480
ACGAATAAAT CCTCGAGTAG CCCAATCCCT GAGAGATTAG GAAGGGTCAG TCCTAGGATT	30540
CCCCACAAG CATACCAATC AAGATACGCT TGACAAGGCT TGCCTTATTC CAAGCATGAA	30600
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TATGGGAGCC CAAGGCTTTC TGTCTGATGT CATCAATGGC TTTTTCATCC TCTTTGAACG	31140
TCAACTGGAT GTGGGAGATG AGGTCGTTCT GACAAATGGA CCGATTACTG TATCGGGTAA	31200
GGTTGTCAGT GTGGGAATTC GTACGACACA GCTTCGTAGC GAGGAGCAAG CCTTCACTT	31260
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GAAGACCTTT CTGAAATTTA CGGTTTGGAC AAGGAAACCA TTGAATACGC ACTGGATAGA	31500
AACGAGCGCG CCCACATGGA CTACCACCGT GAAAGTGAGA CGGTTACCTT TATCTATAAT	31560
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GAGCATCGTC GCCTGATTAC CATTAGTAAT ACCAAGAACG CCTATGTCAT TGAACAGATG	31680
ACTCGTTATC TGGAGAACCA TGACACGCTT TCGATTTATA AGTTTCTCTT TGCCAGTCTG	31740
GAAATCATCA GCAATGCCTA CTATCCTGTC ATTGAGCAGA TGGACAAGAG TAGGGATGAG	31800
GTCAATGACC TCTTGCGCCA GCGAACTACC AAGAAAAACC TCTTTGTCCT GTCTGATTG	31860

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GAGACTGGTA TGGTTTATCT GACGGCAGCT GCCAAACAAA ATCGGATTTT GTTAGAGCAT	31920
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GCCATGATTG AGGCTCATCA GCTGGTATCC ATGACAGACC TAATCTCTCA GATTTTACAG	32040
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TTGACTATCA TTTCACTCTT GCTAGCTGTT TTGGCAGTCG TGACAGGCTT TTTCGGAATG	32160
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ATCTGACAGT CCCAAGCCTG CAGGCGCAGG GAATAAAGGC TGTTTTGGTC GATTTGGATA	32400
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AACGAGCAGT TGAGAAATTT GGGATTGATT ACGTTTACTG GGCCTTGAAG CCCTTCACAT	32580
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GTGACCAACT CATGACAGAT ATACGAGCAG CCCACCGTC AGGGATPCGG TCAATTTAG	32700
TCAAACCTT GGTCCAACAT GACTCAATCA AAACGCAGAT TAACCGAACT CGTGAGCGTC	32760
GTGTTATG	32768

## (2) INFORMATION FOR SEQ ID NO: 72:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 14872 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 72:

CCAGTCACAA AGAAATTGAG CGCGTTCAGC TGAGGATGCA CTATGATGCA AGCTACATTT	60
CATTTGATGG GATATTAAGA AAGGAGATTT TCATGACACT TTTAGATGTA AAACACGTTT	120
AAAAAATTTA TAAACACGT TTTCAAGGCA ACCAAGTAGA AGCCCTCAAG GATATTCACT	180
TTACCGTAGA AAAGGTGAC TACGTGCGCA TCATGGGTGA GTCTGGTCTT GGTAAATCAA	240
CTCTTCTCAA TATTCTAGCT ATGTTGATA AACCAAGTCG TGTCAGGTT TACTTGAATG	300
GAACTGACAC CGCAACTATT AAAAATTCAC AGGCTTCTAG TTTCCGGCGT GAAAAGCTAG	360
GATTTGTCTT CCAAGACTTT AACTTGCTAG ATACTCTGTC TGTAAAGGAC AATATCTTGC	420

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TTCCGCTTGT CTTGTCAAGA AGACCTATAA CGGAGATGAT GAAGAAATTG GTGGTGACAG	480
CTGAGAATCT GGGTATTAAC CAATTGCAAG AGAAGTACCC TTACGAGATT TCTGGTGGTC	540
AGAAACAGCG TGTAGCAGTA GCGCGGCCA TCATCACAGA ACCTGAAATT CTCCTTGCGG	600
ACGAGCCAAC AGGAGCCCTT GATTCCAAGT CATCTGCAGC CTTACTTGAT GTCTTTAATG	660
AAATCAATGA GCGTGGGCAA ACCATCCTCA TGGTAACCCA CTCAACAGCA GCTGCTAGCA	720
GGGCCAAGCG TGTTCTCTTT ATCAAAGACG GCATTCTTTA CAACCAATC TACCGTGGAG	780
AGAAGACAGA GCGTCAGATG TTCCAAGAAA TCTCTGATAC CTTGACTGTC ATGGCAAGCG	840
AGGTGAATTA GTATGTTTCG ATTAACCAAT AAGTTAGCGG TATCGAACTT GATTAAAAAC	900
CGCAAACTCT ACTATCCCTT TGCACTGGCT GTTCTCTTGG CAGTCACCAT CACCTATCTC	960
TTTTACTCCC TAACCTTCAA TCCAAAGATT GCGGAAATCC GTGGAGGAAC CACCATTCAA	1020
GCAACACTTG GATTTGGTAT GTTTGTCGTT ACCCTTGGCT CACCATTTATC GTCTCTATG	1080
CCAATAGTTT TGTCATGAAA AACCGTTCCA AGGAACTGGG TATATATGGC ATGTTAGGCT	1140
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TTATCTTTGG TACTTATCTA TTGTTTAATG CAGGGATTAC AGTCTTCCTA CAAATCTTAA	1620
AGAAAAACAA GAAATACTAT TACCAACCTA ATAACCTCAT ATCTGTTTCC AACTTGATTT	1680
TCCGTATGAA GAAAAATGCG GTTGGACTAG CAACCATCGC TATTTTGTCA ACAATGGTTT	1740
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ACAGTAACCT TGGTATTGCA AATCAAGAAG GAACCAAGTT AACTATTTTT GAAAAAGGAC	1980
AAAACCGTGT CCAACCCACA ACAGTTTTC A TGGTATTGCA CCAAAAAGAT TATGAAAATA	2040
TGACTGGTCA AAAACTGTCT CTATCAGGAA ATGAGGTCGG TCTCTTTGCC AAAAATGACG	2100
GACTGAAAGG ACAGAAAGCT CTAACCTCAA ATGATCATCA ATTTTCTGTC AAAGAAGAAT	2160
TTAATAAAGA TTTCATTGTG AACCATGTT CAAATAAGTT TAATATCTTG ACTACTGATT	2220



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ACAATTACCT TGTTGTTCCCT GATTTACAAG CCTTTTGGGA TCAATTCCCA GATTTCGGCTA	2280
TCTATAATCA GTTTTACGGT GGTATGAATG TAAATGTCAG TGAAGAAGAA CAACTCAAGG	2340
TCGCTGAGGA GTATGAAAAC TACCTCAATC AATTTAATGC TCAATTAGAC ACAGAAGGTA	2400
GCTATGTTTA TGGTAGCAAT CTAGCAGATG CTAGTCTCA GATGAGTGCC CTCTTTGGTG	2460
GTGTCTTCTT TATCGGTATT TTCCTATCCA TTATCTTTAT GGTGCGAACT GTTCTGGTCA	2520
TCTACTACAA ACAAATTCTT GAAGGCTACG AAGACCGTGA ACGCTTTATT ATCTTGCAGA	2580
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CGGATACATA TTCTCCACCA GCCATTGAAA AGGCACCAGC TAAGATAGCC GTAAAACCTG	3420
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CACTTTTCGA TGAATGCGAC TTCTTTGGGA GTCATTTTCT TGGTTCCCTT AGGTAACCAT	3720
CTACGAATGA GCCTGTGTG ATTCTCATTG GTTCCCTTTT CCAAGAGGC ATAGGGATGT	3780
GCATAATAAA TGTGCTCCTC AGAAAATACA TTAGACAAGC GATTGAATTC CGTTCCATTA	3840
TCTGCCGTGA TGGAAAGAAT CTTGTGTTGT TTTAAGATGA GTTTTAGAGC CTGATTGACC	3900
ACATCAGCAC TTTTATTGG AATCAATCGG ATGATCTGAT GTCTACTTTT TCGATCCGTC	3960

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AAGACAAGCA AGCAGTAGTT TTTGCTCTC GTAAGTAGAA CTGTATCAAT CTCATAATGC	4020
CCATTCTCCA AGCGAAAATT GATAGCTTCA AGCCGCTGTT CGATGGATTG ACCAGCAGGT	4080
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TGTTTGCTTA ACCCCAATTT TCCATGATGA ATCCAATAGT AAATGGTTGA AATCCCACG	4200
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ATCTTTTCCT TTAGTTCCTT GGTCAAGCTT GATTTCTTGA CCGAGCGCTT GCGATTGTTT	4320
TCATAAGACT GTTGAGCATA GTCGGCAGAA TAAACCTCTT TGAAGCGCCC TTTTCCAAGA	4380
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TGAAAGCACA CGTCATCTG TGAAACGATC AATAAGTAC GTAATATTG CTAAGTAGA	5100
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CCAATTTATG AGGCCTTGGT GAAGTTACGC AAGAAAAGGA TTGTTCCCTT TGATGTTCCA	5340
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CGTGATGCAG AGGAGCTGGC TGCAGATGCT TTTGGAGCTA GCCATGCCTT TCTAATGATT	5520
GGTGAACAA CTTATCGGT GCAGACTATG ATTCTGGCAA CCTGCAAGGC AGGAGATAAG	5580
ATTATTCTGC CACGAAATGT CCATAAATCT GCTATCAATG CGTTGGTTCT ATGTGGTGCC	5640
ATTCCCATCT ATATCGAGAT GAGTGTAGAT CCTAAGATTG GTATCGCTTT AGGTCTTGAA	5700
AATGACCGAG TAGCACAGGC CATAAAGGAC CATCCAGATG CTAAGGCTAT CCTAATCAAC	5760

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AATCCTACTT ACTACGGCAT CTGTTTCAGAC CTAAAGGGGT TGACAGAAAT GGCTCATGAA	5820
GCTGGCATGA TGGTTTTAGT AGATGAAGCC CACGGAGCGC ATTTGCATTT CACTGATAAA	5880
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GAGCTATCTG AGTATGCCCG CCGTGAAATC AATGCTATCG GTGGCTACTA TGCCTACTCA	6180
AAAGAGTTAA TAGACGGTGT TTCGGTTTGC GATTTTGACG TAACTAAGCT GTCAGTTTAC	6240
ACTCAGGSTA TTGGCTTAAC AGGTATCGAG GTTATGACC TCTTGCGAGA CGAATACGAC	6300
ATTGAGATCG AGTTTGGTGA TATCGGCAAT ATCTTGGCCT ATATTTCCAT CGGCGACCGC	6360
ATCCAAGACA TCGAGCGCTT GGTGGTGCT CTGGCTGATA TTAAGAGACT CTATTCAAGA	6420
GATGGAAGAG ATTTGATAGC AGGAGAATAT ATTCAGCCCG AGTTAGTGCT GTCTCCGCAA	6480
GAAGCCTTCT ATTCAGAAAG AAAAAGTTTA ACTTTGGATG ATTCTGTTGG ACAGGTCTGT	6540
GGAGAATTTG TTATGTGTTA CCCTCCAGGT ATTCCTATCT TGGCTCCTGG TGAACGCATT	6600
ACACGAGAAA TTGTCGACTA TATCCAATTC GCCAAGGAAC GTGGTTGCTC CCTCCAAGGG	6660
ACGGAAGATC CAGAGGTCAA TCATATCAAC GTTATTAAGA GAAAGACAAA CTATAAGAAA	6720
AGTCAATAGT TTTATCTAAA CTATTCTTA TTTCAATTTG ATGATTTGGC GATGATTTTA	6780
GAGCACGGCA AAAAGCCCTT GAATTAGAAG CGGTCAATCG CTTAATTTCT ATCAGCTTAT	6840
CAAATCCTGC CTCAAGCCTT TTCTGAGGAT TAGGGTAGCG TGTCAAGAGT TGGTAGGTAT	6900
ATTCTGAATG CTTTCCAACG ATTTTATCCA ACTCAGGAAA GATGATATCA AGACAACGAG	6960
TGTATTGTAC TTTCCAATCA GACTGTTTTT TCTTGAGACG ATGAATATGT CTAGCCAGTA	7020
TTTTTAGTTC TACTTGCCGA TTATCGTGTG GAAATTGTTT ACGATTGGGG TCAGAAAGAA	7080
GTTTAAGAGC GATGCCATGA GCGTCTTTCT TATCCGTTTT AGTTTTCGGA AGTGATAATG	7140
ATTTGGCAAA TTTCTTGATG AGCAAAGGAT TGTAGGTGTA AACTTTATAT CCTTGTTTAT	7200
GCAGGAAGTT CAGTAGATTA AAGGCATAAT GTCCGGTATT TTCAAGAGCG ATGAGACAGT	7260
CTTGGTTGAG CTGTCGAAGA GACAGATCTA AGAGTTCAAA ACCAGCTTTA TTATTTGAAA	7320
AAGTGAGTGG TTTAAGAACA GTTTTTCCTG GAACATTCOA GGCTGTAACA TCGTGTTTAT	7380
TTTTAGCGAC ATCAATGCCC ACATAAAGCA TGGGAGTATC TCCAGATATA GTATTTCAAG	7440
TCTACTGGGT TATCCACGAA CTTTTTGCCT TGTACCTTA GACGAGATAA AACGTCTATG	7500

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CGTTATCAAA CTCATTACCA ATTGAAACAA AAAACTGTGG TTAGAGCCTT TCGGAAATCG	7560
TCAAGCGATT GGAGGAAATG AACTAATCCA CAGTGGCTTA TTCCAAGTAT ACCACTTGGG	7620
CTTTGGCAGT AGCTAACTGC GCTAAATATA ATATAAGGAG AAATAGATGG ATTTATGGTT	7680
TTCTGAAGTT CATACTCCAG ATGTCAAATT GTCTCTGAGA ACAGCCAAGC AACTTTACGC	7740
TGGAAAAAGT GAATGGCAGG ATATCGAAGT CTTGGATACG CCAGCTTTTG GGAATACT	7800
GATTTTAAAT GGCCATGTCT TGTTCTCAGA TGCGGATGAT TTCGTCTACA ATGAAATGAC	7860
CGTTCACGTT CCCATGGCTG TCCACCCAAA TCCAAAGAAA GTATTGGTTA TTGGGGGTGG	7920
TGACGGCGGT GTTGCCCAAG TATTAACCTT CTATCCTGAA CTGGAGCAA TTGATATTGT	7980
GGAACCGGAT GAGATGTTGG TCGAGGTCG TCCTGAGTAT TTCCAGACT TTGCTGCAGG	8040
GCTAGATGAT CCTCGTGTTA CCATTTACTA CAAAATGGG CTACGCTTTT TGCGAACTG	8100
CGAAGATGAT TACGATATTA TCATCAACGA TGCGACAGAT CCATTTGGCC ATACGGAAGG	8160
ACTCTTTACC AAGGAATTCT ACGGCAATAG TTATCGAGCT CTGAAGGAAG ACGGCATCAT	8220
GATTTACCAG CATGGGAGTC CCTTCTTTGA CGAGGATGAG TCGGCCTGCC GAAGCATGCA	8280
CCGCAAGGTC AATCAAGCCT TTCCAATCAG TCGGTTTAT CAGGCCATA TTCCAAGTAG	8340
CCCAGCTGGC TATTGGTTGT TTGGATTGTC ATCGAAAAA TACCACCCTG TCAAAGATTT	8400
TGACAAGGAA GGCTGGA AAAACCCAGCT TTTCACAGAA TACTACACTG CAACTTACA	8460
CGTGGGAGCC TTTATGTTGC CCAAGTATGT TGAGGACATT TTAGAAGAAG AGGAAGGAAA	8520
AAAATGAGTC GTTTACTAGT TATTGGTTGT GGGGGCGTTG CCCAAGTTGC TATTTCAAAG	8580
ATTTGTCAAG ATAGCGAAAC ATTTACAGAG ATTATGATTG CTAGCCGTAC CAAGTCAAAA	8640
TGCGATGACT TGAAAGCGAA GCTAGAAGGC AAAACAAGTA CTAAAATTGA AACTGCAGCA	8700
CTTGATGCTG ACAAGGTTGA AGAAGTGATT GCCCTGATTG AAAGCTACAA ACCAGAAGCT	8760
GTTTGAATG TAGCTCTGCC TTATCAAGAT TTAACCATTA TGGATGCTTG TTTGGCAACA	8820
GGTGTTCACT ATATCGATAC AGCCAACTAC GAAGCAGAAG ACACAGAAGA CCCTGAGTGG	8880
CGTGCTATCT ACGAAAAACG TTGTAAGGAA CTTGGTTTGA CAGCCTACTT TGACTACTCA	8940
TGGCAGTGGG CTTATCAAGA GAAATTCAAA GAAGCAGGCT TGACTGCTCT TCTTGGTTCT	9000
GGTTTGAAC CAGGTGTAAC TAGTGCTTTT TCAGCTTATG CCCTCAAACA CTATTTTGAT	9060
GAAATCCATT ATATCGACAT TTTAGACTGT AATGGCGGTG ACCACGGTTA TCCATTTGCA	9120
ACCAACTTTA ATCCAGAAAT TAATCTCCGT GAGGTTTCTG CGCCAGGTTT TACTGGGAA	9180
GATGGGAAAT GGGTCGAAGT CGAAGCTATG TCTATCAAGC GTGAGTATGA TTTCCCTCAA	9240
GTGGACAAA AAGATATGTA TCTCCTTCAC CATGAAGAAA TCGAATCATT GGCCAAGAAC	9300

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ATTCCAGGTG TCAAACGCAT TCGTTTCCTT ATGACTTTTG GTCAACTCTA CTTGACGCAC	9360
ATGAAATGTC TTGAAATGT TGGACTCCTT CGTACGGATA CCATTAACTT TAACGGCCAA	9420
GAAATTTGTC CAATTCAATT TTTGAAAGCC TTGCTTCCAG ATCCTGCCAG TCTTGGGCCA	9480
CGTACAGTCG GAAAAACCAA TATTGGATGT ATCTTTACAG GTGTCAAAGA CGGTGTCAAA	9540
AAGACTATCT ATATCTACAA TGTCTGCGAC CATCAGGAAT GTTACGCAGA GGTGGTTTCG	9600
CAAGCTATTT CTTATACGAC AGGAGTTCCA GCCATGATTG GGACAAAATT AGTCATGAAC	9660
GGAACTTGGA AACAAGCTGG AGTGTATAAC CTTGAGGAGT TAGATCCAGA TCCATTTCATG	9720
GAAGCTTTGA ATGAGTATGG TTTGCCATGG GTTGTGGTTG AAAATCCACA AATGGTGGAC	9780
TAATGAAGTT AGAACAAGTA CCAACACCAG CCTATGTTAT TGAATTGGCC AAGTTAGAAG	9840
CTAATTGCCG CATTCTACAA TATGTACAAG AAGAGGCCGG TTGCAAGGTC TTGCTTGCCC	9900
AGAAGGCATA TTCCCTCTAC AAAACTTATC CCTTGATTAG CCAGTATCTA TCAGGTACGA	9960
CAGCTAGTGG ACTCTATGAG GCCAAATTGG CAAGGAAGA ATTCCTGGT GAAGTCCATG	10020
TATTTGCGCC TGCTTTCAAG GATGCAGACT TGGAGGAATT GCTAGAGATA ATGGACCATA	10080
TAGTCTTTAA CTCAGAGAGA CAGTTGCGTA AACACGGTCC GCGTTGTCGA GAGGCTGGTG	10140
TCAGTGTGG TTTGCGCCTC AACCTCAGT GTTCAACTCA AGGcAGATCA CGCGCTCTAT	10200
GACCTTGTG CACCAGGTTT TCGCTTTGGA GTTACTATAG ACAAGATPCC GAGTGATTTG	10260
CTAGATTGTTG TTGACGGACT TCATTTTCAT ACCCTTTGCG AGCAGGGAGC AGATGATTTA	10320
CAACAACCTT TGAAGCAGT AGAAGAACAG TTTGGTCCCT ACTTACATGA GGTAAAATGG	10380
CTCAATATGG GTGGTGGTCA TCATATTACA AGAGAAGGT ACGATGTGA TTTGCTGATT	10440
TCAGAAATCA AGCGTATCCG AAAAATTAC AATCTTGAAA TCTATATCGA GCCTGGTGAA	10500
GCCATTGCGC TTAATGCGGG TTATTTAGCA ACTGAGGTAT TAGATATTGT AGAAAACGGT	10560
ATGGAAATCT TGGTTTTAGA CGCCTCTGCG ACCTGCCATA TGCTGTATGT ACTTGAGATG	10620
CCCTATCGTC CACCTTTGAG AAATGGCTTT GAGTCACAGG AAAAAGCCCA TACCTACAGA	10680
CTTTCTTCTA ATACCTGTCT GACGGGCGAT GTGATTGGTG ATTATAGTTT TGAAAATCCA	10740
GTCCAAATCG GAGACAGACT TTATTTTCAA GACATGGCCA TTTATTCTTT TGTCAAAAAT	10800
AATACCTTTA ATGGTATTGG ATTGCCAAGT CTCTATCTCA TGGACGAACA GGGAGACTGT	10860
AGCTTACTCA AAGCTTTTGG CTATCAAGAC TTTAAAGGGA GATTATCATG ATGGACAGTC	10920
CAAAAAAATT AGGCTATCAC ATGCCAGCAG AGTACGAACC CCATCATGGT ACCCTCATGA	10980
TATGGCCGAC TCGACCAGGA TCATGGCCTT TTCAAGGAAA GGCTGCTAAA AGAGCATTTA	11040

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CTCAGATTAT CGAGACCATA GCAGAAGGGG AAAGAGTCTA TCTTTTGGTG GAGCAGGCCT	11100
ATCTATCTGA AGCCCAATCC TATCTTGGAG ACAAGGTTGT TTATTTAGAC ATTCCCACCA	11160
ATGATGCCTG GGC CGTGAT ACTGGCCCAA CCATTCTCGT CAATGATAAA GGTAAGAAAT	11220
TAGCCGTGGA TTGGGCCTTC AATGCTTGGG GAGGCACCTA TGATGGTCTT TATCAAGATT	11280
ATGAAGAGGA TGACCAAGTA GCCAGTCGTT TTGCTGAGGC CTTGGAAAGG CCTGTCTATG	11340
ATGCTAAACC TTTTGTACTG GAAGGAGGCG CAATCCATAG CGATGGTCAA GGAAGTATTC	11400
TCGTAAGTGA AAGTTGCTTG CTTAGTCCCTG GTCGCAATCC TAAGTTGACT AAAGAGGAGA	11460
TTGAAAACAC ATTATTAGAA AGTCTTGGTG CTGAAAAGT TATTTGGCTT CCTTATGGTA	11520
TTTATCAGGA TGAAACCAAT GAACACGTCG ATAATGTTGC TGCCTTTGTT GGTCTGTCTG	11580
AGCTTGT TTTT GGCTTGGACA GATGACGAAA ATGATCCCCA GTATGCCATG TCAAAAGCAG	11640
ATCTCGAAGT CTTAGAACAG GAAACAGATG CAAAAGGTTG TCACTTCACC ATTCATAAAT	11700
TGCCTATCCC TGCAGTTGCA CAAGTTGTGA CAGAAGAAGA TTTGCCAGGC TACATCTATG	11760
AAGAAGGAGA AGAAAAGCGA TACGCAGGTG AACGACTAGC AGCTTCCTAC GTAAACTTTT	11820
ATATCGCCAA CAAGGCTGTC TTGGTTCCAC AGTTTGAGGA TGTAACGAC CAAGTGGCCT	11880
TAGATATCCT CAGCAAGTGT TTCCAGACC GTAAAGTTGT CGGAATACCA GCCAGAGATA	11940
TTCTCTTAGG TGGTGGCAAT ATCCACTGTA TCACCCAACA AATTCAGAA TAGGAGAAAA	12000
AGATGAGAAA TGTAAGAGTT GCAACCATTC AGATGCAATG CGCTAAGGAT GTGGCAACAA	12060
ATATCCAAAC CGCAGAGCGT TTAGTACGTC AGGCTGCTGA GCAAGGAGCC CAAATTATTC	12120
TCTTGCCCGA GTTGTGTA CATCCCTATT TCTGTCAGGA ACGTCAGTAT GACTACTACC	12180
AGTATGCCCA ATCTGTAGCG GAAAATACTG CCATTTCAGCA TTTTAAGGTG ATTGCTAAGG	12240
AACTACAAGT TGTTTTACCA ATCAGTTTCT ATGAAAAAGA TGGTAATGTC TTGTATAACT	12300
CTATTGCCGT CATTGATGCA GATGGGGAAG TGCTGGGCGT TTATCGAAAG ACCCATATAC	12360
CAGATGACCA TTATTATCAA GAAAAATTCT ATTCACGCC TGGTAACACT GGTTCAAGG	12420
TCTGGAATAC TCGTATGCT AAGATTGGTA TCGGTATCTG TTGGGATCAA TGGTTCCTG	12480
AAACAGCGCG CTGTCTGCA TTGAATGGTG CTGAATTGCT CTTTATCCT ACAGCTATCG	12540
GTTTCAGAGCC AATTTTGGAT ACAGATAGTT GTGGTCACTG GCAACGTAAT ATGCAAGGGC	12600
ACGCAGCAGC GAATATTGTT CCAGTCATCG CAGCCAATCG TTATGGTTTA GAGGAGGTTA	12660
CTCCTAGTGA GGAATAAGGC GGACAGAGCT CCAGTCTTGA CTTCTACGGT TCCTCCTTTA	12720
TGACGGATGA AACAGGAGCT ATTCTAGAAC GAGCTGAAAG ACAAGAAGAA GCTGTTCTGT	12780
TAGCTACTTA TGACCTAGAC AAGGGAGCAA GTGAACGCCT AAAGTGGGGC TTGTTTCGAG	12840

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ATAGAAGACC AGAAATGTAT AGACAAATTA CAGATTAGTG TGGGAGAAAT GAGAGATTCA	12900
TTCTGCTAGA CTAACCTCTT ATTAGTAACATAAGATACT ATGGCATCTA GTAAATCGAT	12960
TTTTATGATT CGCTATTCTT GTCTATTGAT TAGTCCGTAT TTTAAATAT TAGCAAAAAA	13020
GCAAAATAGCA GTAACCTCTG TCTATTGCT TTTCTTTTT ATAGAATATA TTTCTCAATA	13080
GCACGCGCAA CGCCGCTCTT TTCGTTGCTT GAGGTAACGG CATCCGCAAG AGATTGATA	13140
TAATCGCTGG CATTTCCCAT TGCAATCCCA AGCCCTGCAA ACTGGAGCAT TTCGATATCG	13200
TTATTAGCAT CGCCCATGGC CATAATCTCT GAGGAATCAA TCTTCAAAAT CTCAGCTAGT	13260
CGTGAAAGAG CAGTAGCCTT TGTCTGTCCA AGCGGCATG CTTCAATAAT GACAGGCTGC	13320
GAACGAATC CACTGAATCG TTGGCAAAGC TCTTCAGCAA AACGCTGCTC AAAATCGTCT	13380
GTTTGTCTT TTGTTCTTAA ACACATACCT TGGAAACATCC GGAACCTTCC ACTAGTCGCT	13440
TCTTCAAGAG AAATTTCACT CAGGTCTGAA AATACTAGTT TAGCATCATT TTCAATAACT	13500
TGATTGGGCT TGTCAACGAG AACAAAATAA TGTGACTCGT CAAAAGTGT CAACTGAACA	13560
TCACCTTTT CAGCAAGGTC ATAGAGGTAT TCGATGTGAG CTGGACTCAG TTCTTTCCAG	13620
TCAACTAGAC TCCAATCACT GGTCTGGTGA GTTGAACAAC CGTTGTTAAC AATAATATAT	13680
TCGTCTGGA GGTCAAGCTC CAGTTTTTTG TAGTAGGGGA GGACACCGAA AAGGGGGCGA	13740
CCCGTACAGA GAACCAAGTT GACACCTTTT TCAATGGCTT TGTGAATAGC AGTAATGTGT	13800
GCTTGTGGGA TTTCTTGGC TTCATTGAGG AGGGTGCCGT CCATATCCAA GGCTAGTAGT	13860
TTAATCATAG GTCTTCCTCT TTATCTTGC TATTATTATA GCATATTTTG GAGAAGAAAT	13920
TGATAGAAAG CTTGAGACTA ATTGATTTTA TAGTTTAAGA TGTTTGTATG ACAATTCATG	13980
ATTTGAAGAG GATATTTGCG AAAGATATGC TATACTATGT TTGTCAATGT TGCAACTAGA	14040
CAAATTAATA AACCAACTTA ATATAATAGT TTTTTGTAA GTAGGTATGA GTAGCAGATT	14100
ACTCAACTAA TCTGAAGAAT AATGGAGGAA ATATATCATG ATTTTAATGA CAAAAATAT	14160
AAATCTAACA AATGAAGAAT TAGAGCTGAT ACAAGGTGGA GCAGATCCAT ATGGTAAAAA	14220
TCCTAATGGT AGGTACGATT GGGAAATAGA ACCAGTATTA ACTCTGCTGG TTCATGGATT	14280
TTGTCCCAGA GGCACCTATG ATTCAGGATA TATTGGAGGA GGTAATCATC TTGCAAAGG	14340
AAGTGCTGCG AGATTTTAAG TAAATTTAT TAGGAATATG AAGAAACAAG GGGAGAAAAA	14400
AGAGGATTTA ATATGAAAAA ACGAGCTATT CAAATTTTAC TAGCATTGTC CTTAATTTTT	14460
TACAAATCAA CTTGGTTTTG GAGGCTTTTC AATTATCTCG CAAAGCCCTA TCTACCAGCA	14520
AGTCGTGAAT TTTTTCAGAT TCTGCTTTTG ATGGAGAGCG GAGTTCTTTT CTTAGCGGTC	14580

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ATCTATCTAC TGGTTTTTGC AGGAAAGAAA ATTTTTCATT TCAAGTGGCA GCTGAGGTAC	14640
TTCATCTACC TTTTACTGGG CTACATCATT TCATATATGT CTGACTTCCT CTTTTCGTAT	14700
TTTCATATCCC TGTCTTCAAA TCAGATTTCCT TTGAATGAAA CGGTAGAAAT GATGGGGAGA	14760
CAGGAGTTCC CTTATGTCTT GCTCATCGTT TGCTTCATCG CCCCTATTGC TGAGGAATTG	14820
ATTTATCGAG GtGTGCTTAT GACAACCTGT TGCAAAACT CACCTTGGA CG	14872

(2) INFORMATION FOR SEQ ID NO: 73:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 10223 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 73:

CGTGCTATCG GTCTCAAAAC CAATCTGGTC GCTATGGTCA AATCCAGTTG GAAAATCCAT	60
TCTTCTTGGG GCCATCTGCT GGATTGCCAT CATCCTCACC ACTCTTGGTA TGCAGACCCT	120
TATCGGCATT TTCTAATACT CTTGCAAAAT CTCTTCAAAAC CACGTCAACG TCGCCTTGCC	180
GTAGGTATAT GTTACTGACT TCGTCAGTTC TATCTGCAAC CTCAAAACGG TGTTCGAGCT	240
GACTTCGTCA GTTCTATCTG CAACCTCAAA ACGGTGTTTT GAGCTGACTT CGTCAGTCGT	300
ATCTACAACC TCAAAACAGT GTTTTGAGCT GACTTCGTCA GTTCTATCTG CAACCTCAAA	360
ACAGTGTTTT GAGCAGCCCG TGGCTAGTTT CCTAGTTTGC TCTTTGATTT TCATTGAGTA	420
TAACACAAAA GGTAGCCCAT CAGCTACCTT TTTCTTATGC TTCCTCAATC AAGCGAGTAT	480
GTCTCTCTTT GATACAGCGA TTCATCAGCA TATCATCACA TCCACCATCA CGCAAAATCT	540
CTTTCGCTTC TAAACTTTCA AGTCCTAGCT GTGCCCAAAA AATCTTGGCA TCAGCTTTGA	600
GAAAATCAGC CGCCACATCG GGCAGAAATT CACTGCGACG ATAAACATTG ACAATATCTA	660
CAGGAAAAGG AATTTTCAGC AGGCTAGCAT AAGCCTTTTC ACCCAAGATT TCGCCACCTG	720
CCGCCTTGGG ATTGACTGGG ATGATTTTAT AGCCCCGAGC CTGCATTTC TTTGTTACTC	780
GATTGCTGGT TGTTCCTTCA CGGTCAGACA AACCCACCAC AGCAAGGGTT TTA CTGTTG	840
CGAGATACTG ACGAATCAGC CCATCACTTG GATTGATAAA TTCTTGACTC ATAGAAATCC	900
TCCTTTTTC TCAGTATAGC ACATTTTGAA AAGGTTTGCA GAATTATACT ACAAAAAAGG	960
AGGACTAGCC CCCTTTTAT TTAGCCTCGT ACCAGGTTGC CCCTTCATTC TCATCTGCGA	1020
TAAGAGGAAC ACTGAGTTGA ATGGCTTCTT CCATGTTTG TTTCACCAAT TTTTTCATCT	1080
CTACCAATTC AGATTTAGGC ACTTCAAGGA CGATTTTCATC GTGCACTTGT AACAGCATCT	1140



TAGTCTGATA ACCACCTGCA ACCAAGGCTT TATCCAGCTG AATCATGGCA ATCTTGAGAA	1200
TATCTGCTGC CGAACCCTGG ATAGGTGAGT TGATAGCAGT TCGCTCCGCA AAACCACGAA	1260
TATTGAAGTT GCGCGAATTG ATATCTGGCA ACTCACGGCG ACGCTTAAAG AGGGTCTCTA	1320
CATAGCCCTT ATCACGCGCC TCCCGCACCA CTTTCATCCAT GTAGTTTTTA ATACCTGGAA	1380
AACGTTCAAA GTAGGTATCA ATGTAGGCTT TGGCTTCCTT ACGACTAATT CCCAAATTAT	1440
TAGACAAGCC AAAGTCTGAA ATCCCATAAA CCACTCCAAA GTTAACTGCC TTGGCATTGC	1500
GACGGTCGTT TGCAGTCACA TCATCAGGAC GCTCAATGCC AAAGACCCGC ATGGCTGTCTG	1560
AAGTATGGAT ATCTGCCCCC TCTTGGAAGG CCTTAATCAA GTGCTCATCC TTAGAAATAT	1620
GCGCCAAAAC GCGCAATTCA ATCTGTGAAT AGTCAGAGCT GAGTAGCACA CTATCCTCCC	1680
ACTCTGGCAC AAAAGCCTTC CGAATCAAGC GCCCCTGTTC CAATCGGGCA GGAATATTTT	1740
GCAAGTTTGG ATCCACACTA GACAAACGCC CGGTCTGGGT CAAATCCTGC ACATAGCGAG	1800
TATGAATCTT TCCATCAGCC AAAATCCAGT CCTGCAAGCC AATTACATAA GTAGATTGAA	1860
TCTTAGCAAT TTGACGGTAA TCCAGGATTT TCTTAACAAT CGGAGCAATA GGAGCGAGAC	1920
GCTCTAAAAC ATCCACTGCT GTCGAATAAC CTGTCTTGGT TTTCTTAGTG TATTCTAGAG	1980
GAAGTCCCAA TTTCTCAAAG AGAAGCACGC CCAACTGCTT AGGCGAGTTG ACATTAAACT	2040
CCTCACCAGC CAGCTCGTAA ATCTCTTGAG TCAGTTTTTC AATGACAAGC TCATTTTCAG	2100
CCTGCATCTC AAGCAAGGTC TCTTTCTTGA CCATAATCCC AGCAATTTCC ATCTTGGCAA	2160
GGACAAAAGC CAGAGGTGTC TCCATATCAT AAAGAAGCTC TAATTGCCCA TTTTCGCTGA	2220
GTTTTTCAAG TAAATAGGC TCTGTTTCTA CAAAACAGC AAGTTTACAA GCTAAGTGTT	2280
CCAAGAATTT CTCACGTTCA GGAATGGCCT TTTTAACACC CTTACCGTAG AAAGTTTCAT	2340
CATCAACCAA GTAAGTCTGA CCATAAAGAC TAGCGATGGT CGCAATTTCA TTGTCCTCCA	2400
CAGTCGAAAG GAGGTATTTA GCCAAACGGA TGTCAAAAGC AGGCGCCTGC AAATCCACAC	2460
CAAAACGTTG CAAAAGAACT TTAACCTTCT TAAAGTCATA AACTCTCAGA GATGTTTTTT	2520
CTAAGAAATC CTTGAAAATC GGGTCTTGCA ACAGCTCAAG CTTGTCTGTG GCATAGAGCT	2580
TATCCCCACA AGACCAGACA AATCCAACCA AATTATCCGT ATGGTAATTC TCACCAAAAA	2640
GCTCAAAGTG GAAGATAGAC TCTTCACTCA GCATATCTTG ACTGATTTGG TCAACAATAG	2700
TAAATCCAA ACTCTCAGAC ACATCAGCTG ACGACACATT TAAAGCCTGC TTTAGCTGTT	2760
TGAAGCCCAT CTCATCGTAG AATTTCCCAA GATTTTCAAC ATCTGGACCA CTATAGACCA	2820
AGTCCTCTAA ACCAATCGCA ATCGGTGCCT TGGTATCAAT GGTCGCTAGT GTTTTAGACA	2880

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AAAAGGCCTG TTCCTTGTC TGTATGAGAT TTTCCTTCAT CTTAGAAGTC TTCATTCCAT	2940
CAATATTTTC ATAAATCCCC TCAAGCGAAC CATGCTCCAG CAAGAGCTTA ATACCCGTCT	3000
TTTCACCGAC TTTGGTCACC CCAGGGATAT TATCCGACTT ATCACCCTAG AGCGCCTTGA	3060
GATCGATAAA CTGAGCTGGT GTGAGGCCCA TTTCCTTCAT GAGGTAATCT GGCCTAAAGG	3120
CCTCAAATC AGCCACACCT TTCTTGAAA TTTCAACCAC CGTATGCTCA TCCGTAGCT	3180
GAATCAAATC CTTGTCCCA CTGACAATAG TAATATCAA ACCATCCTGC TCTGCTAGCT	3240
TATCCAGCGT CCCAATGATG TCATCCGCT CATACTGAGC CAGATCATAG TGACGAATCC	3300
CCATATGATC CAGCAACTCA CGAATGAAAG GAAATGCTC ACGAACTCA TCAGGAGTCT	3360
TGGCCCGACC ACCCTTATAG TCCGCATACA TCTCTGTCCG GAAGGTCGTC TTCCCGCAT	3420
CAAAAGCCAC CAAATATGA CTCGGCTCAA CCCGCTCAA TAAATGACTC AACATCAACT	3480
GAAAACCATA AATCGCATTG GTATGCAAAC CAGCCACATT CTTAAAACGG TCCAACTGCT	3540
GATACAGCGC AAAAAACGCC CGAAAAGCTA CAGAAGACCC ATCAATCAAT AATAATTTT	3600
TCTTATCCAT ACACCCATTA TAAAGGAAAG AATCAAAAA TACCATTGGG AAGAGCTAGA	3660
GCAAGTATTT TTCAAATTT TTCCGAATA ATAGATAGAG CCAGAGAATT TAGTAAACCT	3720
AGATTAAAA ATGTGCTATA ATATAGTATA TTGAATCTAT AATAGTACAC CTTGACTGCT	3780
AAAATATTT TATAAATTAA TTTGACTTTC CTGATAGAGT TATTCACATC TTATTTCAAC	3840
TCACTATAGA AGGAGGAATA GGAGGATTCT CAGACATCCG GGCATCAGCC CAACTAATGA	3900
TTTGATTGCT AAGAAAATAT TCAGCAATCC AGAAATCACT TGTCAATTTA TTCGCGATAT	3960
GCTGGACTTG CCAGCAAAAA ATGTGACCAT TTTGGAGGGA AGCGATATTC ACGTATTACT	4020
CTCCATGCCT TACTCGGTGC AGGATTTTTA TACCAGTATA GACGTCTTGG CGGAGTTGGA	4080
TAACGGTACT CAAGTAATTA TTGAGATTCA AGTCCATCAT CAGAATTTT TCATCAATCA	4140
CTTGTGGGCT TACCTGTGCA GTCAGGTAA TCAAAATCTT GAAAAAATTC GTCAGCGAGA	4200
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TAGTAATTAT TTCTCAGATG ACCTGGCTTT TCATAGCTTT AGTATGCGCG AAGACACAAC	4320
AGGTGAGGTA TTGGCGATTA CCAACAATGG ACAGGAAAC CATCTGGTTA AGATGGCATT	4380
CTTGGAATTA AAAAATACAG AGAAACCAGC AAAGACAAGG TTCGCAAGCC ATGGTTGGAG	4440
TTTTTCGGCA ACAAGCCCTT TACCCAGCAA CCGCAACGAG CCATTACCCA AGCAATCAA	4500
CTGCTGGACT ACAAGAGCTG GTCCGAGGAG GACAGGAAAA TGTTTAGTCA ACTACATATG	4560
CGAGAAGAAC AAGTCTTGTT AGCACAGGAC TATGCCTTGG AAATGCTAG GGCTGAAGGC	4620
CTTGAACAAG GACTAGAGCG TGGGAAAGTT GAAGGAAGGG CAGAAAGGAA ACTTTTGGCC	4680

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TTCCTAGACA TAGTACGCCA AGGTCTTCTG ACTTCTGAGG TTGCCAGCCA GCAATTAGGT	4740
ATGTCAGTAT CTGAATTTGA GGCAGTGTG TAAAATGGCT CCATAATATC CATAGTGGGT	4800
AAATCCCCTA TGGATATTAT GGAGCCTATT TTGTGTAGAA AAAAAGTCCC ATATGACCTA	4860
TAATGAAAAG CGACAAAACA ACTCATTAGA AAGAATCATA TGAACAATT ACATTTTATC	4920
ACAAAATTAC TAGACATTAA AGACCCTAAT GTCCAGATT TAAACATCAT CAATAAGGAT	4980
ACACACAAGG AAATCATCGC CAACTGGAC TACGACGCCC CATCTTGCCC TGAGTGCGGA	5040
AACCAATTGA AGAAATATGA CTTTCAAAA CCTTCTAAA TTCTTATCT TGAAACGACT	5100
GGTATGCCTA CAAGAATTCT CCTTAGAAAG CGTCGATTCA AGTGCTATCA CTGTTCAAAA	5160
ATGATGGTCG CTGAACTTC TGATGACGTA CAGTCATATT TCTTCTCTT TTATTATATC	5220
ACAGTTTTAA ATCTAGCTTT ACTAGATTCA CCGCTACTAT CTATTTATTC GAAAAAAGA	5280
CGAAAAACC TGAGAATCAT CTCAGGCTTG GTCATTAAAT TTTTCTCA ATATCGAAAA	5340
GTGGAGAAAG TGGTCGTTT TCATGAATAC GTACGATAGC ATCCCTAGG AGATGAGCGA	5400
TTGAAATCTG CTCAATCTTA TCAATCAAA GCTCTTCTGG CAGATAGATG GTATCCAAA	5460
CAACCAATTT CTTAATAGCT GATTTTGGG TATTGTCCGT AGCAGGACCA GAAAGAACTG	5520
GGTGCGTACA GCTTGCATAG ACTTCAACAG CACCAGCTTC CGCAAGAGCA TCTGCCGCAT	5580
GACAAATCGT TCCAGCGTA TCAATCATAT CATCAATCAA GATACAAGTC TTGCCTTCAA	5640
CCTTACCGAT GATATTCATA ACTTCACTAG TATTCATCTT ATCAACGCTA CGACGTTTAT	5700
CAATAATAGC GATAGATGTT TTCAAAAATT CTGCCAATT ACGAGCACGA GTCACCCCTC	5760
CATGGTCCGG GCTGACAACC ACATAGTCAG AACCAACCAT ACCACGACGC TCAAAATAAT	5820
CTGCAATCAG AGGAGCACCC ATCAAATGAT CCACAGGAAT ATCAAAGAAT CCTTGAATTT	5880
GCGCAGCATG CAAGTCGATG GTCAATAAAC GATCCACTCC AGCTACTTCA AGCATATTTG	5940
CGACAAGTTT TGAAGTGATT GGCTCACGCG CTCTCGCCTT TCTATCCTGA CGTGCAATCC	6000
CATAGTAAGG CATGACAACA TTGACAGATT CTGCACTCGC ACGCTTCAAA GCATCTACCA	6060
TAATCAAAAT TTCAAGCAGA TTGTCATTTA CAGGCGAACT AGTTGATTGT AAGATAAAGA	6120
CGTGTTTCCC ACGGATTGAT TCTTCAATGT TGACCTGAAT CTCTCCATCT GAAAATTGGC	6180
GAACACTTGA TTTCCCAAC TCTATCCCAA TCTCCTGCGC CACACGTTCT GCCAATTCTT	6240
TATTAGAAGA AAGGGCAAAC AGCTTTAAAT CAGAAAAAGA CATGATTTC TCCGGTATAT	6300
ATGTATAACT TGTGCTTTTC ACAAGATTTT CCATCTACCA TTGTAGCGCT TTTGCACTA	6360
TTTTTCAATC AAAAATAAAA GAAGGGCACC ATATTGTAC CCTTGCATCA TTCTTTTGAA	6420

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AAATATTCTA GGTCAATCAAC TCATTGTGTT TCTCAACAAA GCAATAAGCA TGATAAAAAC	6480
CATAGAGAGC AATAGCCGTA ACCACTGGAA TCGCTAAAGG CAACTCTGTT TCCAACTCCA	6540
CAAAAGGAGA GTTAAACAAG AAGTGAGTTC CCAAGGCTAA ACCTAGAAAA ATAAGGCCCT	6600
GTTTCTTGCC AACCTTCTGT CCTTTATAGG CTCTGTAAAG CAAGTAAACA CCTACTACAG	6660
CTAGACCTGA AAAAGTCCAG TGAGAGGCAA TTCCTGAGAT GATACGCTCT AAAATTCGCG	6720
AAATAGTAAA GTCAAAGCCC TCTGGCAAAT CCGTACGAAT ATAACCAATA TCCTTAATCA	6780
TTTGGAATCC CAAACCGGAA GCAATTCCAA GTAAAAACAA AGATTTTAAT TTTCGCACAG	6840
GAATCAAAGC CAAAACAAA ACAAGTGACA ATAATTTCAA GGGTCTTCT ACCAAAGGAG	6900
CCGCAATAGC ACTTTCAAAG GCATTTAAAA ATGGACTATC TGGGAAAAGA ACCCCAGTA	6960
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ATAAGACAG AATCAAAACC TTCCTTGCCA ATTCCTATT TTCCAATAC GGAAGAGAAA	7080
ATAAGAGCC GGAATCATGT AAAAGAGAGC TAGAAAGATA GAACTCCCA TTAGTCCATA	7140
TTCCGCACCT GACCTCGAAC CGTCCGTATA GTAGATGGTT TCATACTGTA AACCAATACA	7200
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AAGTATTTAT AATTCTACGA CTGTCATACT TCCTGTATCA ACATTGTAAA TGGCACCAGA	7320
GATAATGACA TCGTCTGGTA TTAGGGGAGA CTCGATAAGC AGTTGCATAT CCTCGGTAC	7380
ACTCTCTTCT ATATCTTGA AGGGCAAGAA GTCTGGTCT GACACATCGA CACCCAATTC	7440
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CATATCCTCA GTCACGAC CACCTGCATT CCGCAAAATA TGAGCATCCC CAAGTGCCAA	7620
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TTTAGGTTTA AGTGGCAGAT TTAAGTCCC ATGTAGGGCA ACATAAGCCT GATTGGCTTG	7740
CATAAACTGT TCAAAATACG ACACGATTCC CTCCTGAAA ATTTGATAGT CAAATATTTC	7800
TCCTATCTTA TCATTTTAA GAGAATTTGT CACGGATTAT GCAAAGACCT TTTCAAGAC	7860
TTCTGAATC GTTGTCACGC CAATGACCTG AATTTCCTTA GGCAGAGTGA TTCCTGTCAA	7920
GGAATTCTTA GGTACATAAA TCTTAGTAAA GCCAGTTTA GCAGCTTCGT TGATGCGTTG	7980
CTCAATACGA TTCACGCGCC GAATCTCTCC TGTCAGCCC AGTTCCTCGA CAAACATTC	8040
CTGAGGATTA GTTGGCTTGT CTTGTAGCT CGAAGCAATA GCAACTGCAA CAGCCAAGTC	8100
AATCGCAGGT TCATCCAAT TAACACCACC AGCAGATTG AGATAGGCAT CCTGATTTTG	8160
CAAGAGAAGC CCGCCCGTT TTCCAAAAC AGCCATAATC AAGCTAGCAC GGTAAAAATC	8220

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AAGTCCTGTC GTAGTACGCT TGGCATTTC AAACATGGTC GGTGTTACCA AAGCCTGAAC	8280
CTCCGCCAAA ATCGGACGCG TCCCTTCCAT GGTACAAACG ATGGAGGAAC CAGTCGCCCC	8340
ATCCAAACGC TCTTCTAGGA AAACCTGACT CGGATTGAGT ACCTCAACCA AGCCGCCCCA	8400
CTGCATCTCA AAAATCCCAA TCTCATTAGT GGAACCAAAA CGATTTTTGA CCGCTCTCAA	8460
AATACGAAAG GTGTGGTGAC GCTCCCCTTC AAAGTAAAGC ACCGTATCCA CCATATGCTC	8520
CAACATACGA GGCCAGCCA AGGTTCCCTC TTTGGTCACA TGACCTACGA TAAAGATGGC	8580
AATGTTATTG GTCTTGGCCA ACTGCATGAG TTCAGCGGTC ACTTCACGCA CCTGAGAAAC	8640
AGACCCCTGC ACCCCTGAAA TCTCAGGAGA CATGATGGTC TGGATGGAAT CAATAATGAG	8700
AAAGTCTGGC TGGATACGCT CCACTTCTGC ACGAACAAC TCATATTTGG TCTCTGCATA	8760
GAGATAAAAC TCACTATCAA TATCACCTAA GCGCTCTGCA CGTAGTTTAA TCTGCTGGGC	8820
AGACTCTCC CCACTGACAT AGAGAACTGT CCCCCTTGG GACAACTGGG TTGAGACTTG	8880
TAGGAGAAGA GTTGATTTCC CAATCCCAGG ATCCCCACCG ATAAGGACGA GACTTCCTGG	8940
TACCACTCCG CCTCCAAGCA CACGGTTGAA TTCCTCCATC TCCGTCTTGG TTCGATTGAC	9000
ATTGATGGAA GTCACCTCAG CTAGTTTCAT GGGCTTGGTT TTCTCACCTG TCAAGGACAC	9060
ACGCGCATTC TTAACCTCGG CAACCTCAAC CTCTCCACA AAAGAAGACC AAGACCCACA	9120
GTGGGGCAA CGTCCAGAT ATTAGGGGA ATTATACCCA CAATTTTGAC ATACAAATGT	9180
CGCTTTTTTC TTTGCGATGA CAAACCTCTT TCTATATCTC TAACTCACAC TCAATCACTT	9240
GGCAAAAATC AATCTTCTCA TTTGGCACAA ACTGGCGCAT GAGCATTCGA TGAGCAACAA	9300
CTACCACAGT CTGATGTTCT CGATACTTAG ACATACATTC TAGAAACCGA GACTTCATTT	9360
CCGTAGCTGT CTCATATTGA ATAGGACTAT TAGGAAGCAA CTCCCCCTTG TTTCTAAAA	9420
ACAGTCTTCT AGCTGTTTCA AAGTTTCTA TTCCTGTTTT ATAGACCTGC CATTCATGTA	9480
ATAAAGGCTC TACTCTTAAA GGAAGACCCG TAGCACAGAC CACATACGAA GCCGTTTCTA	9540
AAGCTCTTGT GACTGCAGAA GATACGATTA TTTCAGCTGA CGAGAGTAAA GGATTTTTCG	9600
TCAATTTCTG GACTTGCTGC CGTCCCATCT CAGACAAGGG TGCCAAATCT ATCCCAAATC	9660
CTATATAAGA ACGCTCCTCT AACTCACGGT AATCTGGCTC CCCATGACGT ACAAAGATAA	9720
TCTTCATTCT AGTGCCCTGT CGATCCAAAT CCACCACTC GAACGCCATC AGCTGCATCT	9780
CCATCTGCAA TTAAGAAAGT AGCAAAAACA GCCTGGACAA TACGCTCCCC AACTTCAAGA	9840
ACAACCTCTT GGTCTGTGAT ATTCTTCATC TGCGCAAAA TATGCCCTTC ATTTCCAGGA	9900
TTTCCATAAT AATCCCATC AATGACTCCA ACTGAGTTAA TTAACCAAA GCCCTTCTTA	9960

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CGAGGATTTG AAGAACGATC ATAGAGGTAG AGAACCTCAG TCGGCTGCAT ATAAGCCTTA	10020
ACCCCTGTCTG GAACCAAGAC AATCTCTCCT GGCACAACAA CTGTACGCAC AGCAACCTTT	10080
AAGTCGTAAC CAGTCGCATG CGCTGTCTCA CGCTTGGGCA ATAAATTTTC ATCTGTAAAA	10140
CTCGAAACCA ATTCAAAACC ACGAATTTTC ATAATTTTCT CTTTCTATT ATCATTATT	10200
CTAGATTATT CTATACTTAT TTA	10223

## (2) INFORMATION FOR SEQ ID NO: 74:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 16535 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 74:

TGGTTCGTGC CTATCGGCG CCTGTCTTG CTGCCATGG CTACACCAAC TATCTCATCC	60
GACGAAAGTA CACCAACCAC TAACGAACCC AACAACAGAA ATACAACCAC CCTTGCCCAA	120
CCTCTTACTG ATACAGCAGC TGGCTCTGGT AAGAACGAAA GTGATATTTT TTCACCTGGA	180
AATGCAAAACG CTTCCCTAGA GAAAACAGAA GAAAAACCTG CTGCAAGCCC AGCCGATCCA	240
GCACCACAAA CTGGACAAGA TCGTTCAAGT GAGCCAATA CTTCTACTAG TCCAGTAACA	300
ACTGAAACTA AGGCAGAAGA GCCCATCGAA GATAACTACT TCCGTATCCA TGTCAAAAAA	360
CTTCCTGAAG AAAACAAGGA TGCTCAAGGA CTATGGACTT GGGACGATGT TGAAAAACCA	420
TCTGAAAACT GGCCAAACGG AGCTTTGTCC TTCAAGGATG CCAAGAAAGA TGACTACGGC	480
TATTACCTAG ATGTCAAATT AAAGGGAGAA CAAGCCAAGA AAATTAGCTT CCTCATCAAC	540
AATACAGCTG GAAAAAATCT AACCGCGAT AAATCTGTAG AAAAAGTAGT TCCAAAAATG	600
AACGAAGCTT GGTTAGACCA AGATTACAAG GTTTTCTCTT ACGAGCCACA GCCTGCAGGA	660
ACTGTTCGCG TCAACTACTA CCGCACAGAT GGCAACTATG ACAAGAAATC TCTCTGGTAC	720
TGGGGAGATG TGAAAAATCC AAGTAGCGCT CAATGGCCTG ACGGAACAGA CTTTACGGCT	780
ACAGGCAAAT ATGGCCGCTA TATCGACATT CCTCTTAATG AAGCCGCAAG AGAATTTGGA	840
TTTTTATTAC TAGATGAGAG CAAACAAGGA GACGACGTGA AAATCCGTAA AGAAAAATTAT	900
AAGTTCACAG ATTTGAAAAA TCATAGCCAA ATTTTCCTAA AAGACGATGA TGAATCGATT	960
TACACAAATC CATACTATGT CCATGATATC CGTATGACAG GAGCCCAACA CGTAGGCACT	1020
TCTAGCATTG AAAGTAGCTT TTCAACACTT GTCGGTGCTA AAAAGAAGA TATCCTCAAA	1080
CACTCCAACA TCACTAATCA CCTAGGAAAC AAGGTAATA TTACCGATGT TGCAATCGAT	1140

GAAGCTGGTA AGAAAGTGAC CTACAGCGGA GATTTCTCTG ACACAAAACA TCCTTATACT	1200
GTTAGCTACA ATTCCGACCA ATTCACTACC AAAACAAGCT GGCGCCTGAA AGATGAGACA	1260
TACAGCTATG ATGGCAAACCT GGGAGCTGAC CTAAGAAG AAGGAAAACA AGTTGATTG	1320
ACCCPTTGGT CACCAAGTGC TGATAAGGTT TCTGTGTGTTG TCTACGACAA GAATGACCCT	1380
GACAAAGTAG TTGGAACGTG CGCTCTTGAA AAAGGGGAAA GAGGAACCTG GAAACAAACT	1440
CTAGACAGCA CAAACAACT CGGAATCACA GATTTCACTG GCTACTATTA TCAATACCAA	1500
ATCGAGCGTC AAGGTAAAC TGTTCCTGCA CTCGATCCTT ACGCTAAATC TCTTGCTGCT	1560
TGGAATAGCG ACGATTCCAA GATTGACGAT GCCCATAAAG TGGCTAAAGC CGCCTTTGTA	1620
GATCCAGCTA AACTCGGACC TCAAGACTTG ACTTATGGTA AGATTCACAA TTTCAAGACT	1680
CGTGAAGACG CCGTTATCTA CGAAGCTCAT GTGCGTGATT TCACTTCAGA TCCTGCCATT	1740
GCAAAAGACT TGACCAAAAC ATTTGGGACT TTTGAAGCCT TCATTGAAAA ACTAGACTAT	1800
CTCAAAGACT TGGGTGTAAC CCATATCCAG CTCCTTCCAG TCTTGTCTTA CTACTTTGTC	1860
AATGAATTGA AAAACCATGA ACGCTTGTCT GACTACGCTT CAAGCAACAG CAACTACAAC	1920
TGGGGATATG ACCCTCAAAA CTACTTCTCC TTGACTGGTA TGTACTCAAG CGATCCTAAG	1980
AATCCAGAAA AACGAATCGC AGAATTTAAA AACCTCATCA ACGAAATCCA CAAACGTGGT	2040
ATGGGAGCTA TCCTAGATGT CGTTTATAAC CACACAGCCA AAGTCGATCT CTTTGAAGAT	2100
TTGGAACCAA ACTACTACCA CTTTATGGAT GCCGATGGCA CACCTCGAAC TAGCTTTGGT	2160
GGTGGACGCT TGGGGACAAC CCACCATATG ACCAAACGGC TCCTAATTGA CTCTATCAA	2220
TACCTAGTTG ATACCTACAA AGTGGATGGC TTCCGTTTCG ATATGATGGG AGACCATGAC	2280
GCCGCTTCTA TCGAAGAAGC TTACAAGGCT GCACGCGCCC TCAATCCAAA CCTCATCATG	2340
CTTGGTGAAG GTTGGAGAAC CTATGCCGGT GATGAAAACA TGCCTACTAA AGCTGCTGAC	2400
CAAGATTGGA TGAAACATAC CGATACTGTC GCTGTCTTTT CAGATGACAT CCGTAACAAC	2460
CTCAAATCTG GTTATCCAAA CGAAGGTCAA CCTGCCTTTA TCACAGGTGG CAAGCGTGAT	2520
GTCAACACCA TCTTTAAAA TCTCATTGCT CAACCAACTA ACTTTGAAGC TGACAGCCCT	2580
GGAGATGTCA TCCAATACAT CGCAGCCCAT GATAACTTGA CCCTCTTTGA CATCATTGCC	2640
CAGTCTATCA AAAAAGACCC AAGCAAGGCT GAGAACTATG CTGAAATCCA CCGTCGTTTA	2700
CGACTTGGA ATCTCATGGT CTTGACAGCT CAAGGAACTC CATTTATCCA CTCCGGTCAG	2760
GAATATGGAC GACTAAACA ATTCCGTGAC CCAGCCTACA AGACTCCAGT AGCAGAGGAT	2820
AAGGTTCCAA ACAAATCTCA CTTGTTGCGT GATAAGGACG GCAACCCATT TGAATATCCT	2880

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TACTTCATCC ATGACTCTTA CGATTCTAGT GATGCAGTCA ACAAGTTTGA CTGGACTAAG	2940
GCTACAGATG GTAAAGCTTA TCCTGAAAAT GTCAAGAGCC GTGACTATAT GAAAGGTTTG	3000
ATTGCCCTTC GTCAATCTAC AGATGCCTTC CGACTTAAGA GTCTTCAAGA TATCAAAGAC	3060
CGTGTCCACC TCATCACTGT CCCAGGCCAA AATGGTGTGG AAAAGAGGA TGTAGTGATT	3120
GGCTACCAA TCACTGCTCC AAACGGCGAT ATCTACGCAG TCTTTGTCAA TGCGGATGAA	3180
AAAGCTCGCG AATTTAATTT GGGAACTGCC TTTGCACATC TAAGAAATGC GGAAGTTTGT	3240
GCAGATGAAA ACCAAGCAGG ACCAGTCGGA ATTGCCAACC CGAAAGGACT TGAATGGACT	3300
GAAAAAGGCT TGAAATTGAA TGCCCTTACA GCTACTGTTT TCGAGTCTC TCAAAATGGA	3360
ACTAGCCATG AGTCAACTGC AGAAGAGAAA CCAGACTCAA CCCCTTCCAA GCCTGAACAT	3420
CAAAATGAAG CTTCTCACC TGCACATCAA GACCCAGCTC CAGAAGCTAG ACCTGATTCT	3480
ACTAAACCAG ATGCCAAAGT AGCTGATGCG GAAAATAAAC CTAGCCAAGC TACAGCTGAT	3540
TCACAAGCTG AACCAACCAG ACAAGAAGCA CAAGCATCAT CTGTAAAAGA AGCGGTTCGA	3600
AACGAATCGG TAGAAAATC TAGCAAGGAA AATATACCTG CAACCCAGTA TAAACAAGCT	3660
GAACCTCCAA ATACAGGAAT CAAAAACGAA AACAACTCC TATTTGCAGG AATCAGCCTC	3720
CTTGCGCTCC TTGGTCTCGG TTTCTTACTA AAAAATAAAA AAGAGAACTA AACTAGCCCT	3780
CCTATAGAAA AATCCCCCAA GCATTATAGC TCGGGGGATT AATTTTGTGA CAATATTTGT	3840
TGTCCTAATA AACTTGATTA GGATTTTSTA TTAAGCCTCT TTCATAGCAA AATAAGCTCG	3900
TACTTTGGGT GCAACTTGTG TTCCGAAGAG TTCAATAGCT CTCAGAACCT GGTATGAGG	3960
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CTGCTCCAAA TATTGCTCAT AACGCAATTC CTGCCAGTGC GGACGGTCTT TGGAAATAGC	4140
ATCCACCACT TGCTTAGTCG GATGGAAATA ATCTTTCACC GCCTGCTCAC CATCTCCGC	4200
AATCCACCCC CAAGAATGGG CTCCCACCTT CAAGTCTTTG TCAGCATGGC CCCTTCGCTT	4260
CCAATCTCAC GATAAGCCTG AATCAACTTT TTAATAAAC GTGGATTACC ACCAATAATA	4320
GCATATACAA TCGGTAGACC AGCCTGAGCA ATCTTCACTG TTGATTGAC ATGACCACCT	4380
GTAGCTATCC ACAAGGGCAA TTTGTCCTGA ACTGGACGAG GATAAACTTC TTTACCAGCA	4440
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AAGTCTAATT TCTCATCAA AAGAGAGTCG TAGTCTTTCA AGTCATAACC AAACAGAGGG	4560
AAAGATCCG TGAAAGAGCC CCTTCCAGCC ATAATCTCCG ATCGTCCATT TGACAAAGCA	4620
TCGATAGTGG CATACTGTTG GAACAAACGA ATCGGGTCCA TGCTTGACAG AATGCTGACT	4680



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GCACTGGTCA AACGGATTTT CTTGGTATTG ACTGCCCCAG CGGCCAGAAC AATCTCTGGG	4740
GCTGATACTG CAAAATCCGC CCGATGGTGC TCACCAATCC CATATACATC CAAACCAACC	4800
TTGTCAGCCA GCTCAATCTC TGCCACCAAC TGGCGAATGC GTTCAGCATG ACTGTAAGTT	4860
TGTCCAGTCC CTTCAAGCTC CGTTATTTCC CCAAATGTTG AAATTCCCAA TTCTACCATT	4920
GTGATTCTCC TTATCTATCT CTGTACTTCA ATTTGAAAA TTATTCTAAC ACGAATCTTG	4980
AGTACAAGCA ACCGATTTGC TCATTAGAAA AAGCCTAGAT AACTAGACTT TTTTAGCTTA	5040
TTCTACCGTT ACTGACTTGG CAAGGTTACG TGGTTTGTCC ACATCGAGGC CACGGTGGAG	5100
GGTTGCAAG TAAGCGACTA ATTGCGTTGG TACGACCATT GAAATTGGTG AGAGGTATGG	5160
ATGTACGGTC GTAAGGACGA TATCGTCGGT ATCTTTGGCT ACATTCTCTT CTGCGATAGT	5220
GAGGACTTTG GCACCACGGG CTGCGACCTC TTGGATATTT CCACGAGTAT GATTGGCAAG	5280
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GTGCTTGAGT TCTCCTGCAG CAAAGCCTTC AACTGGATA TAAGAAATCT CTTTGAGTTT	5400
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GATGAAGAGT GGTTCCTTGC TGAGAAGTGG CATACCGTAG CCCCCTCAG ATGAGATTCC	5880
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TTGAACCTCC AACTATCAG CCTTGACGAT TACCAACTCT TGGTCATGGA TTTCCATGTA	6240
TTGTTAGTT TCACGAATCA TAGCCATGGC GTCTGAGCAG ACCATGTTAT AGCCTTCTCC	6300
AAGACCAATC AAAAGTGGTG ATTTATTTT AGCTACGTAG ATGACTTCAG GATCTTGTGA	6360
GTCAACCAAG GCAAAGGCAT AAGAACCACG GATGATGTGA AGGGCTTTTT TGAAGGCTTC	6420

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AAGAACTGAG AGCCCTTCTT CTTCGCAAA TTTTCCAATC AAATGAACGG CTATTTTCAGT	6480
ATCTGTCTGC CCCTTGAAGT GGTGACCTGC AAGGTATTCT TCCTTGATTT CAAGATAGTT	6540
CTCAATCACC CCATTATGCA CCAAGACAAA ACGTTCGGTC TCAGAGCGGT GTGGGTGAGC	6600
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GTATCAGCA CCATCTAGGA CAAAAATTCC CGCAGAATCA TAGCCACGGT ATTCAAGCTT	6780
TTCAAGCCCT TGAATCAAAA TATCAGTTGC ATTTGTGTTT CCAACAACAC CAACAATTCC	6840
ACACATAGTA TATACGACAC AGGCAAGCTG TGCTTTCTCC TTAATAATTGG TATAGTCTAA	6900
TTCACTTTT ATAGAATCAG CAAAAACAGT ATATACTTGT TTCTTTCACT TGTCAAGAGT	6960
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AATCAGTCAG AGTCCTTTT AAAATCCATT ATTATCGCTT AATTCTTTGA ACCAGTGGCC	7080
TGATTTCTC AGACGACGTT CTTGCGTTTC CAAGTCTAAT TCGACCAAAC CATAGCGATT	7140
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ACGGTAATCA TCTTGAATCA TTCCATCTTG ACGGAATTTT TCTTCCCTT CAACACCCAT	7320
ACCATTCTCA GTCAACATCC ACTCAATATT GCCATAATT TCCTTGATAT TTTGGGCGAT	7380
GTCATAAATC CCTTGCTCAT AAATCTCCCA ACCACGGTGA GAATTGATTT TACGTCAGG	7440
CATCACATAA GGCTCGTAAA AATGTTCTGG TAAGAGTGGA CTCTCTGGAT GCTTAGCAAA	7500
TCGAGGAGCC ATAACACGCA AAGGTTGATA GTAGTTCACA CCAAGGAAGT CCACCGTATT	7560
ATCACGAATG AGTTCCAACT CTTCTCTGT AGCATCAGGT AAAAGACCGT GTTCATGCAA	7620
GATTTCTACC AACTCCTGTG GATAAGTCCC CAAGACAGAT GGATCTAAGA AAGATTGGGC	7680
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ATCCACCTTA TGTGGATAAT GGGCATCATA AAAATAACCA AATTCTACAG GAACGATGGG	7920
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GGCAAAAGGT AAATCAAAAT GATAGAGATT GACTAACAGA CGAATTCCTT TAGCCTTAAT	8100
AGCCTCAAAG ACCTTACGAT AAAATCCAC ACCTTGAGTG TTGACTTTTC CACAGCCTTG	8160
TGGAAAAATC CGTGACCACT GAATAGAAGT CCGAAAGGCT GTGTGACCAG TCTCTAACAA	8220

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AAGCTCAATA TCCCGCTCCC AATTTTCATA AAAAGTCGAT GTCTTATCTG AACCAATCCC	8280
ATTATAGTAA CGATTGGCT CCACTTGGAA CCAGTAATCC CAGAGATTGT CTCCCTTACC	8340
GTCACCAGCT ACACGTCCCT CTGTCTGCGG TCCAGAAGTA GAGGATCCCC AGACAAAATC	8400
CTTTGGAAT CTTAGCATAC ATTTACCTCT TTATCTACTC ATTTCTCCCA TTATACAGAA	8460
AAAACAAGGT AAAAAGTAGT TACATTTTTT CCTTGTTTTT CTTCTGATTA TAGTTTTAT	8520
TTCTTGCTTA GGATTCAAG CGTTTCAAGC ACGTTATCTG CATGAACCTC AATGGTGCA	8580
CCAGTTGCCT TGATCTTAAC TTCTACAATG CCATCGGCCG CTTTTTTACC AACAGTGATA	8640
CGGATTGGAA GACCAATCAA GTCATATCG CTAAATTTAA CACCGACACG TTCGTTACGG	8700
TCATCTGTCA AGACTTCATA ACCAGCTCCC ATCAAGCTTG CTTCAAGTTT TTCTGTCAAG	8760
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AAGAGCGGAG CGTGTGCTC CATCACTGCT GAAAGAAGAC GGCTGACACC GATACCGTAA	8940
CATCCCATGA TGATTGGCAC AGCACGACCA TTTTCATCCA AGACATCTGC TCCCATGCTT	9000
GCTGAATAGC GAGTCCGAG TTTGAAAATA TGACCGATCT CAATACCACG CGCAAAGTTA	9060
AGGACACCTT GTCCATCTGG GGAAATTCA CCCTCACGAA CTTACGGAT ATCCACATAT	9120
TCTGCAGTAA AATCACGGCC TGGGTTTACA CCAGTCAAGT GGTAGTCATC TTCGTTAGCA	9180
CCGACAACCTG CATTCGGAAC ATCTTGTTACC TTACGATCTG CAATAATTTT AATATTCTCT	9240
GGCAAACCAA CTGGTCCAAG TGAACCAAAT CCTGCTTGAA CAACATTGCG CACTTCTTCT	9300
TCGCTAGCAA CGTCAAAGAA ATCTGCTCCC AAGTGATTTT TCAACTTGAC TTCGTTGAGT	9360
TGGTCATTTT CAACTAGAAG GGCTGCAACA AGCTCACCAT CTGCAATGTA GAAGAGGGTT	9420
TTAATCGTTT GTTCTTCTGG AACATTGAGG AAGGCTGCAA CTTATCAAT TGATTTAACA	9480
TCTGGCGTTG CAACACGAGT AACTTCTTCT TCAGCGACAA CACGGTTGCT TGGTTGTAC	9540
TCGTTTGTG CCATTTCTAA GTTAGCTGCA TAGCTAGACT CACTTGAGTA AGCAATGGTA	9600
TCTTCACCAG AGACTATCCA TTTGAGCAAT TCTGCCTTGA TTTCTTCTTG CACTTCTGCA	9660
GGAATTTGCT CAAATGAGGC AACTGACTTG TCCAAGACAA CCCAGCGGTC AAGGTCTGTA	9720
CGAGCAGATG TAATGGCCAT AAATTCTTGG CTATCCTTAC CACCCATGGC TCCACCGTCA	9780
CCAATAATAG CCTTGAAGTC TAAACCACTA CGAGTGAAAA TACGCTCATA GGCTGCTTTG	9840
TACTCATCAT AAACACTATC CAAACTATCA TAGTTAGCGT GGAAACTATA AGCATCCTTC	9900
ATGATAAACT CACGTGTACG AAGAAGTCCA TTACGCGGGC GTTTTTCATC ACGATACTTG	9960

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GGCTGAATTT GATAAAGGTT GAGTGGCAAT TGCTTGTAAG ATTTAACAGA ATCACGGACA	10020
ATAGCTGTAA AGGTTTCTTC GTGAGTTGGA CCTAAGATAA AGTCTGATTT TTCACGGTTT	10080
TTTAGTTTGT AAAGGTCTTC ACCATAGGTT TCGTAACGAC CTGATTCACG CCACAATTCT	10140
GCACTAAGAA GGGCTGGAGC CAACATCTCA ACAGCACCAA TCTTTTCGAA TTCTTGGCGC	10200
ATGATGTTTT TAGCTTTTTC AATCACACGG TTGGCAAGTG GTAGATAAGA ATAAACACCT	10260
GCTGAAACTT GGCGAACATA ACCAGCACGC AACATAAGAG CATGGCTGAT AACTTGAGCA	10320
TCGCTTGGCA TTTTCGGAAG CGTTGGGATA GGCATTTTAC TTTGTTTCAT AATATTCTTC	10380
GATTATCTAA AAAAGAGTCG CATAATGTCA TTCCAAGTCA CAGCAATCAT CAAGACAACC	10440
ATGATGACCA CTCGGCCAA GGTGACATAG GTTTCAATTT CTGTTTCAA TGGTTTGGCG	10500
CGGATGGCTT CTAGGATATT GAGCACAATC TTACCACCAT CCAAGGCTGG AATCGGAATA	10560
AGATTAAAAA TCCCAATATT GATGAAATC ATTGCCAAGA AGTACAAGAT ATTTTCAATT	10620
CCATTTTTAG CAGCATCACT ACTTGCCTTA AAGATAGCAA CAGGTCCACC CAACTTGTTC	10680
AAATCTGGTT GGAAATCAG ATTTTTCAGA GCTGAGAGAA TTCGGAGAGC TGAGTCAGCA	10740
GCAGTTGTAA AACCACCTAC AAACATGGAT AGAAAATCTG ACTTAACCCC CGGTTGAACA	10800
CCTAGAAGGT AACGACCTTG ACTATCTTTG GGTGTAACAG TGACTTGTTC GTCCTCCCC	10860
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ATTTCTGGTA CTCCTACCTT GGCCAAGGCA CCTTGGGGCA TGATATGGAA CTGATTGGTA	11040
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CCTGAGAGAT TGATGCGTTT AACCTTACCA TCATCAGCAA GTGTCAAAC AACAGGCGTT	11400
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CCCATACCGA TGGCAAATTC ACGTACTAAA ATCCCTGATT TCTTGGCAAA GTAGAAGTGA	11580
CCGAACCTGT GCACCACTAC AATAATCCCG AAAACCAGAA TAAAGGTTAA AATTCCGAGC	11640
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AGCAACATAC TATCGAAACG ATCCAAAACA CCACCATGTC CAGGGATAAA TTTCCAGAA	11760

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ATGCTAAAGA AAATAGCAA GACTGACATC TTGTAAATTC CATATGGAAG AGCAACTGTA	11880
CTGTCAACTA TCATAAGGAT AATGGTTACT AAAATTGCTC CTAAAATACC ACCCAAGGCA	11940
CCCTCAAGGG TTTTATTAGG CGATACCCCTT GGTGCTAACT TTCGTTTCCC ATAGTTCATC	12000
CCAACAAGAT AGGCACCACT GTCTGTCGCC CAGACGATAC ACAAGGCTAA GAGAGCCTTG	12060
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AACATGATTG AAATCAAAAC ACTATAGGCA ACCACATGCC CATCAACTGG CAAAAAAGTC	12240
AGGTAATTCT CCAAGGGAAT GGTCAATGCA AAGGTTGCAA AGAGGGTCAA GAGGCCCTCC	12300
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ATTCCGATTG CTATCTGAAG CAAGAGGCC CCAATCATTAA AAATTGGTAG GAAAATAGCC	12420
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CTCTCCAAA TCGGCGATGA CGACGATTAT AGGCAAGAAT AGCTTCCTGC AAGGCCGCTT	12540
CGTCAAAATC AGGCCATAAG GTGTCCGTAA AATAAGCTC ACTATAGGCT CCCTGCCATG	12600
GAAGGAAATT GCTCAAACGT AATTCTCCAC TAGTACGGAT AATCAAGTCT GGGTCTCGTA	12660
AGTCCTTAGG CAAATGCTGA GTAAAGAGAT AGTTACCAAT CAATTCTCTCT GTGATGTCAC	12720
CTGGGTGTAT TTTGGCATCT AAAACATCCT GGGAAATCAA CTTAAGCGCC TGTGTAATCT	12780
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ATTCTCAGC CTTGGTTAAA GCTTCAAAGG TTTGCTTAGG CAGGCGGTCT GTCTCCCCAA	12900
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GGCCATTGCC ATCCATGATG ATGCCGATAT GAGCAGGAAC CTGTGTCGGA ACCTCTACTT	13200
CCACAGCCTT ATCTTTCTTA AAAAATCCAA ACATGATCTT ATTCCTATTC AAAAATCTAT	13260
CGTTTCATTA TACCATATTT CCCCATTTTC TTCTATCACT AAGCTATTTA TTCTCAGGCA	13320
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ATTATTATGA AAAAGTTTAA GGAGTTTAAG TTAAGGTCTT CTTAACTTAT GAACTTAGTG	13440
TACACTCCCT AGCTTAAAGT TTCCTTAAGT ATTTTAAAA ATCAAATTTT TCCATTTCTC	13500

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CTGCCAATTT	TTCTTGGATA	AACGTGTTTG	ATAGAGTTCC	ATTCGGTCTT	CATTTTCTAA	13560
GAAATGAGGA	GTGAGCGAA	CTGAAAAAT	CAAAATATCC	TCCAAACCAT	AAGGTACATA	13620
GAGTTCAAAA	TCTAATTCTT	CATTCAAGCG	CAGTCCAACT	GCCGTACACC	GTCTTGGATA	13680
CTTACTCATA	GCATCACGAG	AACCTGGTATA	GGAAGCAGTG	TGAGGACTGT	GCTGATGCAT	13740
ATAGACCTGA	TTTTTCAATT	CCCACTGGTA	CTGAGGAAAA	TCCTCTCTCA	GCTTTTCTC	13800
CAGTAATAAG	GTTCCTCAT	AAGAAAAATC	TGGATCAAAG	AAAATCACAT	CTATATCTGT	13860
TTCATGATCA	AAAGGGGATT	TGTCTGACAA	AAGATTCCAG	ATGAAATTC	TGACAGAACC	13920
TGCTGCCAAC	CACGAGTCTT	TCAAACCAAG	GTCTCGGATG	ATCGTCAGAA	TGGCCATCAT	13980
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CTAAGTGCTC	ATATGCCTTA	GCAGTCGCCA	CCCGTCCAGA	CCGTGTCCGC	ATGATAAAAC	14100
CTTTTTGAAT	CAAGTAAGGC	TCATACATGT	CTTCAACTGT	CTCACGCTCT	TCGGCGATAT	14160
TCACAGAAAG	AGTTCCTAGA	CCAACAGGTC	CTCCACTGTA	CATCTCAATC	ATGGTGCGAA	14220
GGATTTTTTG	ATCCACATAG	TCCAAACCTT	CATGGTCAAC	ATCCAGCATA	GTCAAAGCCT	14280
TATCGGTAAT	AACATCATCG	ATAACCCCAT	TCCCCATTAT	CTGGGCAAAA	TCGCGCACGC	14340
GCTTGAGGAG	ACGATTGSCA	ATACGAGGGG	TTCCACGACT	ACGTAGGGCC	AACTCAGATG	14400
CTGCCTCATG	GGTGATTTC	ATCTCAAAAA	TATCTGCCGT	CCGCTCGACA	ATTTCTGTCA	14460
AGTCAGCATG	AGCATAATAC	TCCATATGAC	CTGTAATCCC	AAAACGTGCC	CGTAGTGGAT	14520
TTGAGAGCAT	ACCAGCCCGA	GTGTCGCAC	CAATCAAGGT	AAAAGGAGGC	AACTCCAAAT	14580
GAACACTGCG	ACTGCCTTCA	CCAACCCCAA	TCATAATATC	GATGTAGAAG	TCCTCCATGG	14640
CACTATAAAG	CACCTCTTCC	ACTGACATGG	GTAAGCGATG	AATCTCGTCA	ATAAGAGGA	14700
CATCTCCAGG	CTCTAAATCA	TTCAAAATCG	CTACCAAATC	ACCCGCTTTT	TCGATAACAG	14760
GACCAGACGT	TTGCTTGAGA	TTGACTCCCA	GTTCAATGGC	AATGACAAAA	GCCATGGTTG	14820
TTTTCCCAAG	CCCTGGAGGG	CCAAATAAGA	GCACATGATC	CAGCGCTTCA	TCCCGCATTT	14880
TAGCGGCTTC	GATAAAGATC	TGAAGTTGAT	CCTTAACCTT	ATCCTGACCA	ATATATTAC	14940
GTAAATACTG	AGGACGGAGC	GTGCGTTCTA	CTAACTCCTC	ATCACCCTATC	ATCTCATTAT	15000
CTAAAATTCT	ACTCATGGCT	CTATTATATC	AAAAAAAACA	AGCCACAAAC	AAAAAGCCA	15060
CCTGATTGGG	TGACTCCTAA	GTTTAGCACT	TATGTGGTAT	AATATTATAC	GGCACTTCTA	15120
CACCGCTTAC	GAAAGGAGGT	GAGATAGCCC	ATGATGGAAT	TAGTACTCAA	AACTATTATC	15180
GGACCAATTG	TGGTCGGTGT	CGTCTTCTGT	ATAGTCGATA	AATGGCTAAA	CAAGGACAAA	15240
TAGTGTCAAA	AAAGACCTCA	AGCTTATTTG	GTCGTGAGCT	TGGGGTCTTT	TCTAGCCTAT	15300

617

GATATAGAAC TAGTACTCAA TTCCTTTTTA TTATCCCATTA GTTCACGAAT TTTGTCAAAA	15360
CTTTACATTT TCTTCAACCG CTGTACGACA AGACGGTTAA GATTAAGAGA ACGTTAGGGA	15420
TTCTATCAAT TTCATAGAAA TTTTGATTTC GTAAACGAAG AGACAATCTT ACATGTCACT	15480
TCTCATTTAA TACGCCACTA CTAGACAAGC AAAATCATT TACAGTAGT TCCAGTCCTT	15540
CAATTAACAG TCACCTACAA TCAAATTGAG TTTGAACTAG CTGAAGCGAC CACAGACCTA	15600
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CCCCGACCAA AATCCGAAAA ATACCGAAAA ATATCGAAAA ATTATTTTTA GAATAGTCCC	15720
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TATGAAAAAG AAAAGTTTAG GATTTTATTA AATAAAGTTA GGAGGTCTTT ATTTAATAAC	15840
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CAAGGTAATA ATCCAAACAC GAAACCAGTC CACGTTTTTC CAGGACTGGT TTTGATATAG	16080
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TCTTCCATTG CTTCAGATA ATCACTCGTA GCGGAGTACG CRAAGCGCTCA TCTATGCTGG	16260
CGACTATACT TTTTCATATTT CCCAATGAGC AATAGTTTAT CCATCCTCGA ATAGACAAAT	16320
TCAGTTGCTC AATACGTCTT GTTAGGTCTA TACTCCATTT CCTCTGTGTT AGTTTCTTCA	16380
ATTTAACTT AAATCTCCGA ACACTATCTT GATGTGGACG GCTTTTCCAA CCATCTGATA	16440
ATTTCCAGAA CCAAAACCT AGATATTTCA ACTCTCTTGG TCATGTTTAC TTTCAAACCT	16500
AGCCGTTTCT CAATAAACGA CTGACTGAAT ACATC	16535

## (2) INFORMATION FOR SEQ ID NO: 75:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 8136 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 75:

CCAGAGCGTT GCGTCCGAAA GTCTATCCAG ACACGGCTCT TAAAAACAA AAGGAGAAAT	60
GATGCATACT TATTTGCAAA AGAAAATTGA AAATATCAAA ACAACCCTAG GTGAAATGTC	120

618

AGGTGGTTAC CGTCGTATGG TTGCGGCTAT GGCTGATTTA GGATTTTCAG GAACTATGAA	180
GGCTATCTGG GATGACCTCT TTGCCCATCG TAGTTTGGCC CAGTGGATT ATTGCTGGT	240
TTTAGGAAGT TTTCCTCTCT GGCTGGAGTT GGTTTACGAA CATCGTATTG TTGACTGGAT	300
TGGGATGATT TGTAGCTTGA CAGGGATTAT CTGTGTAATC TTTGTATCGG AAGGTCGAGC	360
AAGTAATTAT CTTTTTGGCT TGATTAACTC TGTATTATAC CTTATTTTGG CCCTACAGAA	420
AGGCTTTTAT GGTGAGGTGC TGACGACACT TTAATTACACA GTCATGCAGC CAATTGGACT	480
TCTAGTTTGG ATTTATCAGG CACAGTTTAA GAAGGAAAAG CAGGAGTTTG TCGCGCGTAA	540
ACTGACGGC AAGGGCTGGA CAAAGTATCT TTCCATTAGT GTGCTTTGGT GGTGGCCTT	600
TGGCTTCATT TATCAGTCTA TTGGTGCCAA TCGTCCCTAT CGTGATTCAA TCACAGATGC	660
AACCAATGGG GTAGGGCAA TCCTCATGAC AGCTGTTTAC CGTGAACAGT GGATATTCTG	720
GGCGGCTACC AATGTCTTTT CAATCTATCT CTGGTGGGGA GAAAGCCTGC AAATTCAAGG	780
GAAATATCTA ATTTATCTCA TTAACAGTCT AGTTGGTTGG TATCAATGGA GCAAGGCAGC	840
TAAGCAGAACT ACTGATTAC TTAAGTAGGA AAAGATGTTT GAAAGTGCTG TTTTGAGATT	900
TCGATTAAAA CAGATATAGT TGATAATCAA GGATTTATAG TATGAAAAAG AGGATCGGCG	960
GGTCTCTTTT TGTGTGTGAA AAGATAAAAA ACTCAGTAAC CTAGAAATAA GACAACTGAA	1020
GCTTTACTCT ATATTCAATT TTAGGAATG AGAAGGTCTA GATAAAATTG GACAACCTCC	1080
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CGTCCCACAT CTGCGAGATC AATGATATCC TGAACAGTAG TGGCCTCGTA GCCCTTAGCA	1500
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ATTATAACAA AGGAATGAGA AATATGAAGG CAAAATATGC TGTGTTGGTG GCTTTTCTCT	1740
TAAATTTGAC TTATGCCATT GTTGAAGTTA TTGCAGGTGG AGTATTGGT TCTAGCGCTG	1800
TTCTTGCTGA CTCTGTGCAT GACTTGGGAG ATGCGATTGC AATGGAATA TCAGCTTTTC	1860
TAGAAACAAT CTCCAATCGT GAAGAAGACA ATCAGTACAC CTTGGGCTAT AAGCGGTTTA	1920



GCCTGCTAGG AGCCTTGGTA ACAGCTGTGA TTCTCGTAAC GGGCTCTGTT CTAGTCATTT	1980
TGGAATAATGT CACGAAGATT TTGCATCCGC AACCAGTCAA TGATGAGGGG ATTCTCTGGT	2040
TAGGAATTAT TCGGATTACT ATCAATCTGT TAGCGAGTCT GGTGGTTGGT AAGGGAAGA	2100
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TTATCCTGAT GCGGATTGTT CTTCGATTTA CGGACTGGTA TATCCTAGAT CCTCTTTTGT	2220
CCCTTGTCAT TTCTTTCTTT ATTCTTTCAA AAGCCCTTCC ACGTTTTTGG TCTACACTCA	2280
AGATTTTCTT GGATGCTGTG CCAGAAGGTC TTGATATCAA GCAAGTAAAG AGTGGCCTGG	2340
AGCGATTGGA CAATGTGGCC AGCCTTAATC AGCTTAATCT CTGGACTATG GATGCTTTGG	2400
AAAAAATGC CATGTGCCAT GTTTGTCTAA AAGAAATGGA ACATATGGAA ACTTGTAAG	2460
AGTCTATTCG AATTTTCTTA AAAGATTGTG GTTTTCAAAA TATTACCATT GAAATTGATG	2520
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AGCATCAACA TTAGAAAAA GTGAAAAATA CTTGGGTACT ATCTTATTTG GAATAGAGTA	2640
ATTCTTTTAT TATTAAATA TTTCAAAAAT TGGAAGAGA AGAGCATGTG ATAACTCCA	2700
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CAGAAATATAT TCGCTTCCAC TATGCAAACT GGGCGCTGGT TAAAATCCCT GGTCAACCTT	3600
CTGACTATAC AGAAGGGATG CTCAAGTCCC TTTTGACTCT TGCAGATGTC ATGCCGACAG	3660

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GCTATCATGC GCGCGTGT GCAAAATGTTT AAAAAGGGGA CAAGGTTGTT GTTATCGGTG	3720
ATGGGGCTGT TGGTCAATGT GCTGTCATCG CGGCTAAGAT GCGTGGAGCA TCACAAATTA	3780
TCCTTATGAG CCGTCATGAA GACCGTCAAA AGATGGCTAT GGAGTCAGGT GCGACAGcTG	3840
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CTTCAAGTTA TAAACTGGAA GATATCGACC AAGCCTATAA AGATATGGAT GAACGTAAGA	4200
CAATTAAGTC TATGATTGTA ATCGAATAAA AAACGAATAG GAGTTTGA ACTCTATTCTG	4260
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TAGTAGTAGA GGTGCTCCAG CTCCCCTTGT TCGCTGACCC ATTGGATAAT GGCAATCTTT	5100
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ACGGTTAAAA TACGGTGTCT GGTCTCTTCT GTAACAGATA GGCTCTGGTC GCGGTTGAGG	5220
ACGCGGGATA CGGTCGCGAT AGAGACAGAG GCTAGCTGTG CAATGCTTTT TAAGGTAGCC	5280
ATAAATCCTC CTGATTAGG TTAGTATATC ATGTTTTTCT TCTTTTTACT GATATTTTAC	5340
TAAAATTTTA GTAAAAAGGA TTGACCTTGG AAAATTCCTT GGATATAATA GAAAGAAAAC	5400
GATTACAGT TAAGATGGCT TAACGGACAG TCAAAGGAGA ATTATATG CACAACATCT	5460

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TACTACTGAA GCCCTTCGCA AAGACTTTCT TGCTGTTTTT GGTCAAGAAG CAGATCAAAC	5520
CTTCTTTTCA CCAGGCCGCA TTAATTTGAT TGGTGAACAC ACAGACTACA ACGGTGGGCA	5580
CGTTTTTCCT GCTGCTATTT CCTTGGGAAC TTACGGTGCA GCTCGTAAGC GTGACGACCA	5640
AGTCTTGCCT TTCTACTCAG CTAACTTTGA GGACAAGGCG ATTATCGAAG TGCCTCTCGC	5700
TGACCTCAAG TTTGAAAAAG AGCACAAC TGACCAATTAT CCAAAGGTG TCCTTCATTT	5760
CTTGCAAGAA GCTGGGCACG TGATTGACAA AGGTTTTGAT TTTTATGTTT ATGGAAATAT	5820
TCCAAATGGT GCTGGCTTGT CTTCTTCTGC ATCCTTGGA CTCTTGACAG GAGTCGTGGC	5880
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CTCTAAATAC AATGAACGTC GTGCTGAGTG TGAAAAAGCA GTGGAAGAAT TGCAAGTTTC	6180
CTTGATATTT CAGACTCTGG GTGAATTGGA CGAGTGGGCC GTTGACCAAT ATAGCTATCT	6240
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TGCGTCACAC GTTTCTCTGG AGCATGATTA TGAAGTAACT GGTTTGGAA TGGATACCTT	6420
TGTTACACAC GCTTGGGCAC AAGAAGGAGT TCTCGGTGCT CGTATGACAG GGGCTGGTTT	6480
TGGTGGCTGT GCcATTGCCT TGGTTCAAAA AGATACTGTT GAGGCCTTTA AGGAAGCTGT	6540
AGGCAAACAC TACGAGGAAG TAGTTGGATA CGCTCCAAGC TTCTATATCG CTGAAGTTGC	6600
AGGTGGCACT CGCGTCCTTG ACTAGTCAAA AGGAGGCTCT ATAGTGACCT TAGTAAATAA	6660
ATTTGTAACA CATGTCATTT CTGAAAGCTC ATTTGAGGAA ATGGATCGAA TCTATCTGAC	6720
CAATCGTGTT TTGGCAGGAG TGGGAGAAGG TGTTTTGGAA GTTGAGACCA ATCTGGATAA	6780
ATTGATTGAC CTCAAGGACC AGCTGGTTGA AGAAGCCGTT CGATTAGAGA CGATTGAGGA	6840
TAGTCAGACT GCGCGTGAAA TCCTTGGTGC TGAAGTATG GATTTGGTGA CTCCTTGTCC	6900
AAGTCAGGTC AATCGTGATT TTTGGGCAAC CTACGCCAC TCTCCAGAAC AAGCGATAGA	6960
GGATTTTAC CAACTCAGTC AGAAAAATGA CTACATCAAA CTCAAGGCCA TTGCTAGAAA	7020
TATCGCTTAT CGTGTTCAT CTGACTACGG AGAACTTGAA ATTACCATCA ATCTCTCTAA	7080
GCCTGAAAAA GATCCCAAAG AGATTGTGGC AGCCAAGTTG GTGCAAGCTA GTAATTATCC	7140
TCAGTGTACG CTTTGTCTAG AGAATGAGGG CTACCATGGT CGAGTTAACC ACCCAGCTCG	7200

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TAGCAATCAC CGTATTATCC GTTTTGAAAT GGTGGTCAG GAATGGGGTT TCCAGTATTC	7260
GCCCTATGCT TACTTTAATG AGCATTGTAT CTTTTTAGAT GGCCAGCATC GTCCCATGGC	7320
CATTAGTCGT CAGAGTTTGT AACGCTCTGT GGTATCGTA GACCAGTTTC CAGGATATTT	7380
TGCTGGATCT AATGCCGACC TGCCGATTGT GGGGGGCTCT ATTCTAACTC ATGATCATT	7440
TCAGGGAGGC CGTCACGTAT TTCCTATGGA ATTGGCTCCC TTGCAAAGG CCTTCCGATT	7500
TGCTGGTTTT GAGCAGGTCA AGGCTGGAAT TGTCAAGTGG CCCATGTCTG TCCTACGTTT	7560
GACTTCGGAT TCCAAAGAGG ATTTGATCAA TTTGGCTGAT AAGATTTTGC AGGAATGGCG	7620
CCAGTATTCA GATCCTGCAG TGCAGATTTT GGCAGAGACA GACAGGACAC CGCATCACAC	7680
TATCACACCC ATTGCCCGCA AACGCGATGG ACAGTTTGAG TTGGACTTGG TCTTGCGAGA	7740
CAATCAGACT TCAGCAGAGT ATCCTGATGG TATCTATCAT CCCCACAAGG ATGTCCAACA	7800
TATCAAGAAG GAAATATCG GCTTGATTGA GGTATGGGC TTGGCAATCT TGCCACCACG	7860
TCTGAAAGAA GAAGTGGAGC AAGTCGCTAG CTATCTTGTA GGAGAAGCTG TTACAGTTGC	7920
CGATTATCAT CAGGAGTGGG CAGACCAACT CAAATCCCAA CATCCAGACT AACGGATAAA	7980
GAAAAAGCCC TTGCAATCGT CAAGGACTCT GTGGGTGCTA TCTTTGCGCG TGTAATTGAG	8040
GATGCAGGAG TCTACAAGCA GACAGAACA GGGCAGACAG CCTTTATGCG CTTTGTGGAA	8100
CAGGTCGGAA TTTTACTAGA CTAGGAGCTT TCTCGG	8136

## (2) INFORMATION FOR SEQ ID NO: 76:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 10011 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 76:

CCCATAGTGA AGAGTGGCCA TAAGAAGGTC TTCTAGGCTT AATTTAGGTT TTCGTCCACC	60
TTTTCGCTGT TTAAGTTGAT AAGCTGTTTT TAACACAGCT GAACATCTCT TCAAAAGTCG	120
TGCGCTGAAC ACCAACAAGA CATTAAATC GTGTATCAGT TAGTTGTTTA CTGCTTCAT	180
CATTCATAGA ACTACTATAC CATGTTTTGT TTCGCAGGAA GTCTAATATT GTCAAATACT	240
GGAACGCTCA TTGCTGGGAT ACGGAATAAG ATTGGCCCAG CTTCGATAAC TGGGATACCT	300
GGTTCAAAAC CAAGGCTCTGT TGCAGCGATT GGTGTAAAGA TATCGTAACC TTTCATAAGG	360
TCTTCGTTTA CATCTTTCAC CATAACTGCA TCACAGTGAA CATCGTAACC ACGGTTTGAA	420
AGTTCCTCTT CTAGAGCACT TTTAATTGG TGACTTGAGT TAACACCTGC ACCGCAGGCA	480

623

GCAAGAATTT TAATCATTG GATTTCTCC GATTTTATTT TTTAATAGAC AAGATTAAGC	540
GGTTGCTTCA GCAATGTAAG CATAAAGGGC TTCTGTTCA GAAATTTTG ATAGGTCTTC	600
AAGATGACCA TTTCTGTGA AGAAGTCCAT TAACTGAGCA AGAATGTTG TTTGACTTGA	660
ACTTGAATTA TTGATGATAA AGAAGAGCAA GGATACTTCT ACTTCCTTAC CTGGCGCAAT	720
CATATTATGG AAAGTCACCG GTTCTCTAA TCGAACAACC ACCACTTTCT CAGCTAGATT	780
ATGAACAATA TCTGTGTGAG GAATCATTAC ATTTGCAAGT CCTTTCCTAG AAATTCATA	840
TATAAACCAAG TTGGAATGA CTTTTCACGC GTGATCAAGG CTTACGATA AGTTGGAGTG	900
ACAATTTCTC GTTCTTCAA CAAGCTTGCT ACCTGATCAA AAAGTTATTC TTGATTATCC	960
GCTTCTAAGC AAAACACAAG GTTTTGTCA AAGAAATAAT CTAATACCAT AAGGTTTCC	1020
CTTCTTCCA TTAACTTTAT GCTATAAGTA TAACACTATA TGAAATCGTT GTTAATTACT	1080
TTCTATTCTT TTTTGTCTCT TTTTATATAT TTTTGTGTTG TTTATAGTTT GTTATATAAA	1140
AATAACACA CAAACAATA CTCCAAGCAT TTTTCTGTTC TAATACTCAA TGAAAAACAA	1200
AGAGCAAAC AGGAAGCTAG CCGCAGTTGT TCAAAACACA GTTTTGAGGT TGTAGATGAA	1260
ACTGACGAAG TCACTCAAAA CATGGTTTGG AGGTTGTAGA TGAACTGAC GAAGCAACAG	1320
CCATACATAC GGTAAAGCGA CGCTGACGTG GTTTGAAGAG ATTTTCGAAG AGTATAAAAA	1380
CTAAAAAGC AGACCATCTA AGCCTGCTTT ACTATTGATT CTTATATAAA TTTCCTGTGA	1440
ACAAGGAAAG GCATTTCTGA TAACTTATTC TTCATCCATA CTCAAGACGC TGAGGAAGGC	1500
TTCTTGCGGA ACTTCAACTG ATCCGATGGA TTTTATGCGT TTCTTACCAG CTTTGTGTTT	1560
TTCAAGGAGT TTACGCTTAC GAGAAACGTC ACCACCATAA CATTTAGCAA GTACGTTCTT	1620
ACGAAGGGCC TTGATATCAG TACGAGCGAC AATCTTGTGT CCAATAGCCG CTTGGATTGG	1680
AACTTCAAAT TGTTGGCGAG GGATGATTTT CTTGAGTTTA TCAACGATGA GTTTCCCACG	1740
TTCTGAGGCA AAGTCCTTGT GAACGATAAA GCTGAGGGCA TCCACCTTAT CTCCATTGAG	1800
AAGAATATCC ATTTTCACCA GCTTAGATGG GCGATATTCT GACAATTCGT AGTCAAAGCT	1860
TGCATAACCA CGTGTGGAAG ACTTAAGTTT ATCAAAGAAG TCAAAGACAA TTTCAGCAAG	1920
AGGAATTTGA TAGATAACAT TGACACGGTT ATCATCAATA TAGTCCATAG TCACAAAGTC	1980
CCCACGCTTA CGCTGAGCTA GCTCCATTAC TGCTCCGACG AACTCCTGTG GTACCATGAT	2040
TTGCGCCTTG ACATAAGGCT CTTCAATGGT CGCAATCTTA GTTGGGTCTG GAAACTCAGA	2100
TGGGTTAGAC ACATCCATAG ACTCACCCTC GGTCAAATTA ACTTTGTAAA TAACAGACGG	2160
AGCTGTCTAT ATGAGGTCAA TATTGAACTC ACGCTCTAAA CGTTCCTGGA TAACATCCAT	2220

624

ATGGAGAAGT CCAAGAAATC CACAACGGAA ACCAAATCCA AGTGCCTGAG ATGTTTCTGG	2280
TTCAAACCTGA AGACTAGCAT CATTCACTTG CAATTTTCA AGCGCTTCAC GCAGGTCATT	2340
GTACTTGTGTT GATTGATTG GGTAGAGACC CGCAAAGACC ATAGGATTCA TCTGCTTATA	2400
ACCATGTAAT GGTCTGCGG CAGGATTGGT TGCCAAGGTA ACGGTATCAC CCACACGAGT	2460
ATCCTGAACC GTCTTGATAG ACGCCGCAAT GTAACCAACA TCACCAGTCG CAAGGAAATC	2520
ACGACCAACC GCTTTTGGTG TAAAAATACC GACTTCGGCC ACATCAAAGG TCTTACTATT	2580
GCTCATGAGC TGAATCTTAT CACCAGGTTT GACCACTCCG TCCATGACAC GCACTTGGAG	2640
GATAACCCCA CGGTAAGCAT CGTAAACAGA GTCGAAAATC AAGGCCTTAA GTGGCGCCGT	2700
CACATCACCC GTTGGTGCTG GTACTTTTTC TACAATTTGC TCGAGGATTT CTTCATCCC	2760
AATACCAGCC TTGGCAGAAG CCAAACTGC TTCCTGGCA TCCAAACCAA TCACATCTTC	2820
AATCTCTGTA CGCAGCGCT CCGGATCTGC AGCCGGCAGG TCAATTTTAT TAATGATAGG	2880
CATGATTTCC AAATCATTAT CCAAAGCCAG ATAAACGTTG GCAAGAGTTT GAGCCTCAAT	2940
TCCTTGAGCC GCATCGACCA CCAAATAGC ACCCTCACAG GCAGCTAGCG AACGTGAAAC	3000
TTCATAGGTA AAGTCAACGT GCCCTGGTGT GTCAATCAAG TGGAAAATAT AAGTTTCCCC	3060
ATCTTTTGCA GTGTAATTCA ACTCGATGCG ATTCAACTTA ATAGTAATTC CACGTTCCCG	3120
CTCTAGCTCC ATGCTATCCA AAAGCTGGGC CTGCATTTCA CGACTTGAAA CCGTCTCTGT	3180
TTTTTCCAAA ATGCGGTCTG CTAGAGTTGA TTTTCCGTGG TCAATATGGG CGATAATAGA	3240
GAAGTTACGG ATCTTCTCCT GTCGTTTTTT CAATCTTCT AAGTTCATGA TTCTCTCCT	3300
TTCAGGGTAT CTATTTATTA TAAATTGTTT TTGATATTTT GACAAGACCA TACCTGCTA	3360
GGAGTACTAA TCTTCAGCGA CAAAGCCGTC ATTTTCGATA AAGTGGTGT CTGTCAATCC	3420
TTGGTCTGTA AAGACAATCC CGTGAAGGAC ACCACCATAA ACAGCTCCTC CATCCATTCC	3480
AATCTTGCCA TCTTCTGTAG TCCAAAGCTC AGATGTACCG CGTTCTTGCT GTAACAAACC	3540
ATAGACCGGT GTATGACCGA AGACAATGGT TTTTCCAGTA TGATTTTCAG CTCGCTGGAA	3600
TGGTTTCTA AGCCATACTT TTTTATAATC TGTGTTTCA TGCCAGTCGT CCAAGGTCAA	3660
ATCAATACCT GCGTGAACAA AGATATACTT GTCTGTCTCT ACTACAAATG GCATTTGACG	3720
AATGAATTCG ACCAAGTCTG CCGCTTCAGC GCAACCCGC TTGGCATCTT CTACTCCATC	3780
AACTGGTGCA TCCAAGGGAC GACCTAGGAT AGAGTTAATG GTTGTATCTC CACCATTGCG	3840
ACTATAATGG TCATAACTTT CTCTGCGGTC ATCTAGCCAA GTCAAAAACA TATACTCGTG	3900
GTTCCTGGAC AAACAGATAG CCCCTTGATT GTCCACCAAG TCCTTGACCA TTTCAAGAAC	3960
ACGGTGACTA TCCTCACCTC TGTCATCAA ATCACCTAGA AAGAGCAACT GGGGCTGACC	4020

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ATCCCAGGTT TTGAGAAGGT CTTCCAGCAT CCCAGCTTTT CCGTGAACAT CTCCAATTAC	4080
ATAATAATCT GTCATCTTAT TTCTCCCTGT TTCTCAACAA TTCTCTTGCT TGCCTCAGGG	4140
CTGCTTCTGT CACATCATCA CCTGCCAACA TCTTGGAAC TTCCTCCACT CGCTCTTCGA	4200
CCGTCAAGAG ACGAACAGTC GAAACCGTTG AATGGTCATT ACTAATCTTC TCAATAAAGA	4260
ATTGATAATC TGCAATCGCA ATTACTTGTG GCAAATGGGA GATAGCCAAA ACCTGACCAT	4320
GCTGACCAAT TTTATGAATT TTCTGAGCAA TAGCTTGAGC AACACGACCT GAAACTCCCG	4380
TATCCACCTC ATCAAAGACA ATGCTAGTCT TGCCTTCTTT ACGTGAAAAG GCAGACTTAA	4440
TGGCTAACAT GAGACGAGAT AATPCCCTC CAGAAGCAAC CTTAACCAAG GGTTTAAAGT	4500
CTTCTCCAGG GTTGTTGAA ATATAAACT CAACCATTTT ATTTCCCTCA CGACTGAATT	4560
TTCCCTTACT AAAACGAACC TGAACTGGG CTTTTCCAT ATAAAGATCT TGCAGTTCTT	4620
GTTTAATCTC AGCTTCGAGT TGCTGAGCCA AATTATGACG AGCAGAAGCA AGTTGACCTG	4680
CCAAATTGAC AAGATTGACT TCCAACCTCT TAAGCTCTGC TTCCATGTCC TCAGACGAAA	4740
GATTATTGCC TGTCAAGAGA TTGTATTCTT CCGTAATCTT GGCAAAATAA AGCAAAACAT	4800
CATCAACAGT CCCACCATAC TTACGAGTAA TAGTATGAAG GAGGTCCAAA CGATTCTCAA	4860
CCTGCATCAG GCGATTGCCA TCAAAATCAA GGTCTCTCAAT GATAGCTTCC AAACGTTTGC	4920
TAATGTCTTC TAAAACATAG TAGGTCTCAG ACAGATAGCT TGAAATTTCA CGGTATTGAG	4980
GATCATACTC TTCGACACTT TCCATGTGAT TCATAGCTGA ACGAACATTG GCCAGACTTG	5040
AAAAATCTTC ATTGTCCAAC ATACTGTAGG CATTGCTCAG TGTATCCGCA ATATTTTTGT	5100
GGTTGAGGAG TTTATCTCGC TCTTGATTGA GAGCCAAGTC TTCTCCAGCC TGCAAGTTTG	5160
CTGCCTCAAT CTCTGCCATT TGAAATTCCA ACATTTCGAT ACGTGCCTTG TGTTCCTGTT	5220
GGTTTTCTTT GACTTCCAGA ACCTGCTTGC GCATTTTCCG ATAGGCATCA AAACTCGTTT	5280
GATAGGTTTC TTTCAAGTCC CAAAAGCGG CATCACCAA TTTATCCAAC ATCTGGATAT	5340
GCAGTTGGGG ACGCATTAA TCCTCATGGT CATGCTGACC ATGAATATCT ACAAGATGTT	5400
GCCCAATAGC TCGCAAAACA GACAGATTAA CCATCTGACC ATTTACACGG CTGATACTAC	5460
GACCATTTTG CAAGATTTCC CGACGGATGA TAATTTTCATC ACCTAATTCT AAACCTTGCT	5520
CATCAAAAAT TTCCTGTAAA AGACGACTAT TCTCAACTGA GAAAGCCCC TCAATCTCTG	5580
CCTTTGGTGC ACCATGACGA ATAACATCTG TCGTCGCACG AGCTCCCAAC ATCATATTCA	5640
TGGCATCAAT GATAATCGAC TTCCCTGCAC CCGTTTCACC AGTCAGGACA GTCATCCCTT	5700
TTTCAAAATT GAGGGAATA GCCTCAATAA TGGCAAAGT TTTTATCGAA ATTTCAAGTA	5760

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ACATATAGAC CTACCAATTT TTTACTTGTT CAAAGATTTC CTCTGCTAGA CTTCCACTTC	5820
TGGCAATGAC TAAATCGAG CTATCATCAG TCAAACAGCT AAAAATCTTG TCTGCAAAAG	5880
TCTCGATTAA CTGAGCTTTT ACAAAGCCG TATTTCCTGG AATAACTTGG AGATTGATCA	5940
TCTTATCCAT CAATTCAGCC GATTGATAT TGTCTTCAGC CAGTTCGAGA CTTTTTACGA	6000
TTGATTTTGG CAATTCGTAG ACATAGGTGT TGTCTCTCAA AGGAATTTTG ACAATACCTA	6060
ACTCTTTGAT ATCTCGGGAT ACCGTCGCCT GAGTGGCAGT GATACCTGCT TCTTTCAAAT	6120
GTTCTACAAT TTCTTCTTGC GTGCCGATTT GATAATCTGT CACCAATCTT CTAATTTTTT	6180
CAAGTCTCTC TTTTTTATTC ATTTTAAAT TGACTATGCG CCCTCTCTAC TGCTTCTTTA	6240
ATCTCAGCAA GAATCTGATT GCTTGCTGAC TTTTCTTTTT TCAAATACGC TAAAAATTCA	6300
ATATTTCCAT GTCCACCTTG GATGGGAGAA AAGTCCAAGC CAAGGACTGA AAAACCTACC	6360
TCTACTGCCA TAGCTGTAC AGATTCAAGG ACATTCTGAT GAACCTTAGC ATCTCGAATA	6420
ATTCCATTTT TCCCAATCTG CTCACGTCCT GCCTCAAACCT GAGGTTTGAC AAGTGTACC	6480
ACCTGACCTT GATCAGCCAA GACACGGTGC AAGGCTGGCA AAATCAGACT AAGGGAATG	6540
AAACTCACAT CAATACTGGC AAAGCTCGGC TCCTGCTCGA AATCAGTCTT TTCAGCATAG	6600
CGGAAATGA ACTGCTCCAT GCTGACAACT CGTGGGTCTT GGCCTAATTT CCAAGCCAAC	6660
TGATTGGTAC CAACATCGAC TGCAAAGACC AACTTGGCAC TATTCTGTAG CATGACATCG	6720
GTAAACCTC CAGTAGAGGC CCCGATATCA ATCGTAGTCG CGCCATCCAC CGACAAATCA	6780
AAGACCTGCA AGGCCTTTTC CAGTTTCAAA CCACCACGGC TGACATACTT GAGTTTCTCC	6840
CCCTTGAGTT TTAATTCGGT GTCATCTGGA ATTTTCTCTC CTGGCTTGTC AAACCGTTCT	6900
CCATTAAGGA CTGCTACGAC TAGGCCAGCC ATCACACCTC GCTTGGCCTG CTCTCTCGTT	6960
TCAAACAACC CCTGTTTATA AGCTAGTACA TCCACTCTTT CCTAGCCAT TGATTCTCAA	7020
ACTTTCTACT AACTTTACAA TCGATTCTGT TTCAAAGGGA AGCTGCTGGG CAATTTCTTC	7080
TAATTTTCA TTAGCTTGAT CCAGGGTTTG GTTACAAAAG GCAATGGACT CTTCCAAGCC	7140
CAACAGGCA GGATAGGTTG ATTTTCTGTC CTGCAGATCC TTTTGAGGTG TCTTGCCGAT	7200
TTCTTCAAAA CTAGCTGTCA CATCCAGTAC ATCATCTCTG ACTTGAAAAG CAAGTCCAAT	7260
CAATTCACCC ACAGTTTCA GCTTCACCTG CATTTCAGGT GACAATTCAG CTATAATAGC	7320
TGCCGCTTGG AAGGGATAGG CTAGTAACTT CCCAGTCTTA TTGGCATGAA TAGTCTGAAG	7380
TTCTTCAAAA GACAAGTGCT GGTGTTGCCC CTCCATATCC AAAACTTGCC CTGCTACCAT	7440
ACCCAGACTA CCTGAAGCAA GGGATAAGTT GGCAATCAAG TCCACCTTAA TCTGACTTGG	7500
CAAATCTGCC TGCCTAATCA AGGCATATGA GTCTAAGAAT AAGGCATCTC CAGCCAAAAT	7560



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GGCCATAGCT TCACCGAATT TCTTGATGATT GGTAAACCGC CCTCTTCGAT AATCGTCATC	7620
ATCCATAGCA GGAAGGTCAT CGTGAATCAA GCTCCCTGTA TGAATCATCT CTAAGGCAGT	7680
AGCTACCTGC GCGTGAGCAG GTTTGATGGT AACCTGCAAG GCTTCCAGAA CTTCTAACAA	7740
GAGAAAAGGC CGAATACGCT TGCCACCAGC ATGAATAGAA TAGAGAACAG ACTCCCCTAA	7800
ACTAGAGGCA AACTGCTGGT CTCCATAAAA ATCTTCCAAA GCCGACTCGA CAAGAGCTAA	7860
TTTTTCTTGC TTTTTCATTC AAAATCACTT TCTGTCCCGT CTTCTTGCAT GACCTTGACC	7920
AAGGTCTTTT CAGCCTTGTC CAGCGTAGCT TGGAGCTCTT TTGACAAGAC CATGCCCTTT	7980
TGAAAGGCAG TAATCGCATC TTCCAGAGCA ATTTCAACCAT TTTCCAAACT TTGGACAATG	8040
GT'TCCAGTT CTGCTAGATT TTCTC'AAT TTCTTTTGTT TTGACATCTT TAACCTCTAA	8100
TTCTACTTGA CCATCTCGCA TCAAAAGCGT TACTTGGTCT TTTTCTTCA AACTCTCAAC	8160
CGAATCTACA ACGGACTCTT CTTTTTGTGAC AATAGCATAA CCACGCGCCA CGATTGCGCT	8220
AGTATCCAAC ATGAGCAAAG CTTCCGAAAG TCGCTTGGCC TCAGCAACCT TGGCGTCATA	8280
AACTAACGCC ATTTGGCTAC CTAAGAGCTT GTCCAACCTGT CCTAAACGGT CTTGATAGCG	8340
TTGGATTTTG GTAACAGGTG ATAATTGTAC TAATTGATGA GTTCTTGCTT GAACTAATTG	8400
TTTGTATATCA GAAATCCGAG TTCCGAAACT TTGTTTCAA CGCAGTTGCA GTTGGTCCAA	8460
GCGTTGCAAA TAACCGTCAT ACAAGCGCTC AGGTTGTCTA AAGATAACAG ACTGACTGCA	8520
TTTTTTTCAA GCCTCTTGT TCTTAGATAG AACATTTGCG ACTGCCGTTA CCATCCGTTT	8580
TTCTGTATTT TGCAAAATGAG CTAATACATC CAACTTGGTC ACAGGTGTTG CCAGTTCAGC	8640
CGCCGCTGTT GCGGTTGCAG CCGGTCGATC TGCCACAAAA TCTGCCAAGG TCACATCCGT	8700
CTCATGCCCC AACTAGAGA TAACTGGCAA ACGAGATTCA AAAATAGCTC GTACCACAAT	8760
TTCTTCGTTA AAGGCCCAGA GATCCTCAAT AGAACCACCT CCACGACCAA TAATGAGCAA	8820
ATCCAAATCG TCCCGTTGAT TAGCACGCGC AATATTTCTA GCAATTTCTT CCGCAGCCCC	8880
TTACCTTGA ACCTTGGTCG GATAAAGAAG GATGTCAACA CCTGGGAATC GCCTGCTGAC	8940
GGTCGTGATA ATATCTCGAA TAACGGCTCC ACTACGGCTG GTTACTACAC CAATTCTCTT	9000
AGAAAATTGG GGCAGAGCTT GCTTGAAGCG TTCTTGAAAC AGGCCTTCTT CTGTCAATTT	9060
TTTCTTAAGT TGTTCAAAC GAATCGAAG CGCCCCAACC CCATCAGGCT CAGCTTTTTT	9120
AATGATGATG GAGTAGCTAC CACTTGGTTC ATAGACCTGT ACACGCCCAA TCACATTGAT	9180
CTTCATTCCT TCTTCCAGGT CAAACCCTAA TTTCTGATAA ATCCCAGACC AGATGGTCCG	9240
TTGAATAACT GCATGGTCAT CCTTTAGGGA GAAATATTGG TGAGTAGGTC GTTTACGAAA	9300

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GTTGGAACT TGACCAGTTA AATAGACCCG TTCCAAGTAT GGGTCTTTAT CGAATTTTCAT	9360
TTTCAGATAC TTGGTCAAAG TTGTTACCGA TAAATACTTT TCCATCTCCA CCTACTATTC	9420
ATTTACTTGC TCTTTCATGG GTATTATTAT ACCAAAAATA TGCCTAAAAA TCTCCATTTA	9480
TGTACCATTA TGAGGGAAAA ATAGAAAAAG GAGGCAAGGC CTCCACATGT GATTATTTGC	9540
TGTTTCGAGC TTCTTCCAAA ATCTTTGCAA TCTTGGTCGT CAACAGGTCG ATAGCCACGG	9600
TATTGCTAAC CCCTTCAGGA ATGACGATAT CAGCATAACG CTTAGTTGAC TCGATAAACT	9660
GGTGTGACAT TGGTTTGACC ACACCTAAGT ACTGGTTAAT AACGCTATCA AGGCTACGGC	9720
CACGCTCCTC CATATCACGC TTGATACGAC GAATAATGCG CACATCGTCA TCCGTATCCA	9780
CAAAATCTT GATATCCATC AAATCGCGCA GACGTTGTC CTCCAAGACC AAAATACCTT	9840
CAACGATAAA GACATCTTGA GGTTCCTGAC GATAGGTCTT GCTACTCCGT GTATGCTCTG	9900
TATAGTCGTA GGTGCGGATG TCCACCGGAC GCCCTGCCAA CAATTCCTTA ATCTGCTCGA	9960
TCATCAAGTC TGTATCAAAG GCAAAAGGAT GGTATAGTT GGTTTTGACG G	10011

(2) INFORMATION FOR SEQ ID NO: 77:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 5365 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 77:

CGTGTGGTCT TAAAAATAGA AGACAAAGAA CAACTGTTG GAGGCTTTGT CCTTGCAGGC	60
TCAGCCCAAG AAAAAACCAA AACAGCTCAA GTTGTGGCTA CTGGACAAGG TGTTGCTACC	120
TTGAACGGTG ACTTGGTTGC TCCAAGTGTT AAAACTGGAG ATCGTGTCTT AGTTGAAGCC	180
CACGCAGGTC TTGATGTCAA AGATGGCGAT GAAAAGTACA TCATCGTAGG CGACTAACAT	240
TTTGGCAATC ATTGAGGAAT AGAAGGAGAA AGTAAGTATG TCAAAAGAAA TTAAATTTTC	300
ATCAGATGCC CGTTCAGCCA TGGTTCGTGG TGTCGATATC CTTGCAGACA CTGTTAAAGT	360
AACCTTGGGA CAAAAGGTC GCAATGTCGT TCTTGAAAAG TCATTCCGTT CACCCTTGAT	420
TACCAATGAC GGTGTGACCA TTGCCAAAGA AATCGAATTG GAAGACCATT TTGAAAATAT	480
GGGTGCTAAG TTAGTATCAG AAGTAGCTTC TAAACCAAT GATATCGCAG GTGACGGAAC	540
TACGACTGCA ACAGTCTTGA CCAAGCTAT CGTCCGTGAA GGAATCAAAA ACGTCACAGC	600
AGGTGCAAAAT CCAATCGGTA TTCGTCGTGG GATTGAAACA GCAGTTGCCG CAGCAGTTGA	660
AGCTTTGAAA AACAACGCCA TCCCTGTTGC CAATAAGAA GCTATCGCTC AAGTTGCAGC	720

629

CGTATCTTCT CGTTCGTGAAA AAGTTGGTGA GTACATCTCT GAAGCAATGG AAAAAAGTTGG	780
CAAAGACGGT GTCATCACCA TCGAAGAGTC ACGTGGTATG GAAACAGAGC TTGAAGTCGT	840
AGAAGGAATG CAGTTTGACC GTGGTTACCT TTCACAGTAC ATGGTGACAG ATAGCGAAAA	900
AATGGTGGCT GACCTTGAAA ATCCGTACAT TTTGATTACA GACAAGAAAA TTTCCAATAT	960
CCAAGAAATC TTGCCACTTT TGGAAAGCAT TCTCCAAAGC AATCGTCCAC TCTTGATTAT	1020
TGCGGATGAT GTGGATGGCG AGGCTCTTCC AACTCTTGTT TTGAACAAGA TTCGTGGAAC	1080
CTTCAACGTA GTAGCAGTCA AGGCACCTGG TTTGGTGAC CGTCGCAAAG CCATGCTTGA	1140
AGATATCGCC ATCTTAACAG GCGGAACAGT TATCACAGAA GACCTTGGTC TTGAGTTGAA	1200
AGATGCGACA ATTGAAGCTC TTGGTCAAGC AGCGAGAGTG ACCGTGGACA AAGATAGCAC	1260
GGTTATTGTA GAAGGTGCGA GAAATCCTGA AGCGATTTCT CACCGTGTG CGGTATCAA	1320
GTCTCAAATC GAAACTACAA CTTCTGAATT TGACCGTGAA AAATGCAAG AACGCTTGGC	1380
CAAATTGTCA GGTGGTGTAG CGGTATTAA GGTGGAGCC GCAACTGAAA CTGAGTTGAA	1440
AGAAATGAAA CTCCGATTG AAGATGCCCT CAACGCTACT CGTGCAGCTG TTGAAGAAGG	1500
TATTGTTGCA GGTGGTGGAA CAGCTCTTGC CAATGTGATT CCAGCTGTTG CTACCTTGG	1560
ATTGACAGGA GATGAAGCAA CAGGACGTAA TATTGTTCTC CGTGCTTTGG AAGAACCCGT	1620
TCGTCAAATT GCTCACATG CAGGATTGTA AGGATCTATC GTTATCGATC GTTTGAAAA	1680
TGCTGAGCTT GGTATAGGAT TTAACGCAGC AACTGGCGAG TGGGTTAACA TGATTGATCA	1740
AGGTATCATT GATCCAGTTA AAGTGAGTCG TTCAGCCCTA CAAAATGCAG CATCTGTAGC	1800
CAGCTTGATT TTGACAACAG AAGCAGTCGT AGCCAATAAA CCAGAACCAG TAGCCCCAGC	1860
TCCAGCAATG GATCCAAGCA TGATGGGCGG GATGATGTAA GCTTTCTATA GAAAACAACT	1920
TATAAAAAAC ACAAAGGAG GGAATGACTA ACCCTTCTTT TTATAGGCTC TTTGTCAACT	1980
GTAGTGGGTT GAAGTCAGCT AAGCTCGAGA AAGGACAAAT TTCGTCTTT CTTTTTGAT	2040
GTTCAAAGCG ATAAAAATCC GTTTTTTGAA GTTTTCAAAG TTTTGAAAA CAAAGGCATT	2100
GCGCTTGATA AGTTTGATGA GATTATTGGT CGCTTCCGGT TTGGCGTTAG AATAGTGTAG	2160
TTGAAGGGCG TTGATAATCT TTTCTTTATC TTTGAGGAAG GTTTTAAAGA CAGTCTGAAA	2220
AATAGGATGA ACTTGCTTAA GATTGTCCTC AATAAGTCCG AAAAATTCTT CCGGTTCTTT	2280
ATTCTGAAAG TGAAACAGCA AGAGTTGATA GAGCTGATAG TGATGTTTCA AGTCTTGTGA	2340
ATAGCTCAAA AGCTTGCTA AAATCTCTTT ATTGGTTAAA TGCATACGAA AAGTAGGACG	2400
ATAAAATCGC TTATCACTCA GTTACGGCT ATCCTGTTGT ATGAGCTTCC AGTAGCGCTT	2460

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GATAGCCTTG TATTCATGGG ATTTTCGATC CAATTGGTTC ATAATTTGAA CACGCACACG	2520
ACTCATAGCA CGGCTAAGAT GTTGTACAAT GTGAAAGCGA TCCAACACGA TTTTAGCATT	2580
CGGGAGTGAA ACAGTCTGGG AGACTGTTC AGCCTGAGCC TAGAAATTTG AAAGCGAAGC	2640
TGTTTAGCCA AGTCATAGTA AGGACTAAAC ATATCCATCG TAATGATTTT CACTTGACAA	2700
CGAACGGCTC TATCGTAGCG AAGAAAGTGA TTTCGGATGA CAGCTTGTGT TCTGCCTTCA	2760
AGAACAGTGA TAATATTAAG ATTATCAAAA TCTTGCACAA TGAAACTCAT CTTTCCCTTA	2820
GTGAAGGCAT ACTCATCCA AGACATAATC TTTGGAAGCC GAGAAAAATC ATGCTCAAAG	2880
TGAAAGTCAT TGAGCTTGGC AATGACAGTT GAAGTTGAAA TGGCCAGCTG ATGGGCAATA	2940
TCAGTCATAG AAATTTTTTC AATTAACCTT TGAGCAATCT TTTGGTTGAT GATACGAGGG	3000
ATTTGGTGAT TTTTCTTTAC CAGGGGAGTC TCAGCAACCA TCATTTTGA ACAGTGATAG	3060
CACTTGAAAC GACGCTTTCT AAGGAGAATT CTAGAAGGCA TACCAGTCGT TTCAAGATAA	3120
GGAATTTTAG AAGGTTTTTG AAAGTCATAT TTCTTCAATT GGTTCGCCA CTCAGGGCAA	3180
GATGGGGCGT CGTAGTCCAG TTTGGCGATG ATTTCCCTGT GTGTATCCTT ATTGATGATG	3240
TCTAAAATCT GGATATTAGG GTCTTTAATA TCGAGCAGTT TTGTGATAAA ATGTAATTGT	3300
TCCATATGAA TCTTTCTAAT GAGTTGTTTT GTCGCTTTTC ATTATAGGTC ATATGGGACT	3360
TTTTTTCTAC AACAAAATAG GCTCCATAAT ATCTATAAGG GATTTACCCA CTACAAATAT	3420
TATAGAGCCG AAAATTCACA TCTAATATAT GCAGACTACT TTGAAATGAA ATTAAAAAAA	3480
TTATTAAAGG ATGACACAAA AGTTTTTGAA AAATCTACAT TCAAATTTGT AGAAGGATAT	3540
AAAATATACC TGACAGAATC TAAAGAATCT GGAATTAAAC AAATGGACAA TGTCATAAAA	3600
TATTTTGAGT TTATTGAATC TAAAAGTATT GCTTTATATT TTCAAAAACG ATTAAATGAG	3660
CTGATAGATT AAATAGCATT TTCTCTGTTG AGATATTGTT TTTAAAAATAT TGTACTAAAT	3720
GATTGATGCT ATGTGGAAAT ACAAAAAAAT GTTTTGTATA CGAAGTTGAC CTGTATTTTT	3780
TATACTAATC ATTTTCGTAT TTTTGTATT AAACGATATA AGTTTGTGT AAACCTTACAA	3840
GGAATAAAGA CATTAAAAAA TAACAGTATA TCTATTGTT TTATATATTT TACGAATTCT	3900
GCATAAATCT CTTTCTAGTA ATGTGTTGTA ACTCTGCTAT AATAGATTTA TTCTTTTTTG	3960
TGTTTACACA ATTTATTTTA TAGTACCAA AAAGGTCAGG ATTTTGTTC TGACCTTTGA	4020
CAACTTTACC GATTCTTTAG TTCTACATAG CGCTTGATC AAATGTTTAC ATAGGCTTCT	4080
GAGAAAGGAC CACGTCCATT GTTAATCCAA TCAACAAGAA TTTTGACATG TTCTTTTAAA	4140
ATATAGTCCA AGTCATCAGA ATAATTCATT TTGCGTTTGT GACGCTCGTA CTCTTCAACG	4200
TCCAAGAGAC GTTTTTCCTC ATCTGTAAAA ATTTTAACAT CCAATCGTA ATCAATATAC	4260

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TTCAGTGCTT CTTCATCCAG ATAGTAGGGG CTAGCCATAT TGCAATAGTA AGAAGTTCCA	4320
TTATCACGAA TCATGGCAAT GATATTAAAC CAATATTTCT TGTGAAAGTA AACAATAGCC	4380
GGTTCTCGAG TGACCCAACG ACGACCATCA CTTTCGGTAA CAAGTGTATG ATCGTTGACA	4440
CCAATAATGG CGTTTTCTGT TGTTTTGTAGT ACCATGGTGT CCCGCCAAGT TCGGTGGAGA	4500
CTCCCATCAT GCTTATAACT TTGAATTGTA ATAAAGTCGC CTTCTTTTGG AAGCTTCATA	4560
ACTAACCAAC TTTCTACAAT TTATAAGTTT ATCATTTACT ATTGTACCAT AAAATTACCC	4620
AAAACTGTG AATTTCACTT GGAAATATTA AAGATATTCT CTAAGAGCGC TTGCTATATC	4680
CGAAAAATCG TAGCCCTTTC GTGCTAAAAC TTGAGTTAAA CGCTGCTTCA GTTCGTATCC	4740
TTCATACTTT CGGGCATACT TAGTATATTG CTTATCAAGT TCCTTGAAGA TGAGTTCCTG	4800
AGTCGTTTCT TCATCAACTT GACTATCCAA TTCGTCAAAG GCAATTTTAG CATCAAAATA	4860
AGAGAAGCCC TTGTTAGTCA AGTTCTGGAT AATCTTATCT TGCAGGGCAC GAGCTGGAAG	4920
TTTTCCCTCA TATTTTTTCA ATAGTTTATT GGCTACACGT TGAGCAACTT CCGAAAAATC	4980
AAAATCATTC AAGATTCTTT CTATAGTAGA TTTTGAAATT CCTTTTGTG CTAATTTCTG	5040
AGTCAGTACA TAAGTCCCT TGTCTCCTGA AAGTTGATTG GCATTGATGA TAGCATAAGC	5100
GTACTGGCTA TCATTAATCC ACTTCTCTTC TTTAAGATTA GCAATGACTT GAGAAACGAT	5160
GTTTTCATTA ATATCATATT TTTTCAGATA TTCTCTGACC TCTTTTTCAG TACGTGCTTT	5220
AAAGGATAAG TGGTAGAGGG CCAGATTCTT ACCATAAGAA AATTGAGCAA AGTCTTGAAT	5280
CTCTTCAAT TCCTCTTCGC TTATCACCTT ATCTCTCGAT AACATAAAAC GAACAATTGT	5340
GTCTTCGGTG ATATAGCATT TGTCG	5365

(2) INFORMATION FOR SEQ ID NO: 78:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 3636 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 78:

TTTCCAGAAA GAAGTTGAGT AAAGTCTTTA TCAAAGAGAA TGACTCCGT ATTGGAAC TG	60
ACATTAGGTT TTATTCTAC TTTACTAGCG TCCGCCCTAG CATTTTCTAA ATCTTTAATC	120
TCTTCTGTTG CCCTATTTAT AGCCAGCTGA ATAACTGCTT GAGGATTTTC ACTCAGTCCA	180
TGAAGCTTAT CGTCCACCGA AGTATAAAGA CTCGAATGCA TGACTTGTA AATAATCAGA	240

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GTCATTGTAG AAAAAATCAG GGTGAAGACA CCGAAGTTGC GGATAAAATA ACTAAAGTCA	300
TCCGCATACC ATGTTTTTTT AAGTTTACTG AACATCTTTT AAAAGATACC CAACACTACG	360
CAAAGTTTGC AAATTTCTCTG CAAAAGTGGT TCCCTTTAAT TTCTTACGGA CTTTGTAAAC	420
ATAGACTTCG ACAACCGAAA TCGTTGTATC ACTATCAAAT CCCCATAGAC GGTCAAAAAT	480
CTGCGTCTTA GGCAAAATCA CATTTTGATT TTGAAGGAAA TAACTAGTA AATCGAACTC	540
TTTCCCCAGC AATTCGACAG GAGTATCTTC AACTTTAACG GTATTGGTTG ATAAATTAAC	600
CACGATATTC CCATAAGTCA AGGTGTTTTC ATTAACTTC CCTGAACGTT TGAGAAGGGC	660
CTGAATCCGC ATTTTAAAGT CTTCTAGGTA GAAAGGTTTG GTCAGATAAT CATCCGCTCC	720
CAGTTCAAAT CCATGTCCTT TGTCATCCAA ACTTTCCTTG GCAGTCATAA TCAGAACTGG	780
TGTCGTAATT CCCTTTTCAC GCAATTCTTT TAAGACTTGG AAACCATTTT TTTCTGGCAA	840
CATCAAATCC AGCAAAATCA AGTCATAGAC ACCACTCTCA GCTTCGTAGA GACCTTCTTC	900
TCCATCAAAT ACCTGCATAA CATCCGCAA ATCGTCTAAA AAGTCAAATA CTGAATTGTA	960
CAGACCTAGG TCATCCTCAA CCAATAAGAT TTTTATCATG AGAACTCCT CTTATTAAA	1020
ACTATTATAC CAAATTTGCC TTAACAAAAA CTCAACTCTC TGCATTTTAC ATGAGATAGC	1080
TGAGTTTCT TTTTATTTTA GGCTTATTTA TGCATTTCCG TATTGAAGAA CAACTGCTTC	1140
GACTGCAGCT TTTTCACGGC TAATCAAGTC AACACGCGCT GCAATTTCCT TGATTCCCAT	1200
ACCGATGTTA CGGCTAAGAG CAAGGTCAGA AAGTTGCGGT TCAAAGAACT CCTTGTATTTC	1260
CGCCAAGCGT TGCTGAGTCT TAAATACATG AGCAGGAAGG ATAACAAAGC TATCAAAGCT	1320
CATATCTCCT CCAAGGGCTG CCTTAATCCA AGCCCAGTTT TCACGCGCCC AAGACCAAGC	1380
TGTTTTCTGA GTTGCTTGAT GAGCTAGGAA TTGGTAATAC CAAGCAGACA AGTCCTGTGG	1440
TTTGACCACA AATTTGTCCT TCCAAGAAGT AATCAGGTTT TGGATATTAT CCGCATCTGT	1500
ACTGTATGCA AGAGCTGCTG CCAACTGGCG TTAAAGACA GCATCTGTTG CGTGAGTATA	1560
AGTATCAAGA TAAAGTGCTA ACAAGTCTTT AGTCTCATGA TGTTCATCT CATTAAATCAG	1620
AACTTGAGAG CGAATAGCTG CTGGGAGTCC TGCAAGATTC TCCTTGTGTG TTGCGAAGAT	1680
TTGGCTAGCG ACTTGACTAG CTTCTGCATC ATTTGAGCGA ATCATCATCG AAACAGCCAG	1740
CTGACGAACC AATTCATCCT CATCTGATTC TCCGTCTTTA GCTTCAAAAC CAAGACGGTC	1800
ATAGTTATGA CGAGCCAATT TAGCAACCG TCCTTTGAAG GCTGTTTCAG CATCCGTTCC	1860
TTTCATCAATA AAGCGCTCAA GGGCTGAAAT CACTTGAGAA ACAGCTGAAA CCACCAGATA	1920
AGACTCTTCC TTAGCAAGTT TATCAAGAAC TGGAAGCAAG TCTGCATAAG AAATGTGCCC	1980
TGCCTCAGCC AACAAACGAC GTTCTTGAAC AATTTGCAGT TTGCTTGTGT TATCAAGTGT	2040

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CTCTAGCTCA GCAAGAACAG CTGCTAACAA GTCTCCTTGA TAGTCGGTAA TATAGTGGGC	2100
AGTATTTTCA GTGTGAGAC GAAGAGCTCC TTCATTTTCA GCAAGAAGAG CTGCGTAGCC	2160
AGGGATTTTCG ATACTTTTTCAG TTTTCGAGTGT ATCAGGCAAG CCTTTCAGT TGCTATTGAG	2220
GGGCACCACC CAGAGACGGT TCTTGCTCTC GTTCTCACCG ATGAAGAATT GTTTTGTGA	2280
AATCTTCAAG ACATCATTTT CAACTTTAAC AGTAAGAACT GGGTAACCAG GCTGTCCAA	2340
CCAAGAATCC ATGAAGGCTG CGACATCACG TCCTGACGCT TGACCAAGGG CATCCCAAAG	2400
GTCACTACCA ATGGTGTGTC TGTATTGGTG TTTTTCAAAG TAGGCGTGCA AACCTTTCAGC	2460
AAAATCAGCA TCTCCTAGCC AACGGCGAAG CATGTGCATG AGACGGCTTC CTTTGGCATA	2520
GACGATAGCG CCGTCAAAGA GTGTATTGAT TTCATCTGGA TGTTTAACTT CGACGTGGAC	2580
AGACTGAACG CCATCAGTAG CGTCACGTTT AAGAGCAAGA GGTACTCCAC CTGTTGGAA	2640
ATCTTCAAAG ATATTCCAGC TTGGTTCGAT GGTATCCACA CAGACGTATT CCATCATATT	2700
AGCGAAACTT TCATGAGCC AAAGGTCATC CCACCATTTT ATAGTCACGA GGTTCCTCAA	2760
CCATTTGGTA GCCAATTCAT GGGCCACAAC AAGGGCAACT TGTTGACGGC TAGCAAATGT	2820
AGAGTTCTCA TCGACAACCA AGTAAACTTC ACGGTAGGTC ACAAGACCCC AGTTTTCCAT	2880
AGCACCAGCT GAGAAGTCAG GAAGGGCGAT GTGGAGAGAT TGAGGAATTG GGTACTTAAC	2940
TCCATAGTAA TCTTCGTAAA ACTCGATAGA GCGAACAGCG ATATCCAGTG AGAAATCAAG	3000
ATTTGAAAGT GGATGTGCTT TGGTTGAGTA GACACCTACC AGGGTACCAT TTTTAGTTTT	3060
AGCGGTCAAC CCTTGCAAAT CACCAGCAAC AAAGGCCAAC AAGTAAGAAG ACATGCGAGG	3120
TGTTGTCTCA AACTTCCAGA TACCTGTTTC CTTACGGTTT TCAACATCGA TTTCTGGCAT	3180
GTTTGACAAG GCCAATTCAC CTTCTGCTTG GTCAAAGCGA AGAGAGAGGT CAAAAGTTGC	3240
TTTGGCTTCA GGCTCATCCA CACATGGGAA AGCTTCGCGC GCAAAATGGC TCTCGAACTG	3300
AGTAGACAAG ACCTCCTTCT TGAATCCATC AACTGTATAA TAAGAAGGGT AAATCCCTGT	3360
CATGTTGTCT GTAATTTTAC CAGAAAAGGC AAGAACCAAT TCAACTTGAC CAGCCTCAGC	3420
CAATTCGATA TGAAGGGCTT CATGTGCATG GTCAACTGTA AATGGACGAG CTTGACCTGC	3480
AACTTCTACA GAGGTGATTT CCAAATCTTT TTGGTGGAGG GAGATGCGGT CACTCTGTGC	3540
TTGACCAGTG ATGGTCACTT TCCAGAAAA AGTCTTGGTC TCACGACTCA AATCTAAAAA	3600
TAAATCATAA TGTTCAAGAA CAAATTGCTT AATGGG	3636

(2) INFORMATION FOR SEQ ID NO: 79:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 5066 base pairs

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(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 79:

ATAGCGTGTA ATAATCGATT TTAGAGGTAC CATAAGCCAC CTCCTACAAA TAGAAACCGA	60
TATAAATCAA TGCCTTCCAC CCTTAGACTT CCCTAGTTCC TGTCTCAAGC GAAACATTTT	120
TTTGAAACAG GAATAAGTTA ACCAATTCAT ACCAATAGCT AGCAGAATAA AAAGAAACCA	180
AATGCCCCAT AACTTGATAT CTGTCACATT TCTCAAGACG GTATTGAAAA ACAGAACTGA	240
AACAACGTGC CAAGCAAGGC TAAAAAGAGA ATAGAAGGGG ATGTAAAACC AGTAAAAATA	300
ATAAAAAAAT GGAAAAAACT TACTATTTCT GTTGGCCTTT TCAATCCAGT TATCAAATA	360
AAAGTACGGT GCTAAAAGTA AGAATTTAAA CAAATGTTCC ATCACCAGCA TCCCCCTTC	420
TTTTGATAGC GTTTTCTATT ATTTTATTAT ATCAAAAAA TCCGGAACGT TCATTCCAGA	480
TTCTACTTTT TTATTGCGT TTCTTGCGA TGAGATGAAT CGGTGTTCCC TCAAAAACAA	540
AGGCCCTGCG GATTTGATTT TCCAAGAAAC GCAGGTAAGA AAAGTGCATG AGTTCTTCTT	600
CATTGACAAA GATGACAAAG GTTGGTGGTT TGGTTGCCAC TTGGGTCGCA TAGAAAATCT	660
TGAGACGTTT TCCTTTGTCT GTCGGTGTG GGTGATGGC AATGGCATCC ATGATGACAT	720
CGTTCAAGAC AGCTGATGGA ATACGTGTAT TTTGACTTTC GCTGATTTGC TTAATCATCT	780
CAGGAAGTTT GTGGAGACGT TGCTTGGTTA AAGCTGATAC AAAGATAATC GGTGCGTAAG	840
GCAGGTATTG GAACTGCTCA CGGATATCTT CTTCCCAGTT TTTCATAGTG TGGTTATCTT	900
TTTCAAGCGT ATCCCCTTG TTGACCACGA TAATCATCCC TTTACCAGCT TCATGGGCAA	960
ATCCTGCGAT ACGCTTGTCT TACTCACGAA TGCCTTCTTC CGCATTGATG ACCATCAAGA	1020
CCACATCTGA ACGGTCAATA GCACGCATGG CACGCATAAC AGAGTATTTC TCAGTATTTT	1080
CATAAACCTT ACCAGACTTA CGCATACCAG CCGTATCAAT CATGGTAAAC TCTTGACCAT	1140
CTGTATCTGT AAAGTGGGTA TCAATGGCAT CACGAGTTGT TCCAGCAACA GGAATAGCAA	1200
TAACACGGTC TTCTCCCAAG ATAGCATTGA TCAAGCTTGA TTTTCCAACG TTAGGACGAC	1260
CAATCAAGCT AAACCTAATG ACATCTGGAT TTTCTTCCTC ATATTCATTT GGAAGATTTT	1320
CTACGATCGC ATCTAGCACA TCCCCTGTAC CGATTCCATG GACAGATGAG ATAGGCAATG	1380
GTTCACCCAA ACCGAGAGCA TAGAAATCAT ATATATCATT TCTCATCTCA GGGTTGTCCA	1440
CCTTGTGAC TCGAGGATA ACTGGTTTGT GGGTCTTATA AAGCTTACGA GCTACGTATT	1500
CGTCTGCATC AGTAATTCCT TCCTTACCAG ACACGACAAA AACGATAACA TCTGCTTCTT	1560



CCATGGCAAT TTCTGCCTGG TGCTTGATTT GTTCCATGAA AGGAGCATCG ACATCATCAA	1620
TTCTCTCTGT ATCAATCATG CTAAGAAGAC GATTGAGCCA CTCACCCGTT GCATAAATAC	1680
GGTCACGTGT CACTCCTTCG ACATCTTCTA CAATGGAGAT TCGCTCACCA GCGATCCGAT	1740
TAAATAGGGT TGATTTCCTA ACATTGGGAC GTCCTACAAT GGCAATAGTT GGTAGGGCCA	1800
TAATTTCTCA CTTTCTACAA TAATTTCTTC TGTTCAAGAT TTTTCTAGT TGAGCTTGGT	1860
TCAGCTTGAC CAAACTGTTT TGCTAGGCGC TGACTCCAGC TTGTGGTCCG ACGCGCCCCA	1920
GCATAGTCAG CCTGAACACG GTCATAAGCT TGGATTGCCT CAGTTGACTG TTCTTGGTAT	1980
TCTTCCTCAA AGACAACATT CTCTAGTGGC AGTCTCGGTT TCATATCATG ATGTTGATTT	2040
GGCACACCCA GTGCCATCCC AAAGACAGAA TAGGTGTAGT CAGGTAGGTT AAAGAGCTCT	2100
GCCACTTCTT CAGACTTGTA TCGAACCAAA CCGATAATCA CACCACCATA GCCCAAGCTT	2160
TCAGCTGCCA ACAAGGCGTT TTGTCCAGCA AGAGCTGCAT CGACCGAACT AATCAAGAGA	2220
CCTCCACAC CTGGGGTTG GAAGGTGTCG GTATGAAGTC GGGCTCCCTT TTCTGCTCGG	2280
TTCAAATCTC CGACAAAGAG AAGGAAAACA GCAGACTGGC GAATGGCTTC TTGAGGTACC	2340
AATTCATACA AGGCATCTTT CTCTCTTGA CTTCGTACCA CAATCACAGA GTAGGATTGG	2400
AAATCTTCC AAGATGATGC CATCTGGGCT GCTGTCAAAA TCTCATTTAA GTCTACTTGG	2460
GGAATTTCTT GCTCTTTAAA CCTGCGCACT GAAGTATGAG CTTTCATCAA TTTAATGGTT	2520
TCTGTATCG ACGGTTTACT CCTTCTAAAC GAGTCTCCTC AGCCAAATAA CGGATGCGTT	2580
CCATGACCCG TCTGGCTTCC CAGGTTTCGT CATTTCCATG TTTCACCTTC GCAAAATGCT	2640
TCTCCAAATC TTCAAAGTTG AAGTTGGATG TGAAAAAGGT CGGTAAATTT TCCTGCATCC	2700
GATATTGGAG AATGACCTGC AGGATTTTGT CACGCACCCA AACGGTTGAT TGCTCGGCGC	2760
CAATATCATC TAAATCAGG ACCTCAGACA GCTTAATCTC ATCCACCAAG GTCTTAACAT	2820
TGCCATCACT GATAGCATTT TTGACATCAA TGACAAAGCT AGGATAGTGG AGGAGAGTTG	2880
ATGAAACACC ACGTTTTTCT GATAAATCAT GAGCTAAGGC CGCCACCATG AAACTTTTAC	2940
CCACACCAAA GTCTCCATAT AAGTAAAGAC CTTTTGGAAT AGCTGGATAT TGCTCCACGA	3000
AGGCTAGTAG CTTTTCAAAA ACTGGAAGC GCCCAAATC ATCCAAGTCA ACTTGAGCCA	3060
AACTAGCTTT CTGAGACTG GCTGGTAGAT TGATTAACTT GAGACGGTTC TTAATAGCCG	3120
CTTCTTTTTC AGCCGCGATT AGCTCAGGAG TTTCTTCATA TGAAACATCT GCATAACCAT	3180
GATTCTTAAC CAAAATCGGC TTGTAGCCTT TGGCAATATA ATCCGTATCC CCACGGAGAA	3240
ACTTGTCACG CTCGGTGATG TACTGATTAA ACTTGAGAT ACTGCGATTT AATTCCTTTG	3300

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GAGTTAAGGA TTCTTGCTGG ATAAAGGCCG CAACATCAGG GTCCTTCATG ATTTTCTGGA	3360
CCAAATCTTG ATAATAAAAA CGGCTGGGTT GACGTTTGAG TACGTCTCCG ACACTTTCCA	3420
TCTAATCTCC TCCTTTTCT AATCGAGCTA ATAGTTCTTG CTTCTTACGT TCTAGTTCCA	3480
GACGAGTTTC CTCGCTGGTT TCATTCCTAT ATTCAAGATT ACTCCATTTA GGAACATTGG	3540
TTTTTTCTGG GGCAGTCTGA TTCTGTTTTT GTGTTTTTGC TTTCTGCCCT CGATCAGGAA	3600
TTCTGAAAAC GGCCTCTTCT GCCGAATGAA TCTTTTGATA GGCATAGTCA TTGGCTACCT	3660
TCATGGCATA TTTCTCATG ATATTTGCCG AATCCACCTT ATTAAAGGTC AATAAGAGAA	3720
TAATATTGAT GACTTCGTCC AGTAAGCCCA AGCCAGCCAT CTGTTGCAAG AGTTCTCTTT	3780
CTGTTTGGGT AATGGTTCCC TTGCGTGTTT GCTTGATTTC TGCTAAGAAC TGCAGGGCAG	3840
TTTACTTTT AGCTTCTTTG ATAATGGTCG CTCCTTAAG ACTAAAGTCA GAGGAACTG	3900
GTTTTTGAGC AATTTTTTCA CGCATGCGTT TGTTTGAAAT AACCTGGGAA ACAGCTGTTG	3960
ACTTGCCAA TTGATAGGTT TCAAACCAAG TCCATTCTTT CTCCTCGGCA ATAGCAAAGA	4020
GGTTTAAGAC ATCGGACTGC TCATCCGCAA AACGAAGTCC ATCTCGAGCC ATCAGCTGGC	4080
GAAAATGTTT CAAGTCAAAA TCATTGGCCA CTTTCTTCTT GAGACCAAG TCTTCTTGAC	4140
TGCCTAGTTC TGCCAATCTT GGAAAGACTT GATTGAGTGA GACAGGTATT TCTTACCAT	4200
CAGCACTTTC AACTTTCAAA TCCTCCACAG CTACATCGCC AATCTTTTTC TCTAAGAGTC	4260
TGCGATAAAC AGGATGCCCC AAGAAGTCTT GACTAGATAG AGGAGCATGG AGGGCTAGCT	4320
GATAAACATC ACCCTTTTGA TAGAGGGTCA AGAGATTAAA AGCAGATAAG ATTTTCAATG	4380
ATTTTATCAG TCTATCCATC CCAAAGTTGA GATGGTTGAG AATGCTTGAA AAAAGATATT	4440
CCTTTCTACC ATTATCCCAA AAAGTATTG TATAAAGATA AAGGCTCAGT GCCTCCTGAC	4500
CGATAATCGG GAGGTAGCAC TGTACCAGAG ATGAGGTATC TTGCGACACC CGATTATTCT	4560
TTAGATAAGA AAAACGGTCA ATTGGCTTCA TTTATCTTTC CTTTTTCTTT TTAGAGGACT	4620
GGGTGATTTC TTGGAGCAAG CTCTCTAACT CACTGACATC CTTAAACTA CGATAGACAC	4680
TAGCAAAACG TACATAGGTA ATCTCGTCCA ATTCAAGCAA CTCCTCCATG ACGAGTGAAC	4740
CAATGTCTTC ACTTTGAATT TCATTTTCAT TTCGACCACG GAGTTTCTGT TCGATACGAT	4800
TGACTACCAT GTTGATTTC TCACTTGACA CAGGACGTTT CTGGGCTGAG CGGATAATCC	4860
CATTAAAGAT TTTATCTCTG GAGAATTGTT CCCGTGTGCC ATCTTTTTTA ACAACCACTA	4920
AGGTTCTTTC TTCTACTCGT TCGTAGGTTG TAAAACGGTG TTGGCATTGC TCGCACTCAC	4980
GTCTTCTACG AATGGTGTTC CCTTCTCTG CTGGCGACT ATCGATAACA CTTGACTTGG	5040
TAGCCCCACA TTTTGACAG GGTACC	5066

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## (2) INFORMATION FOR SEQ ID NO: 80:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 9607 base pairs.
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 80:

CACTTGAAGT ATTTGAAACA GCTATGGAAA ACATCATGCC TGTACTTGAA GTACGTGCAC	60
GTCGTGTTGG TGGTCTAAC TACCAAGTCC CAGTTGAAGT TCGTCCAGAA CGTCGTACAA	120
CACTTGGACT TCGTTGGTTG GTAACAATCG CTCGTCTTCG TGGTGAACAC ACAATGCAAG	180
ACCGTCTTGC AAAAGAAATC TTGGATGCTG CTAACAACAC TGGTGCAGCA GTTAAGAAAC	240
GTGAAGATAC TCACCGTATG GCTGAAGCTA ACCCTGCATT CGCACACTTC CGTTGGTAAG	300
ATAGGATGCG AAAGCGTTAA GAAAGTCCCA GAGAAAATAG GGAATCGAAG CAGGTTGCCG	360
TTGCAACCAA TGAGATTTCAT CTTTTCTCC AGACTTTTAG CTTGAGCTCA ACTAAATCAT	420
GATGCTAGGA ACGGTAAGGA TGCAAGGTAA AAATAGGAAA CTGACGCAGT ATTCGACGAA	480
TACAAGGAGT TTTATCTTTT TCACGCAGCA TCCCGTTCCA GCTCACATCG GCTAACTAAC	540
TTTAGCCCGG GTTCAAATTA GCTAAATCGA TTAGTATTAG CTATAACTCA GCTTACCATC	600
TCGTAAGTTG AAACCAACAA TAGCATGAAA ACATTGAGAA CGGTTAGGTC CTGCCTATCC	660
GTTTTTATTA AAATCGTGTT ATAATAGAAT AGAAATCAAA AATAAATAGG AGAAACAAAC	720
CTCATGGCAC GCGAATTTTC ACTTGAAAAA ACTCGTAATA TCGGTATCAT GGCTCACGTC	780
GATGCCGGTA AAACAACAAC TACTGAGCGT ATTCTTTACT ACACTGGTAA AATCCACAAA	840
ATCGGTGAAA CTCACGAAGG TCGGTCACAA ATGGACTGGA TGGAGCAAGA GCAAGAACGT	900
GGTATCACGA TCACATCTGC TGCACGACA GCTCAATGGA ACAACCACCG CGTAAACATC	960
ATCGACACAC CAGGACACGT GGACTTCACA ATCGAAGTAC AACGTTCTCT TCGTGTATTG	1020
GATGGTGCGG TTACCGTTCT TGAATCACA TCAGGTGTTG AGCCTCAAAC TGAAACAGTT	1080
TGGCGTCAAG CAACTGAGTA CGGAGTTCCA CGTATCGTAT TTGCCAACAA AATGGACAAA	1140
ATCGGTGCTG ACTTCCTTTA CTCTGTAAGC AACTTCACG ATCGTCTTCA AGCAAATGCA	1200
CACCCAATCC AATTGCCAAT CGGTTCTGAA GATGACTTCC GTGGTATCAT TGAATTGATC	1260
AAGATGAAAG CTGAAATCTA TACTAACGAC CTTGGTACGG ATATCCTTGA AGAAGACATC	1320
CCAGTGAAT ACCTTGACCA AGCTCAAGAA TACCGTGAAG AATTGATTGA AGCAGTTGCT	1380

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GAAACTGACG AAGAATTGAT GATGAAATAC CTCGAAGGTG AAGAAATCAC TAACGAAGAA	1440
TTGAAAGCTG GTATCCGTAA AGCGACTATC AACGTTGAAT TCTTCCCAGT ATTGTGTGGT	1500
TCAGCCTTCA AAAACAAAGG TGTTC AATTG ATGCTTGATG CGGTTATCGA CTACCTTCCA	1560
AGCCCACTTG ACATCCCAGC AATCAAAGGT ATTAACCCAG ATACAGACGC TGAAGAAATT	1620
CGTCCAGCAT CTGACGAAGA GCCATTTGCA GCTCTTGCCT TCAAGATCAT GACTGACCCA	1680
TTCGTAGGTC GTTTGACATT CTTCCGTGTT TACTCAGGTG TTCTTCAATC AGGTTTCATC	1740
GTATTGAATA CTTCTAAAGG TAAACGTGAA CGTATCGGAC GTATCCTTCA AATGCACGCT	1800
AACAGCCGTC AAGAAATCGA CACTGTTTAC TCAGGTGATA TCGCTGCTGC CGTTGGTTTG	1860
AAAGATACTA CAACTGGTGA CTCATTGACA GATGAAAAAG CTAAATCAT CCTTGAGTCA	1920
ATCAACGTTT CAGAACCAGT TATCCAATTG ATGGTTGAGC CAAAATCTAA AGCTGACCAA	1980
GACAAGATGG GTATCGCCCT TCAAAAATTG GCTGAAGAAG ATCCAACATT CCGCGTTGAA	2040
ACAAACGTTG AAATGGTGA AACAGTTATC TCAGGTATGG GTGAACCTCA CCTTGACGTC	2100
CTTGTGTGATC GTATGCGTCG TGAGTTCAAA GTTGAAGCGA ACGTAGGTGC TCCTCAAGTA	2160
TCTTACCGTG AAACATTCGG CGCTTCTACT CAAGCACGTG GATTCTTCAA ACGTCAGTCT	2220
GGTGGTAAAG GTCAATTCGG TGATGTATGG ATTGAATTTA CTCCAAACGA AGAAGGTAAA	2280
GGATTCGAAT TCGAAAACGC AATCGTCGGT GGTGTGGTTC CTCGTGAATT TATCCCAGCG	2340
GTGAAAAAG GTTTGGTAGA ATCTATGGCT AACGGTGTTT TTGCAGGTTA CCCAATGGTT	2400
GACGTTAAAG CTAAGCTTTA TGATGGTTCA TATCACCAGT TCGACTCATC TGAAGTGGC	2460
TTCAAGATTG CGGCTTCACT TTCCCTTAAA GAAGCTGCTA AATCAGCACA ACCAGCTATC	2520
CTTGAACCAA TGATGCTTGT AACAATCACT GTTCCAGAAG AAAACCTTGG TGATGTTATG	2580
GGTCACGTAA CTGCTCGTCG TGGACGTGTA GATGGTATGG AAGCACACGG TAACAGCCAA	2640
ATCGTTCGTG CTTACGTTCC ACTTGCTGAA ATGTTGCGTT ACGCAACAGT TCTTCGTTCT	2700
GCATCTCAAG GACGTGGTAC ATTCAATGATG GTATTTGACC ACTACGAAGA TGTACCTAAG	2760
TCAGTACAAG AAGAAATTAT TAAGAAAAAT AAAGGTGAAG ACTAATCCGT CCTCACTCTA	2820
GAAGGAAGTC ACTTAGTGGC TTCCTTTTGT CTTTAAAAA TACCTCTAAA TATGGTAAAA	2880
TAGTAGAAGA ATAATGTGAG GAAAATGAAT GTCAAATAGT TTTGAAATTT TGATGAATCA	2940
ATTGGGGATG CCTGCTGAAA TGAGACAGGC TCCTGCTTTA GCACAGGCCA ATATTGAGCG	3000
AGTTGTGGTT CATAAAATTA GTAAGGTATG GGAGTTTCAT TTCGTATTTT CTAATATTTT	3060
ACCGATTGAA ATCTTTT TAG AATTAAAGAA AGGTTTGAGC GAAGAATTTT CTAAGACAGG	3120
CAATAAAGCT GTTTTGTAAA TTAAGGCTCG GTCTCAAGAA TTTTCAAATC AGCTCTTGCA	3180

GTCTACTAT AGGGAGGCTT TCTCTGAAGG TCCATGTGCT AGTCAAGGTT TTAAGTCCCT 3240  
TTATCAAAAT TTGCAAGTTC GTGCTGAGGG TAATCAGCTA TTTATTGAAG GATCTGAAGC 3300  
GATTGATAAG GAACATTTTA AGAAGAATCA TCTTCCTAAT TTAGCCAAAC AACTTGAAAA 3360  
GTTTGGTTTT CCAACTTTTA ACTGTCAAGT CGAGAAGAAT GATGTCTCTGA CCCAAGAGCA 3420  
GGAAGAGGCC TTTCATGCTG AAAATGAGCA GATTGTTCAG GCTGCCAATG AGGAAGCGCT 3480  
CCGTGCTATG GAACAACTGG AGCAGATGGC ACCTCCTCCA GCGGAAGAGA AACCAGCCTT 3540  
TGATTTTCAA GCGAAAAAAG CTGCAGCTAA ACCCAAGCTG GATAAGGCGG AGATTACTCC 3600  
TATGATCGAA GTGACGACAG AGGAAAAATCG TCTGGTATTT GAAGGGGTG TTTTGTATGT 3660  
GGAGCAAAA GTGACTAGAA CAGGTCGTGT TTTAATCAAC TTTAAATGA CGGACTATAC 3720  
TTCAAGTTTT TCTATGCAA AGTGGGTAA AAACGAGGAA GAGGCCAGA AGTTTGACCT 3780  
CATCAAGAAG AATTCTTGGC TCCGAGTTCG AGGGAATGTG GAGATGAATA ACTTCACACG 3840  
CGATTTGACT ATGAACGTAC AGGATCTGCA GGAAGTTGTT CACTATGAGC GGAAGGATTT 3900  
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TGCTTTGCCA GAGGTCGAAG AGATTGTTGC AACAGCTGCT AAGTGGGGAC ACAAGGCGGT 4020  
TGCTATCAG GACCATGGGA ATGTCCAGTC CTTCCACAT GGCTATAAGG CGGCTAAGAA 4080  
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CGTCTATAAC GAAGTGGAGA TGGACTTGTC AGAAGCAACC TACGTGGTCT TTGACGTGGA 4200  
AACGACGGGA CTTTCAGCTA TCTATAATGA CTTGATTGAG GTTGCGGCTT CTAAGATGTA 4260  
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CTTTACTACA GAGTTAACTG GAATTACAGA TGATCATGTC AAAAATGCCA AACCCTAGTA 4380  
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TCAGCCAGTT ATTGATACGC TGGAGTTTGC TAGAAACCTC TATCCTGAGT ATAAACGCCA 4560  
TGGTTTGGGG CCTTTGACCA AGCGTTTTGG TGTGGCCTTG GAACATCACC ACATGGCCAA 4620  
CTACGATGCG GAAGCGACTG GTCGTCTGCT TTTCATCTTT ATCAAAGAGG TAGCAGAAAA 4680  
ACATGGTGTG ACCGATTAG CTAGACTCAA CATTGATCTA ATCAGTCCAG ATTCTTACAA 4740  
AAAAGCTCGG ATCAAGCATG CGACCATCTA TGTCAAGAAT CAGGTAGGTC TAAAAATAT 4800  
CTTTAAGCTG GTTTCCTTGT CTAATACCAA GTATTTTGAA GGAGTGCCAC GGATTCCGAG 4860  
AACGTTCTA GATGCCCATC GAGAGGGCTT GATTTTAGGT TCAGCCTGTT CAGAGGGTGA 4920

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AGTTTTTGAC GTGGTCGTTT CTCAAGGTGT GGATGCGGCG GTTGAGGTGG CCAAGTATTA	4980
TGATTTTATC GAGGTCATGC CACCGGCTAT CTATGCACCC TTGATTGCCA AAGAGCAGGT	5040
CAAGGATATG GAGGAATCC AGACCATTAT CAAGAGTTTG ATAGAGGTTG GAGACCGCCT	5100
TGGCAAGCCT GTTCTGGCTA CGGGAAATGT TCACTATATC GAACCGGAAG AAGAGATTTA	5160
TCGTGAAATT ATCGTCCGTA GTTTGGGACA GGGTGCATG ATTAATCGAA CTATCGGTCA	5220
TGGTGAACAT GCCCAACCAG CACCACTTCC AAAGGCTCAT TTTCGAACGA CTAATGAGAT	5280
GTGGATGAA TTTGCCTTTT TGGGAGAGGA ACTGGCTCGT AAAGTGGTTA TTGAAAACAC	5340
CAATGCCTTG GCAGAAATAT TTGAATCCGT TGAAGTCGT AAGGGTGACT TGTATACGCC	5400
TTTCATCGAC AAGGCTGAAG AAACAGTTGC TGAGTTGACC TATAAGAAAG CTTTGTAGAT	5460
TTATGGAAAT CCGCTGCCAG ATATTGTGA TTTGCGGATT GAAAAAGAA TAACATCCAT	5520
ACTGGGGAAT GGATTTGCTG TGATTTATCT GGCATCGCAG ATGCTGGTGC AACGTTCTAA	5580
TGAACGGGGT TATTTGGTTG GTTCTCGTGG GTCTGTCGGA TCTAGTTTCG TTGCGACCAT	5640
GATGGGATT ACGGAGGTCA ATCCTCTCTC TCCTCACTAT GTCTGTGGTC AGTGTCACTA	5700
CAGTGAGTTT ATCACAGATG GTTCGTACGG TTCAGGATTT GATATGCCCC ATAAGGACTG	5760
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TAGCGCCAC TTGGATGTGC GTGATATCTT TGGTGAAGAA TATGCCTTCC GTGCGGGAAC	5940
GGTTGGTACG GTAGCTGCCA AGACTGCCTA TGGATTTGTC AAAGGTTACG AGCGAGATTA	6000
TGGCAAGTTT TATCGTGATG CAGAAGTAGA ACGCCTCGCT CAAGGAGCGG CGGGTGTCAA	6060
GCGGACAACA GGCCAACACC CGGGGGGAAT CGTTGTATT CCGAACTACA TGGATGTCTA	6120
CGATTTTACG CCTGTCCAGT ATCCAGCAGA TGATGTCACG GCTGAATGGC AGACCACTCA	6180
CTTTAACTTC CACGATATCG ATGAGAACGT CCTCAAACCT GATGTACTGG GACATGATGA	6240
TCCGACTATG ATTCGAAAAC TTCAGGATTT GTCTGGTATT GACCCTAATA AAATTCCTAT	6300
GGATGACGAA GCGGTGATGG CACTCTTTTC TGGGACTGAT GTGCTAGGGG TAACACCTGA	6360
ACAAATGGA ACGCCTACGG GTATGTTGGG GATTCCAGAG TTTGGAACAA ATTTCTGACG	6420
TGGAATGGTA GACGAAACCC ATCCGACAAC CTTTGCAGAA TTGCTTCAGC TGTCTGGTCT	6480
GTCCACGGT ACTGATGTTT GGTGCGGAA TGCTCAGGAT CTGATTAAGC AAGGAATAGC	6540
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TCTGGAACCT AAGATGGCCT TTACCATTAT GGAACGGGTA CGTAAGGGTT TGTGGCTAAA	6660
GATTTAGAA GAGGAGAGAA ATGGCTATAT CGAAGCAATG AAGGCTAATA AGGTGCCAGA	6720

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GTGGTATATC GAATCCTGTG GGAAAAATTAA GTACATGTTT CCTAAGGCC ATGCGGCAGC	6780
CTACGTTATG ATGGCCTTGC GTGTAGCTTA CTTCAAGGTT CACCATCCTA TTTATTACTA	6840
CTGTGCTTAC TTCTCCATTC GTGCTAAGGC TTTTGATATC AAGACCATGG GTGCGGGCTT	6900
GGAGGTCATC AAGCGCAGAA TGAAGAAAT CTCTGAAAA CGGAAGAACA ATGAAGCCTC	6960
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ACTGGTGCGG GCGCGTGAAG AGGGAGAATT CCTCTCTAAA ACAGAACTAC GCAAGCGTGG	7200
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CTATGGAAAG AGGGTGAGAG TATGTCAAAG ATGAGTATAA GCATCCGCTT GGATAGTGAG	7440
GTTAAGGAGC AGGCCCAACA GGTGTTTAGT AATCTGGGAA TGGATATGAC AACAGCTATT	7500
AATATTTTCC TTCGTCAGGC AATTCATAT CAGGGATTAC CTTTGTGATG TAGACTAGAC	7560
GAAAATCGGA AGTTGCTCCA AGCGTTAACG GATTTAGACC AAAATCGTAA TATGAGCCAG	7620
TCTTTTGAAT CAGTCTCAGA TTTGATGGAG GACTTACGTG CTTAAGATTC GTTATCATAA	7680
ACAGTTTAAA AAAGATTTTA AGTTGGCTAT GAAGCGTGGT TTGAAGGCAG AATTATTAGA	7740
AGAAGTTTGG AATTTTCTGG TTCAAGAAAA AGAACATCCT GCCAGAAATC GTGATCATTC	7800
ATTGACGGCA TCCAAGCATT TTCAAGGAGT TCGTGAATGC CATACCCAGC CAGATTGGCT	7860
TTTGGTTTAT AAAGTAGACA AGTCGGAATT GATTTTAAAT TTGCTGAGGA CAGGCAGTCA	7920
CAGTGATTTA TTTTAATCTA TTTTAAGGGG GTTCTCATGA AACTAAGAAT ATTTGCGGAA	7980
GATAAGCCCG CTAAGAAGGT ATTTGAATAT CAATTAGAAC TTGCTGATCG TACAATTCTT	8040
CTATCGACAG CACTCTTGTC AGGTGCTATT GCTTTAGCAG GAATCTTTTC TGCTTTGAAA	8100
GAAAAATAAA AATAGAAAAG AGAAAACAGA ATGGTTTTAC CAAATTTTAA AGAAAATCTA	8160
GAAAAATATG CGAAATTGTT GGTGCGAAC GGAATTAACG TGCAACCTCG TCACACTTTG	8220
GCTCTCTCTA TTGATGTGGA GCAACGTGAA TTGGCACATC TAATCGTGAA AGAAGCTTAT	8280
GCCTTGGGTG CGCATGAGGT CATCGTTCAG TGGACAGATG ATGTGATTAA CCGTGAGAAA	8340
TTCTCTCATG CCCCATGGA GCGTTTGAC AATGTGCCAG AATACAAGAT TGCTGAGATG	8400
AACATCTCTT TGGAGAATAA GGCTAGCCGT CTTGGAGTTC GTTCATCTGA TCCAGGTGCC	8460

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TTGAACGGAG TGGACGCTGA CAAGCTTTCA GCTTCTGCTA AAGCTATGGG ACTTGCCATG	8520
AAGCCTATGC GTATCGCAAC TCAATCTAAC AAGGTTAGCT GGACTGTAGC AGCTGCAGCA	8580
GGACTTGAGT GGGCTAAGAA AGTCTTCCCA AATGCTGCGA GCGACGAAGA AGCAGTTGAT	8640
TTCTTTTGGG ACCAAATTTT CAAAACCTGC CGTGTCTACG AAGCAGATCC TGTTAAGGCT	8700
TGGGAGGAAC ATGCAGCCAT TCTCAAGAGC AAGGCCGATA TGCTTAATAA GGAGCAATTT	8760
TCAGCCCTTC ACTACACAGC GCCAGGAACA GATTTAACAC TTGGTTTGCC AAAGAACCAC	8820
GTTTGGGAAT CAGCTGGTGC TGTCAATGCA CAGGGCGAAG AATCTTGCC AAATATGCCA	8880
ACAGAAGAGG TCTTCACAGC GCCTGACTTC CGTCGTGCAG ATGGTTATGT CACTTCTACA	8940
AAACCGCTTA GCTACAACGG AAATATCATT GAAGGCATTA AGGTGACCTT TAAGGATGGA	9000
CAAATCGTAG ATATCACTGC TGAGAAGGGT GATCAGGTTA TGAAAGACCT TGTCTTTGAA	9060
AATGCGGGTG CGCGTGCCTT GGGTGAATGT GCCTTGGTAC CAGATCCAAG TCCAATTTCT	9120
CAGTCAGGCA TTACCTTCTT TAACACCCTT TTCGATGAAA ATGCGTCAAA CCACTTGGCT	9180
ATCGGTGCAG CCTATGCGAC TAGCGTTGTT GATGGAGCGG AGATGAGCGA AGAGGAGCTT	9240
GAAGCTGCAG GGCTTAACCG TTCAGATGTT CACGTAGACT TTATGATTGG TTCTAACCAA	9300
ATGGATATCG ATGGTATTCG TGAGGATGGA ACGCGGGTAC CTCCTTTCCG TAATGGGAAT	9360
TGGGCAAATT AAGGAGATA TATGTTAGGA AGTATGTTTCG TTGGTCTCCT AGTGGGATTT	9420
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GGTGGATCG GAGCCTTTCT AGGTCACCTG CTCCTTGGA CTTGGGGGCC AGTTTATCA	9540
GGAACAGCTA TTATCCCAGC GATTTTAGGA GCCATGATTG TTTTAGCTAT TTTTGGAGA	9600
CGAGGAA	9607

## (2) INFORMATION FOR SEQ ID NO: 81:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 14231 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 81:

CTACAAGATA ATTCCAGCTA TAACATCCGC TATAATAGTA AGACCGAGCT CTATGATAAG	60
GCTCATTAGT TTCACCTCCT CTCACGAACC CATAGGAACG TAATCGGTAA CCGATGACAA	120
AAATAGTATA CCACAATACA TTTAGATCAT CAAGGTCAC TAAATCTTGA AATATCAGAT	180
CTAAGAGAAA AATCTTTAAA ATCAGAAAAA CGCATAATAT CAGGTGTGCA AAACTTGAT	240



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ACTATGCGTT TTATTGTGGG AAGGTTTACT CCATTTTCTC CTGAAATTGA GTTTTGTGCC	300
AGCCTCTGTT TTTAGGGTTG CTAAGAAAAT AATGTCATGT GGTGAATATT TGTAAATCAG	360
TCAGCAGACA GAACGATACT CTTCGAAAAT CTCTTCACAT CATGTCAGCT TCGTCTTTCC	420
GTATATATGT GACTGACTTC ATCAGTTCTA TCTACAACCT CAAAACAGTG TTTCGAGCTG	480
ACTTGATCAA TTTTCAAATC TGTACTTTGA GCAAGCTGAG ACTAGCTTCC TATTTGATTT	540
TCATTGAATA TCAGAAACCC ATTCTCCATC AAATAATTCG ACTGCGTCTA ATAATTTTTG	600
ATCTGGCAGG GTGTCTGAAA TAAAGGTTGT GTATTGAGAG AGGGGATTAA TTTTAAAAA	660
TCCAGTCTTG TAAATTTAG AACTATCAAT CAGTAAGATG GTTTCATGGG CTTTGTCAAT	720
AATATCTCTT TTTGAAATAG CTGGGTGAG AGAAGCTTCA TAAACATATT GGTCAATCAAT	780
ACCTCTTGCT GAACAAAATG CTAAATCGAT ATTAATAATGA TCTAATAAAG AATTTTCCTT	840
ATCATAGTTG ACCACGGAAC AGGATTGATG TTTGACCTCG CCAGATGTGA TAAAGATTTT	900
GGAGCTATCT TTAACAGTTT CAGATAGGGT TGTGTCAGTA TGTAAACCAT TTGTAAAAAT	960
AATCAAATTA TCAAGTTCAG AAAGATAGGG ACAGAGTTCG TAGACAGTAG TACTAGAATC	1020
TAGATAGATA CACATACCAG ACCGAATAAA GTCTTTAGCG AGACTAGCGA TTAGTCTTTT	1080
TTGCCTAGTA CTTTCTCCTT CACGTATTTG ATGAGAAAGT TCAATTGTGT TCATAGAGGA	1140
CAGGGTCACG TATCCGTGCT TTCTTTTGAT AAGACCTTGA TTTTCTAAGA AAATTAAATC	1200
ACGAGCTAAG GTACTTGTGC TGGAGAAAGT GATTTCTGCC AGCTCTTTTA CGGCAATTCT	1260
TTTTTCTTTT TTGATAATTT CAATCAATTC AAGTACACGT TCATCTTTTA TCATAAGCTC	1320
CTCCTAATTT ATCATTTCAA CTATATTATA GCACAAATG GAGGAATTTG AATTATTTT	1380
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AAACGTGGGG ATTATAATAA AGTTAATCma GGACGAAGAG AGAAGAAAAA TGGAAAGCGGT	1500
TTTAGCAATA GATTTAGGTG CGACTTCTGG AAGAGCAATC GTTGGTTACC TTTCTGAAAA	1560
TAACTAGTA ATGGAAGAAA TAAATCGCTT TTCTAATCTA CCTATTAGAG TAAAAGGGCA	1620
TTTATCTTGG GATATTGACT TTCTACTAGC TAAAATTCTT GAAAGTATCC GCTTGGCTAA	1680
TACTAGTTAC AAGATTTTAT CTATCGGTAT TGACACATGG GGAGTTGATT TTGGACTGAT	1740
TGATAATGAA GGTAAGCTGT TATTACAACC TGTTCATTAT CGTGATGAAA GAACAAAGGG	1800
AGTGTTAAAG GAAATATCTG AAATGACTGA ATTAGAAAAA CTGTATTGAG AGACAGGAAA	1860
TCAGATTATG GAGATAAATA CCTTGTTTCA ACTCTTTAAG GCACGTCAAG AATCTCCTGA	1920
CTCTTCTAT AAGACCAATA AGATTCTTTT AATGCCAGAT TTGTTTAATT ATCTCTTGAC	1980

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AGGTAAGTTT GCTACAGAAA AAAGCATTGC TTCAACAACT CAATTATTTG ATCCTAGGAG	2040
TCAAAATTGG AATCAGAATA TCTTAAAACT ATTTGAATTG GATTCATCTT TACTTCCTGA	2100
AATTGTTTCA GAGGGAAATG TTCTTGGAAG GATAAAAGAG GAGTATGGTT TAGGCGATAT	2160
TCCTGTTGTG AATGTTTGTA GTCATGATAC AGCAAGCGCG ATTGTCTCAG TACCTAAGAC	2220
AGAAGGTAGT TTATTTATTT CATCAGGTAC TTGGTCTTTG GTTGGAGTGG AACTTACTTC	2280
ACCGATTCTT ACTACCGAAT CCTTCAGTTA TGGATTTACA AATGAAGTCG GTAAAGATGG	2340
AGTGATTACA TTTCTGAAGA ATTGTACAGG GTTGTGGATC ATAGAGGAAC TAAGACGTTT	2400
ATTTGAACGA AGAGGGAAAG CCTATTCTTT TGATGATATT AGGACAATGG TGGAGAAAGA	2460
AAAAGAAAAT CTTCTCTGA TTGATCTGA ATCAACTGAA TTTGCAACAG AATCTGATAT	2520
GCACAAGACT TTGACAGAAT ATCTAGCTTA TCATCATGAA ACTAGAGAGT GGACAGATGG	2580
ACAACTATTT AAGATTGTTT ATGAAAGCCT AGCTGAAACG TATAGGAAAG CGATAGAGTT	2640
ACTAGAAGAA CTAACCTATA AGGTTTATAA GAGGATATAT GTGATTGGAG GAGGTGCTAG	2700
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GACTGAGGCT ACAGCTGTGG GGAATATTGT TGTGCAGCTC ATAGCTATGG GACAATTAAA	2820
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TGTGCAGGAA GGGGGGATAA TTGGTGAATT GAAAAATATT TAGTGTTTTG ATATGAGGAG	3000
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AGATTTGACG AAAGGAACAG GTGGGAATCT CAGCGTTTTC GATCGTGAAA AACAATTGAT	3120
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GGCAGGGAAA GATGTTCCGG TAGCTGAGTA TGCAACATAT GGCACGAAAG AATTGGCTGT	3420
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AAAAATTTAT TGTTTAGCTA AGAATTTTGG AGAGCCAGTA GTTCTTCCTG ATGAGGAGAT	3600
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TTAAACATA TACCGAAAAA TATTTCTCCA GATTTATTGA AGACTTTAAT GGAAATGGGA	3720
CATGGAGATG AAATAGTATT AGCTGACGCG AATTATCCTT CTGCCTCATG TGCAATAAAG	3780

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CTAATTCGTT GTGATGGTGT AAATATTCCA GAATTATTAG ATTCCATTCT GTATTTAATG	3840
CCATTAGATA GTTACGTCGA TAGTTCAATT CAGTTTATGA ACGTTGTTTC GGGTGATGAT	3900
ATTCCTAAGA TATGGGTAC CTATAGACAG ATGATTGAAG GTCATGGTAC AGATCTTAAA	3960
ACGATTACTT ATCTTAGAAG AGAAGACTTT TATGAACGTA GTAAGAAAGC TTATGCTATT	4020
GTTGCTACAG GAGAAACTTC ACTTTATGCT AATATTATCC TTAAGAAAGG AGTAGTTGTT	4080
GAAAGAGAAA ATGTTCAATA GAGGAATTTT AGTTGCCAGT CATGGTAATT TTGCTAGCGG	4140
AGCTCTCATG ACCGCAGAAA TGTTTGTGG TGAGACAACA AATGATAGAG TTAGGACATT	4200
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TAATAATGTG GCTTGTAC GGTTTTAAA TTTGGATTCA GTTGATATTG TAACAGGGTT	4380
TAATATCCCT CTCCTAGTGG AATTAATATC AAGTTATGAT TCAAAAATCA ATTTAGAAGA	4440
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ATCTCAGAAG ATAAAACACG ACAATCTATT TTAAAGATTT CTGCACCGGT AGGTTTAAAA	4680
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AAATGAGGT ACCTCAATGT AGGACAGATG AGTAAAACGG AGGAAATGA AAAGGTAACG	4860
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ACGAGAGTTG AAATCAAAT GGTTCCTAAT GATAAAGTTA CAATGTTGGA AAAATTTTTA	4980
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GTTGGGATTA TTGCCACTAT TGAATAAT GGACCGTTAT TTATGATTCA CCGTCCGTTA	5100
GTTACAAGTG CAATGGTTGG CTTAGTATTA GGAGATTTC ACAAAGGTGT TCTTATTGGT	5160
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ACTATTTTCA GTGCGATTAT TGGTACTGCA TTTGGTATTT TATCTGGTCA AGGAGAAACT	5280
GCTGGTATCG CTATAGCAGT TCCAATTGCA GTTGCTACCC AACAGTTGGA TGTCTTTGCA	5340
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TCAAAGATCG GTTTTTATCA TTATTCAAGT TTGGTTTAA TCACGTTATT TAAAATTGTA	5460
CCAATTTTCC TAGCTATTAT GCTTGGAGGG GAATATGTGG CAGACTTGTG TGCTAAGGTT	5520

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CCACCAATCG TTATGCAGGG ACTTAACTCT GCAGGTGCTT TACTACCTTC AATGGGTTTT	5580
GGTATGCTTT TAAATATGAT GCTCAAGAAA AATATGTGGG TATTCTTGTT GATTGGATTC	5640
ATTTGTTCTG TGTATGGAGG AATGTCAACC ATTGGGATCT CACTAGTTGG TATTGCGGTA	5700
GCATACTTCT ACGATATGAT TGGGAAGCAA CCACAAGAAA CAACCTCAAG TAGTGATGTT	5760
GAGGAGGATC TTGATCTATG ATGAATAATA AAGTAACTAA AGTTGAACCT AAAAAAGTTT	5820
TCAAACGAAG TTTTATGTAT GGTCTTTCAT GGAACCTATGA GAGAATGCAG AACCTAGGTT	5880
TTCTATATAC AATTCTTCCA GTATTGAAAA AACTATACCC AGACAAAGAT TCAGCTTCTC	5940
CTGCAATGAA ACGTCACCTT GAGTTTTTCA ATACTCATCA AACAGCGGCA CCATTTATTC	6000
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CACTAGTTCC TATCTGTTTT AGTATTGGTG CGTCTTATTC TAAAGACGGC GGTGCTTTAG	6180
GTATCTTTAT CGCCTTAATA TTGTTTAATA TTATTAATAT TCCTGTTAAA TATTTGCGTT	6240
TGAAATATGG GTATACTAAG GGTCTAGTC TTATCCAAGA AAATAATACA AAAGGAACAT	6300
TGAATCGCGT TACGAGTATG GCGACAGCAT TAGGGCTAGT ACTAGTGGGT GGTGTGATTC	6360
CATCAATGGT TGGTATTAAT TTTGGATTAG AATTTAAGCA GGGGGAACCT GTTATTTCTG	6420
TTCAAGAAAT GATTACAAAA TTAATTCCAG GATTATCCC TATGGCTTTG ACTTTATTAA	6480
TGTGTAATTT AATTAGAAAA GGAAAGAATC CGGTTGTACT AATCTTTAGT GTTATGGCTA	6540
TTGGAGTTAT TCTAGTTGTT TTAGGAATTT TGAAGTAGTA GAAAGTGTGG AGGTGCTATT	6600
TGGGATATCA CCTCCATTTT GGAAGAGAGG TAAAGAGTGA AATTATGGTA TAAGAAAGCT	6660
GCCGCAAATT GGAATGAAGC CTTGCCGATT GGAACCGTC ATTTAGGTGG TATGATTTAT	6720
GGTTCAGCTA CAAAAGAATG TATTCAACTA AACGATGAGA CTATTTGGTA TAGAGGAAAG	6780
TCAGATAGAA ATAATCCAGA CTCACTATTG CATCTTAAAA AAATTCGGGA ATATCTTTTA	6840
GATGGAGAAA TTCAGAAAGC CGAAGAATTG ATAAAGTTAA CAGTGTTTGC TACCCCAAGA	6900
GATCAAAGCC ACTATGAATT ACTTGGGGAA CTTTACATTG AGCATATAGA TATTCAGTCT	6960
TGTGCTCTTT CATTGTATGA AAGAGAGCTA GATTTAGATA CAGCTATTTT TAATGTTGTG	7020
TTTGAGCCTA ATAGTTGTAA TTTACAAATA AAAAGAGAAT ATTTTACGAG TTTTAATAAG	7080
AATATTTTAT GTTGCCGTAT AGTGTCATCA GTTCAAAACA CATTAAATTT AACATTAAAT	7140
TTGGGTAGAA ATAAACGGTT TAATGACGAA GTATCTAAAC TGGATTCAAG TACAATTTTA	7200
ATGTCGGCCT CTGCTGGAGG TAGAAAAGGT GTTCAGTTTA AAGTAGTATG TCATTCTAAG	7260
GTACCGGATG GTGAAGTAAG TGTATTGGGA GAGACAATAG TTATTCGGAA TGCTACAGAG	7320

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GTATTTCTTT ATCTCAAATC AATGACGGAT TATTGGGGAA ATATAGATAT TTCTTCTCTT	7380
CAGGGAGAAT TTAGTAGTAT TGATTACTTT ACAGAAAAAG ATGAACATGT AAAAAAATAT	7440
CAGGAGCAAT TTAATAGAGT TGATTTTAAA CTAGACTATA GTAAAGGTTG TCTTAGCATT	7500
CCAACGAATC TACTTCTTGA AAACACTAAA AAGTATAGTA ACTACTTGAC TAACTTGTTA	7560
TTTCATTATG GAAGATATCT GTTAATATCG TCTAGTCAAC CGAATGGTTT ACCTGCCAAT	7620
CTTCAAGGAA TATGGTGTGA TGAATTAAAT CCAATTTGGG GTTCTAAATA TACGATTAAT	7680
ATTAATACTC AAATGAATTA TTGGATGGTA GGTCCATGTG ATTTACCAGA AGTAGAATAT	7740
CCATTATTTG ATATGCTCGA AAGAATGAGA GAACCGGAA GACTAACCGC TAAGAAAATG	7800
TATGGAGCTA GAGGTTTTAC AGCACATCAT AATACGGATG GTTTTGGCGA TACGGCTCCC	7860
CAATCTCATG CCATGGGGGC TGCAATTTGG GTATTAACTA TTCCATGGTT ATGTACTCAT	7920
ATTTGGGAAC ACTATTTATA TTTCCAAGAT GAGCGTATTC TTACGGAACA TTTTGAAATG	7980
ATAAAGAAG CATTTCTTTT CTTTGAAGAT TATTTATTTG AGGTGGATGG CTAATTGATG	8040
ACAGGTCCAA GTGTCTCACC GGAAAAATAA TATCGCTTAA AAAATGGTAT TGAAGGAAAT	8100
GCTTGTCTAT CATCTACAAT TGATAATCAA ATTCTAAGAT ATTTTGTGTA TTCATGCATT	8160
GGCATTGCAA AACAATTAGG AGACAATTCG GATTTTATTA GTCGTGTGAA GGAGTTAAAA	8220
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TATGAAGAAG TAGAGCCTGG GCATAGACAC ATTTACCTC TATTTGGGCT TTATCCTTAT	8340
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CATTTTTTTG CGAGACTATA TCAAGGTGAA CCTGCTTATA ACCAGATTAA TGGTTTGTTA	8580
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GGAGGATATA AGGTATCGTT TGCTTGGAAT AATGGGGATA TAACATTCCT AAAATTGGAA	8820
GGAGGAAACA AAGATCAAAA AGTAAGAGTA AGAATATATG GCAAAAATAC TGATGTACAA	8880
AATATTGAAT TGGTATTTAA TTCAGAAAAA ATTATTGAGT TAAATTTTTA GGTATAAGTC	8940
ATGAATAAAG AAAAAATAA AAGAAAATTA ATCACAATAT TGTTTGTATG TATTGGGATG	9000
TTATGTTTTG GATTGTTAGC AGGAGTTAAG GCTGATAATC GTGTTCAAAT GAGAACCACG	9060

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ATTAATAATG AATCGCCATT GTTGCTTTCT CCGTTGTATG GCAATGATAA TGGTAACGGA	9120
TTATGGTGGG GGAACACATT GAAGGGAGCA TGGGAAGCTA TTCCTGAAGA TGTAAGCCA	9180
TATGCAGCGA TTGAACCTCA TCCTGCAAAA GTCTGTA AACCAAGTTG TATTCACGA	9240
GATACGAAAG AATTGAGAGA ATGGTATGTC AAGATGTTGG AGGAAGCTCA AAGTCTAAAC	9300
ATCCAGTTT TCTTGTTAT TATGTCGGCT GGAGAGCGTA ATACAGTTCC TCCAGAGTGG	9360
TTAGATGAAC AATTCCAAAA GTATAGTGTG TAAAAGGTG TTTTAAATAT TGAGAAATTAT	9420
TGGATTTACA ATAACCAGTT AGCTCCGCAT AGTGCTAAAT ATTTGGAAGT TTGTGCCAAA	9480
TATGGAGCGC ATTTTATCTG GCATGATCAT GAAAAATGGT TCTGGGAAAC TATTATGAAT	9540
GATCCGACAT TCTTTGAAGC GAGTCAAAAA TATCATAAAA ATTTGGTGTG GGCAACTAAA	9600
AATACGCCAA TAAGAGATGA TCGGGGTACA GATTCTATCG TTAGTGGATT TTGGTTGAGT	9660
GGCTTATGTG ATAAGTGGG CTCATCAACA GATACATGGA AATGGTGGGA AAAACATTAT	9720
ACAAACACAT TTGAACTGG AAGAGCTAGG GATATGAGAT CCTATGCATC GGAACCAGAA	9780
TCAATGATTG CTATGGAAT GATGAATGTA TATACTGGG GAGGCACAGT TTATAATTTTC	9840
GAATGTGCCG CGTATACATT TATGACAAAT GATGTACCAA CTCCAGCATT TACTAAAGGT	9900
ATTATTCCTT TCTTTAGACA TGCTATACAA AATCCAGCTC CAAGTAAGGA AGAAGTTGTA	9960
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TATCAAGGAC TTTATTGAA TGATGAAACA ATGCCTTTAT ATAATAATGG GAGATATCAT	10080
ATTCTTCCTG TAATACATGA GAAATTTGAT AAGGAAAAGA TTTCATCTAT ATTCCCTAAT	10140
GCAAAAATTT TGAATAAAAA TAGTGAGGAA TTGTCTAGTA AAGTCAACTA TTTAACTCG	10200
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ATTTATAATA GTAATGCTAA TATCAATAAA AATCAGCAAG TAATGTTGCC TATGTATACT	10320
AATAATACAA AGTCGTATC GTTAGATTTG ACGCCACATA CTTACGCTGT TGTAAAGAA	10380
AATCCAAATA ATTTACATAT TTTATTGAAT AATTACAGGA CAGATAAGAC AGCTATGTGG	10440
GCATTATCAG GAAATTTTGA TGCATCAAAA AGTTGGAAGA AAGAAGAATT AGAGTTAGCG	10500
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CATTATACTT ATACAGAAAA TTGGGATGAG AATACCCATG TTTATACCAT TACGGTTAAT	10680
CATAATGGAA TGGTAGAGAT GTCTATAAAT ACTGAGGGGA CAGGTCCAGT CTCCTTCCCA	10740
ACACCAGATA AATTTAATGA TGGTAATTTG AATATAGCAT ATGCAAAACC AACACACAA	10800
AGTTCGTAG ATTACAATGG AGACCCTAAT AGAGCTGTGG ATGGTAACAG AAATGGTAAT	10860

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TTTAACTCTG GTTCGGTAAC ACACACTAGG GCAGATAATC CCTCTTGGTG GGAAGTCGAT	10920
TTGAAAAAAA TGGATAAAGT TGGGCTTGTT AAAATTTATA ATCGCACAGA TGCTGAGACT	10980
CAACGTCTAT CTAATTTTGA TGTGATTCTA TATGACAATA ATAGAAACGA AGTTGCTAAG	11040
AAACATGTTA ATAATTTGTC GGGTGAATCT GTTAGTCTAG ATTTCAAAGA AAAAGGAGCA	11100
AGGTATATTA AAGTTAAATT ACTAACGAGT GGAGTGCCTT TGAGTTTAGC AGAAGTAGAG	11160
GT'TTTTAGAG AATCAGATGG TAAGCAATCT GAAGAGGATA TAGATAAAAT AACAGAAGAT	11220
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GAAAAGTTAA TTATTTATAA TAGAACAGAT GCTGAAATTC AGAGATTATC AAATTTTGAT	11880
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AAAATCAAT GTTTGCGCAA CAATTACAGT TACACCATGC TGGTGTATG GTAGTGAAAC	12420
TATGGATATG TCTCCAGATA TTCCTCATGC TATTTGGGGA TTTAATGGGA CAGAACGCCC	12480
AGGAGCTGTC TATCTTGCGAG CTGTACTAGC TTCACATGCT CAAAAGGGA TTCCAGCCTT	12540
TGGGATTTAT GGAAGAGATG TTCAGGAAGC TAGTGACACA GATATTCCAG AAGATGTCAA	12600

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AGAAAACTT TTACGCTATG CGCGTGCAGC TCTTGCAACT GGCTTGATGA GAGACACTGC	12660
TTACCTATCA ATGGGTAGTG TTTCGATGGG GATTGGTGGT TCTATTGTAA ATCCGGATTT	12720
CTTCCAAGAA TACTTAGGAA TCGGAAATGA ATCGGTAGAT ATGACGGAGT TCACGCGCCC	12780
TATGGACCGT GGTATTTACG ACCCTGAAGA GTTCGAACGT GCGCTCAAAT GGGTGAAAGA	12840
AAACGTAAAA GAAGGATTCG ACCATAACCG TGAAGACCTT GTTTTAAGCC GTGAAGAAAA	12900
AGATAGACAA TGGGAATTTG TTATTAAGAT GTTCATGATT GGACGTGACT TAATGGTTGG	12960
TAACCCAAGA CTTGCTGAAC TTGGTTTGA GGAAGAAGCG GTTGGTCACC ATGCTTTAGT	13020
AGCTGGTTTC CAAGGTCAAC GTCAGTGGAC AGACCATTTT CCAAATGGGG ACTTTATGGA	13080
AACTTTCCTC AATACTCAGT TTGACTGGAA TGGTATTCGA AAACCATTG TATTTGCGAC	13140
AGAGAATGAT TCACTAAATG GTGTGTCTAT GCTCTTAAAT TATCTATTAA CAAATACTCC	13200
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ACATACTTTA GAGGGTCGTG CTGCAGCTGG CTTCTTACAT CTAATCAACT CTGGTTCTTG	13320
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AGTAACAATG GTACGTCTCA ATCTTCTAAA AGGGGTGGT CCAGTGCTAC AAATTGCAGA	13560
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AGGATGGCCA ACTACTTGGT TTGCTCCACG TTGACAGGA AAAGGTGCTT TCAAGTCTGT	13680
CTATGACGTC ATGAATAATT GGGGAGCTAA TCACGAGGCC ATAACATATG GACACATTGG	13740
AGCAGACTTG ATTACCTTGG CTTCTATGTT GAGAATTCCT GTCAATATGC ATAATGTACC	13800
TGAGGAAGAT ATCTTTAGAC CTAAAAATTG GTCCTTATTT GGAACAGAAG ATCTAGAATC	13860
AGCAGACTAT CGTGCATGTC AGTTGTTGGG GCCACTACAT AAATAAACT TGTTTATATA	13920
GGAGGTGAAC TTACGTCCTT CCTATCCTTT TAAAAAGATT TGTAAACAA TTCACAAATA	13980
ATTGAAAACG AATACAAAA GTAATATAAT GATGTTAAAT AGATAGCGCG GAGGCGCAGG	14040
AGGAAAATTA TATGGCTATA TTTTATGTTT CCGCAGTCAA CCTATTGGA AAAGGTGTTG	14100
TAAATGAAGT GGGTCCTTAT ATCAAGGAAC TTGGCTATAA AAAGGCACTT TTGGTGACAG	14160
ATAAGTACAT CGAAGGCAGT GATATTTTAC CTAAGACTTT AAAACCACTG GATACAGAAG	14220
GAATCGAATA T	14231

(2) INFORMATION FOR SEQ ID NO: 82:

(i) SEQUENCE CHARACTERISTICS:



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(A) LENGTH: 16995 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(x1) SEQUENCE DESCRIPTION: SEQ ID NO: 82:

AGTTCTCTTA	ACTTTTTTAG	GATGGCATT	TCCGCTCTCA	GGTACTCATT	TTCTGCTgAA	60
GACGTTCTAA	TTCTGTCTC	TCTTCAGGTC	TCGTTTTTGG	CTTACGTCCC	ATTTTAGGTA	120
CTCTCCCTCT	TGTTTTCTCA	ACAATAGTAT	ACCCGTTTTT	CCTGTATTGT	GCTAGCCAGT	180
TAAGAAGTAT	CGTACGACTT	GGGAGACCGT	ATTCAAGAGA	AACCTCTATCT	TTAGTCCAGC	240
CTTCATGTCA	GACTTTATTA	CTCATTTCTT	GTTTTAAATC	AGGAGAATAG	TAACGATTTT	300
TTCTTTTTTT	GACGAACCT	ATTCGTAAC	GATCAATCAA	TTTAATCATG	TACCTAATAT	360
TAGAATTGCT	TATCCCAAT	TTATTTGAAA	GCTTCTCTAA	GCTATATCCT	TGTTTTCTAA	420
GTTCATAGAT	CTGAACTTTA	TCATCATAAG	TTAGTTTCAT	AATAAAACA	CCCCAAAAGT	480
TAGATTTTTT	CTGTCTAACT	TTTGGGGTGT	AGTTCATGTA	CACCTGATAT	GATGCGTTTT	540
ATAATTTTAA	AGCCTTTTTG	CCCAGCCTCG	TCAAAAGTAA	TGTTTTGACA	CAAAATCTGT	600
GACAAAACCT	TAGTTTTAAA	GGTTTTTAAC	TTGTATATA	CTAGTTTAA	GAAAAGGAGG	660
ATGATCTAAT	GGAAGAAAAA	GTATCATGTA	AAGTCAGGGT	TCAAAACTA	GGGACATCGC	720
TTTCAAATAT	GGTTATGCCC	AATATTGGAG	CATTTATGTC	TTGGGGAGTA	TTGACTGCCC	780
TCTTTATCGC	TGATGGCTAT	CTGCCAATG	AACAGTTAGC	TACTGTTGTT	GGTCCTATGT	840
TAACGTATTT	ATTGCCAATC	CTGATTGGTT	ACACAGGTGG	ATATATGATC	CATGGCCAAC	900
GTGGTGCCGT	TGTAGGAGCT	ATTGCTACTG	TTGGTGCAAT	CACAGGTTCT	AGTGTTCCTA	960
TGTTTATCGG	AGCTATGGTA	ATGGGCCAC	TGGGAGGATG	GAATATCAAG	AAATTTGATG	1020
AGAAATTCCA	GGAAAAAATT	CGTCCCGGAT	TTGAAATGTT	AGTTAATAAC	TTCTCAGCTG	1080
GTCTCGTTGG	TTTTGCATTA	TTGCTTTTGG	CTTTCTACGC	AATCGGTCCA	GTCGTATCGA	1140
CTCTTACTGG	AGCTGTTGGG	AATGGTGTG	AGGCTATTGT	CAATGCTCGC	CTCCTTCCTA	1200
TGGCTAATAT	TATCATCGAA	CCGGCTAAAG	TCCTTTTCCT	CAATAATGCC	CTCAATCATG	1260
GCATTTTTAC	TCCTCTGGGA	GTAAGACAGG	TAGCTCAAGC	TGTAAGTCA	ATTCTCTTCC	1320
TATTGGAAGC	TAATCCTGGA	CCAGGTCTGG	GAATCTATT	AGCTTATGCT	GTATTCGGTA	1380
AAGGTCTGTC	TAAATCTTCT	TCTTGGGGGG	CAATGGTTAT	TCATTTCTTC	GGAGGGATTG	1440
ATGAAATTTA	CTTTCCTTAT	GTTATGATGA	AGCCTACTCT	ATTTTTAGCT	GCTATGGCAG	1500

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GAGGTATCTC TGGAACTTTT ACTTTTCAAC TCTTAGACGC-TGGTCTTAAA TCTCCAGCTT	1560
CACCAGGTTT TATTATTGCG ATTATAGCTA CGGCGCCAAA AGGTGTTTGG CCCCATCTAA	1620
ATGTTCTTTT AGGTGTTTTA GTGGCAGCAG TTGTTTCTTT CCTTGTAGCA GCCCTTATTC	1680
TTCATGCAGA CAAGTCAACT GAGGATTCGC TCGAAGCTGC TCAGGCGGCT ACCCAAGCAG	1740
CTAAGGCTCA GTCTAAAGGT CAGTTAGTAT CAACTTCTGT TGATGCAGTT GTTTCGACAG	1800
ACTCAGTGGA AAAATCATT TTCGCCTGCG ATGCTGGTAT GGAAGCTCT GCTATGGGAG	1860
CTAGTATTCT TCGAGATAAG GTTAAAAAAG CAGGTCTAGA GATTCCAGTA TCTAATCAGG	1920
CAATCTCAAA TTTGCTTGAT ACACCAAAAA CATTAAATGT TACTCAGGAA GAACTGACAC	1980
CAAGAGCTAA AGACAAGAGT CCAAGTGCTA TTCATGTTTC TGTTGATAAT TTCTTAGCGT	2040
CCTCTCGTTA TGATGAAATT GTAGCTTCAT TAACAGGAGC TTCTCCAATA GCAGAAATTG	2100
AAGGAGATAT ACCAACTTCA GCACCAGTAG ATAGTCAGGA AAGTGACCTT AACCATATTG	2160
ATGCTGTAGT AGTTGCTTAT GGTAAAGCAC AGGGAAGTGC AACTATGGGC TGTGAAACGA	2220
TTCGGGCTAT TTPTAGAAAC AAGAATATTC GTATTCCAGT TTCTACTGCC AAAATTTCAG	2280
AATTAGGTGA ATTTAATCTT AAAACATAA TGATTGTAAC AACTATTTCT TTACAGGCAG	2340
AAGTGCAGCA AGCAGACCG AATTCTCAAT TTCTTATTGT GGATAGTTTA GTAACAACAC	2400
CAGAATATGA CAAAATGGCT GCTAGAATGT ACAAATAGAA CTAGAGGTTT CTAAATTACG	2460
AATGCTATTA ACCAAACGAG AAGAACAATT ATTGAAGGCT TTCCTACATG TAGGGAAGCT	2520
TTCAATGCAA GATATGACTG AAATCTTACA GGTTCATCT AGAACAATTT ATCGAACTTT	2580
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CTATATTTTG ACTGGAGAGT TGGATGATTT GCCGACAGAA CTTGAAGTGT TAGTTGAGTA	2700
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TCGGATTTCT GGTGATTGAG TTGGTAAGAG AAGATTTTGT GCTATTTTAC TGACAACTG	2940
TATCTCAGTA GCAGATTTTT CAACCGGTAA TTTTGGGAGC TTTGATATTT TAGAAGCAGA	3000
TAGAACTGGG CTGGCCAGTC AGATTGTTAA TAAGCAACTG TCAGGTTTTC CAGATATGGA	3060
TGCTAGGATG AAGATGTTTT TTGCGATCTT GTTATCTCTT ATAGTCCAGG AGCAAAACAT	3120
TGAAAATTC AATAATACTA GTAAGCAGGC TTTGGAAATT TCTCAAAAAA TTTTCAAGC	3180
TTACTCTAAG CAGACTGCAC AATTTTATAG TATTCAGGAA ATTATCTATT TTGCGAGCAT	3240
CTTGGATGAA TTAATCATT AACGTCAGGA CAATCCGCTC TTTACGGAGA AATTGATGG	3300

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TGAATTTTTC TACAATATTT CAAATCTGAT TGATACGGTT TCCATGTATA CCAAGATTGA	3360
CTTTTTTAAG GACAAGGTTT TATTCATTT TCTTTTCCAT CATATTCGGC TCAGTTTAGG	3420
CGTCCCTATC CTTTTTCAGG GTGAAAATTT GCCAGAATCT ATCCAGATTT TAGTTGAAAG	3480
GAATAAATTT CTTTATACAG TCATCAGTCT TTTAGTGAAT GATATTTTTC CGAAATATCT	3540
TCATACAGAG TATGAGTATG GCATGATTGC CCTACATTTT ATCTCTAGCT TAGGCCGTAG	3600
TCCAGAGATT TATCCAGTCC GTGTTTTGCT TTTAACGGAT GAACGTCGGG TCACTAGAGA	3660
TTTATTAGTC AGTAAAATTA AGAGTGTTGC TCCTTTTGTA GAGTTGATAG ATATTCAATC	3720
TCTAGTAGAT TACCACAGTA TTGATCTCAG TCAGTATGAT TATATTTTAT CTACCAAGCC	3780
GCTGACTAAT CAGGAAATCG ATGTAATTTT TAGTTTTCCA ACCGTCAAAG AATTGCTTGA	3840
ATTACAGGAA CGACTTCAGT ATGTACAGGC ACATCGTACA ATTGTCGCGC GTGATGCTAT	3900
CGCTCCAGAG AAAAGTTATG ACTTGCAAGA TTATTTAATA TCTAGTAGTC AGCTTTTGAG	3960
TCAATTCGAG TTGGTTCAAT TGGAGAATAA TCAATCATTT GAGCACACGG TAGAACAAAT	4020
CATCCAATAT CAGAAGAATG TGAGTGACAG AGCTTACCTA ACAAGAAAAT TGTATCTCA	4080
CTTCCAGAAAT AGTCCTATGG CTATTCCTAA TACTGGTCTG GTGCTTTTAC ATAGTCAGTC	4140
TAGCAAAGTA ACAACAAATA GTTTTACTAT GTTTGAACTC AAACCTACCTA TCTCCGCATT	4200
GTCAATGAAA CGAGAGGAAG AAGAGGTCAA AAGGTGCTCG CTAATGCTAA TGTCTAAAGA	4260
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TCITTATACA GAGATTTACA AGACGGGAAA TCAATCCATT ATTTATCAGA TGCTAAATAC	4380
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AGCTATCTGT TTACATGGGT AACTTTATCG CCATACCGCA TGAACAGAT GCAGCAAAAA	4620
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ACTTAGAAAT TATTCAGAAA ATTTCTATCT TCTGTGCAGA TGATAGATAAT GTTCTTAAAC	4800
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AAACATTCTG TTCATTTTGG TGCCGGTAAT ATCGGTCGTG GTTTTATAGG TGAAATTCTA	4980
TTTAAAAATG GTTTCATAT TGATTTTGTG GATGTCAATA ATCAGATAAT TCATGCTCTG	5040

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AATGAAAAGG GCAAGTATGA AATTGAAATT GCACAGAAAG GACAGTCTCG TATAGAAGTA	5100
ACTAATGTGG CTGGCATTAA TAGCAAAGAA CATCCTGAGC AAGTCATTGA AGCGATTCAA	5160
AAGACGGATA TTATTACTAC TGCAATCGGA CCTAATATAC TCCCTTTTAT CGCCGAACCT	5220
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AGGATTGTTT CAGCACAAAG TCACGAAGAT TCCCTTTTTG TTGTGGTCGA GCCCTTTAAT	5460
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TATGAAGAAG ATTTAGAACC CTTTATTGAG CGAAAACTTT TTTCAGTCAA TTCTGGACAT	5580
GCAACTTCAG CTTACATTGG TGCGCATTAT GGTGCCAAGA CAATTTTGA AGCTCTTCAA	5640
AATCCTAATA TTAATCTCG GATTGAATCT GTATTAGCTG AAATTCGGAG TCTCTTGATT	5700
GCCAAATGGA ACTTTGATAA AAAAGAATTG GAGAATTATC ACAAAGTCAT TATAGAACGA	5760
CTTGAAACC CTTTCATAGT GGACGAGGTT AGTCGCGTAG CTCGTACTCC AATCCGAAAA	5820
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TATAAAACC TACTTAAAC AGTTGGCTAT GTCTTTGACT ATCGCGATGT AAATGATGAA	5940
GAAAGTATTC GATTAGGTGA ATTGTTGGCT AAACAATCAG TCAAAGATGT TGTATACAA	6000
GTTACAGGTT TAGACGACCA AGAATTGATT GAGCAAATG TAGAGTATAT TTAATCTTTT	6060
TCGAAAATCT CTTCAAATCA GGTAGCATC GCTTTGTCTT AGGCATATGT TGTCTATCT	6120
ACAACCTCAA AGCAGTGCTT TGAGCTGACT CCGTCAGTCT TATCTGCAAT CTCAAACAC	6180
TGTTTGAGTT ATCTGCGGTA ATCTTTCTAG CTGTCTTTG ATTTTGTGTTG TTATTTATAA	6240
GGTAAAAGAA GCTGGACAAA AAGTCTTCAA AATCGGGAAA AGGCAGCCTA TCGGGTGTTC	6300
AAAAATCTTG ATAGGATGTC CTTTATTATG GAAAGCCTTA TTGGATTTTC TCCTCAGATT	6360
GAGTTTTTGA TCAGCTTTAT GAGATAGGTC TTGCTAGAGA TGTAGCCCAT CATGTTATTT	6420
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GAGAAGAACG AACCAAGCAA TTTTGAACG AATTCTTTTCG AATGCGATCT ATATAGTAAA	6540
ATGAAACAAG AACAGGACAA ATCGATCAGG ACAGTCAAAT CGATTTCTAA AAATGTTTTA	6600
GAAGTAGAGG TGTAATATTC TAGTTTCAAT CTACTATATA ACTGAAAAAT TAGATAAATT	6660
AGTTTTTGAA AATGACTAAC CAAAAGATAT CCAAAGTAGT CTAAAATTGT CTATACTTTA	6720
TGAGTGTTTT AGTTAGGAAA AAGGCTTGTT GTCTATAATT GTCTGCATTA GTCTAGATTT	6780
TATTTATAGA AAATGTTATA ATAGACTGTA TTTAAAAAAT TTTAAGGAGA AATGACAGAA	6840

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AAGACCAAAT CAAACCAGAA TTGGACCGTG TCTTCAAGTC AGTGAAGAAA TCTCTTAATG	6960
TTCCAGGTTT CCGTAAAGGT CACCTTCCAC GCCCTATCTT CGACCAAAAA TTGGTGAAG	7020
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AAGAAGCTGG TCTTGAAGTG GTTGCCCAAC CAAAAATTGA CGTAACTTCA ATGGAAAAAG	7140
GTCAAGACTG GGTATCACT GCTGAAGTCG TTACAAAACC TGAAGTAAAA TTGGGTGACT	7200
ACAAAAACCT TGAAGTATCA GTTGATGTAG AAAAGAAGT AACTGACGCT GATGTCGAAG	7260
AGCGTATCGA ACGCGAACGC AACCACTGG CTGAATTGGT TATCAAGGAA GCTGCTGCTG	7320
AAAACGGCGA CACTGTTGTG ATCGACTTCG TTGGTTCCTAT CGACGGTGTT GAATTTGACG	7380
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CATCAATCCC TGCCGTCCCT CGGTACATAG GAGCCAGAAC TTGGATATCA CGGGCGGGAA	8880
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CCTCAATTAC ATCAGCCATG GTTCCTGTGA CAATGATTTC AAAATCATCA AAATCCTCTG	10440
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GTCAGGTGTG ACAAAGGCAG CCACAACCTGC AAGCCCACCA AAGTAGGAAC CATTTCCCAC	12060
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AAAGAACTG GCGTATTTTT CAGCCCCTTC ACCCTGAAGC AAGATTTTTC CAGAAGTATA	12180
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AGCCAGACTG GTTTGATAGT GTTCAAGAAA AGCCTGAATA TCCTTTTCGC TTGGTGTGAG	12300
TGTGATACTT GCCATAGTTT CTATTGTACC ACAAAGCAG TAAAATTGT AAAAAGTAC	12360
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TCAAATTTAC ATTCGGGAAA AAATCGTTAA CCTTGACAAG CGAACATGAC AACCTTTTAA	12480
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GCCGTGAGAT TGAATTTGAC GATAAGGAGC AAGAGCTAGA AGAACTCCGT CACAAGCTTG	12660
TGACTGTGTA GCAAGAACAG AGCAAGATTG AGGATTCCTT ATGATTTTAT TCCTTCTTCT	12720
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GCCGTCAGGT TTTACCACTC AAAAACACCT ACCGCAATAA GATTGCAGGT GTCGTTTCATG	13980
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CCGTCGCAAA TGATGTCTAT TTTGGTCAAG ATTTAACAGC TATTGTCATT ACAGGTCCCA	14340
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TGAAACGAAC TTCTGGGCGA GGACCTCAAG CTAGACTGGA TCTTCGAGGC AAGCGCTATG	15480
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AAGTTGATAT CATCCATGGT ATCGGAACAG GAGTCATCCG TGAAGGAGTT ACCAAATACT	15600
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GTGCGACTAT TGTCACTTTT AAAGGATAGC AGTATTCTGG ACTTTATAAA GTAAAACTG	15720
TTGAACTAAT TTTTACTAAT AAACACATTG ACAAAGCCA ACATTTTTTG TAAAATTAGA	15780
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ATGACTGTAA ATGGACGGAA CTCTGGAGAG ACCGTAAAGG CACCGAAGGG CAAGGCAGGC	15900
AACTGCTCAA ACTCTCAGGT AAAAGGACAG AGCTAGGATA GACCGCTTTT TAGCATTAT	15960
CTAAGCATTC CAGAGTACAT GTATCTTGCA TGTGCTCTTT CTTTGGGGT TGAAACGATA	16020
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GATTTCCATG ACAGGAACCT TTATTGATAC CCTCATCATT TGTACTCTAA CTGGTTTGAC	16980
CATCTTGGA ACTGG	16995

(2). INFORMATION FOR SEQ ID NO: 83:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 28473 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 83:

CCGGGGCTTT TGTAGTATAA TAGAGATACG TTTTGAAAGT AGGAGGTATC TATGGACTTA 60

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ACTAAGCGCT TTAATAAACA GTTAGATAAA ATTCAAGTTT CGTTGATTCTG TCAGTTTGAC	120
CAGGCTATTT CGGAGATTCC TGGGGTCTTG CGTTTGACCT TGGGGGAACC TGATTTTACA	180
ACGCCAGACC ATGTCAAGGA GCGGGCAAG CGAGCGATTG ATCAGAACCA ATCCTACTAT	240
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TACCAACTGG ACTATGCTCC TGAAAATGAA ATCTTGTTA CAATTGGGGC GACAGAGGCT	360
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GCTTATCCAG GCTATGAACC GATTGTTAAC TTAGTTGGGG CAGAAATTGT TGAGATTGAT	480
ACGACTGAAA ATGTTTTGT CTTGACTCCT GAGATGTTGG AGAAGGCCAT TTTGGAGCAG	540
GGTGATAAGC TCAAGGCGGT TATTCCTAAC TATCCAGCCA ATCCGACAGG AATTACCTAC	600
AGTCGAGAGC AGTTAGAGGC CTTGGCAGCT GTTTTACGCA AGTACGAAAT TTTGTGTGTC	660
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CTGGTAAAA CGATGCCGAC CCATGAAGAA GGAATATATC CAACGTCGGG ACTATATCAT	960
CGAAAAAATG ACTGCTCTTG GTTTTGAGAT TATCAAACCA GACGGTGCCT TCTATATTTT	1020
TGCTAAAATT CCAGCGGGCT ACAATCAAGA CTCCTTTGCT TTTCTGAAGG ATTTTGCTCA	1080
GAAGAAGGCC GTTGCCTTTA TCCCTGGTGC AGCCTTTGGA CGTTACGGGG AAGGCTACGT	1140
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GTCATGACTT TTCCAAGAT TAATAGTGAC CTCTTTGTCA TGGCCTATGC GACCTATGTG	1500
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TGCCATCGGG TTGGTCAGGC TTTTGACTTT TCTTTCAAAT ATGGAGCCTG CCTCTGTCCA	1740
GAGCATTATC ATGAGGATAA GAGACGTTGT CATCTCAATC CCAATATCCC CTATCTGCTC	1800

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AATCAATTTC AAGCTATTGA TTTTGAGACT TTGGAGACCA TTTCGCTCAA GCCTGGAATC	1860
AAGCAAGAGC TACGCCAATT TATGGATCAA TTATATGAAG AGTACGTTGG GATTACCTA	1920
AAATCAAAGA AATTTATTGA TTCCCTAGCA GACTGGGGAC AATTACTAAA AGAGGAAAAG	1980
AAATGAAAAA AATCGCAGTA GATGCCATGG GGGCGGATTA CGCACCTCAG GCCATTGTTG	2040
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TTTTCTTTAT	TCCATTAGGT	GTTTGTTC	CTTTGATAAA	AACTAATTTA	TCTAGTTTAA	16680
GAATAGTCGG	GACAGGTTTC	TTGATTAGTT	TATTGTTTGA	GTGCTTACAG	TATATTTTAG	16740
CAATAGGTAT	AACAGATATA	ACGGATTGGA	CTTTAAATAC	GCTAGGTGTC	TGTGTAGGCT	16800
TACTGATTTA	TCAAATTTTT	ATAAGAGTGT	TCAAATCACA	GACTAGAAAA	TGGATCAATA	16860
TCTTAGGTAT	GCTTAGCCTT	GGTTTTGCTT	ATCTTGTMTT	ACTGTTACTG	CATTTACTTA	16920
GTGTTTAACT	AATGATTAAA	AAGGAGAATA	TAATGACTAA	ACGCGTCTTA	ATCAGCGTCT	16980
CAGACAAAGC	GGGCATTGTT	GAATTTGCC	AAGAACTCAA	AAAACCTGGT	TGGGAGATTA	17040
TCTCAACAGG	TGGAACCTAAG	GTGCCCCTTG	ATAATGCTGG	GGTGGATACC	ATTGCTATCG	17100
ATGATGTGAC	TGGTTTCCCA	GAAATGATGG	ACGGTCGTGT	GAAGACCTC	CACCCAAATA	17160
TCCACGGAGG	GCTTCTCGCT	CGTCGTGACT	TGGATAGCCA	CTTGAAGCG	GCTAAGGACA	17220
ACAAGATTGA	GCTCATTGAC	CTTGTTGGTG	TCAACCTTTA	CCCATTTAAG	GAAACTATCC	17280
TTAAACCAGA	TGTGACTTAT	GCTGATGCAG	TTGAAAATAT	CGATATTGGT	GGGCCATCTA	17340
TGCTTCGTTT	AGCAGCGAAA	AATCATGCCA	GTGTTACAGT	TGTGGTAGAT	CCTGCTGACT	17400
ACGCTGTGGT	TTTGATGAA	TTGGCAGCAA	ACGGCGAAAC	CTCTTATGAA	ACTCGCCAAC	17460
GTTTAGCAGC	CAAAGTATTT	CGTCACACAG	CGGCTTATGA	CGCCTTGATT	GCAGAATACT	17520
TCACAGCTCA	AGTGGGTGAA	AGCAAGCCTG	AAAACTCAC	TTTGACTTAT	GACCTCAAGC	17580
AACCAATGCG	TTACGGTGAG	AATCCTCAAC	AAGACGCGGA	CTTTTACCAG	AAAGCTTTGC	17640
CTACAGACTA	CTCCATTGCT	TCAGCCAAAC	AGCTCAACGG	GAAAGAATTG	TCATTTAATA	17700
ATATCCGTGA	TGCAGATGCT	GCTATCCGTA	TCATCCGTGA	CTTCAAAGAT	AGTCCAACCG	17760

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GTGTAGTCGG TGGACTTCTC GTGCAAAATC AAGACGTGGT CAAGGAAAGC CCAGCTGACT	18120
GGCAAGTGGT GACTAAACGT CAGCCAACTG AGACAGAAGC GACTGCTCTT GAGTTCGCTT	18180
GGAAGCTAT CAAGTACGTC AAATCAAATG GTATTATCGT GACCAACGAC CACATGACAC	18240
TTGGTGTGG TCCAGGTCAA ACCAACCGTG TGGCTTCTGT TCGCCTTGCC ATTGACCAAG	18300
CCAAAGATCG TCTGGACGGG GCGGTCCTTG CTTCAGATGC CTTCCTCCCA TTTGCGGATA	18360
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GTGACCAAGA ATCCATCGAA GCAGCGGATA AATACGGCTT GACTATGGTC TTTACAGGTG	18480
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GTTC TAGAAG GGGTGATTAA AGAAGGTCGC CCTTATCTGG GAGTTCTTTA CGCAGGGCTT	19440
ATCCTGACAG CTGATGGACC GAAAGTCATT GAGTTCAACG CTCGGTTCGG AGATCCAGAA	19500

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ACTCAGATTA TCTTGCCCTCG CTTGACCTCT GACTTTGCTC AAAATATCAC AGATATCCTG	19560
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GCATCCAAGG GCTACCCGCT AGACTATGAA AGGGGCGTTG AGTTGCCAGC CAAGACAGAA	19680
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CAAGACTGCG ACTGGTGGCT ACGATGGTCA TGGACAAAAG GTTATTGCT CAGAAGCAGA	21240
CTTGGAAGCA GCCTATGCCG TAGCAGACTC AGCAGACTGC GTCTTGAAG AATTTGTCAA	21300

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TTCTGAAAGT CTAGTAGACA AGGCTAAAGC TATGGCAGTG CGAATCGCAG AACAACTCAA	21480
CTTGCTCGGA ACTCTCTGTG TGGAAATGTT TGGCAGAGCT GATGACATCA TTGTCAATGA	21540
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ATGACTGGTC TGGCGCGTGT CATTCGTGGT CACATGATTA CGGCTTATGA AAACGTCGCT	23040

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CAAAAACAGC CTACTCTTGG GACAACCAAG TAGACTTTAA ACCACTTCTT GAGGCAGATT	23340
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AACAGCGAGC TTCAATCTCG CTGTTTATTT TTTATCGAAA AGACTTAGTC TTCTTTTCTT	23520
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GCTAGGTATT GAGGTGATGC GAGGTTATAT CCCCACCAGC CTTTAGACCA GTAAGAAATC	24840



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AATTTGCCAT AGAGTTGATA CCACTTGAGG TAGTACCAGC CTTGGGCACT AGTCGCATCG	25020
TTGGCGTATT CGTCAGTACC AAAGTTGAAA ATCTTTGTTT TACCTGCAAA GAAGTCCATG	25080
TATTTACCGA TGAGGGCTTT TACAAAGTTC ATCGCTTCTT CGTTTTTCAA GTCCATAGTT	25140
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AGATCGACAG TACGGGCTGA TTTCTTCCCA AAATAGCTAA AGTTAGGGTT TTGGATTCCC	26520
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AGACCGATAC CTTTATCTTT GGCATAGTTA ATCAGATCTG TCATTGACT TTCTGTTAAG	26640
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CGCTGTGTGT TTTTATGTTT CATTGCAAAA CCTCCTGATT GCATTGTAT ATTGATAGCG	27480
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AATGATCGC CGCGTAGACC CAATTTTCC AAGTAAACAA GCTTGTTCCT GCGTTCAATT	28200
GAAAGAACAG TTACCTTATC ATCTTTAGCA TTGAAGAGTT CAATATCTGA AAACCTTACA	28260
AGCTTGTGTT TGCGTGACG TGAACGAAG GTTCCTTTTC CTTGTTGGCG GACAATATAG	28320
CCATCTTTGG CAAGGTCGTT TAAGGCGCGA ACAACTGTGA TAGAGCTGAC ATCGTACATT	28380

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GAAATGAGTT CTGCTTCAGT GTAAAATTTA TCTCCACTGC TAAACTGCCC AGAGATGATT 28440  
TTATTTTTTA ATTCGTCTTT TATGTATTGA TGG 28473

(2) INFORMATION FOR SEQ ID NO: 84:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 6749 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 84:

CCTGATGGGT GGTATGCGAG GATACAGTTC TGAAAATCGC CGTTACTTAA TTAATGGACG 60  
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TAACACCATC TTGAAGAATG CTGCTCTTGC TCGTCGTTTC AACGAAGTGA AGGTCAATGC 720  
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AATGGAAGCT TCAGATATCG AACGTTTGAA AGATATGGCT CATCGCTTGC AAGACAAGGT 1200  
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AGAAGATCGG GATAAACCAG AATTGATGGA CCGTTTGAAA CCCTTCTTCC GTCCAGAATT	1740
CCTCAACCGC TTTAATGCAG TCATCGAGTT CTCACACTTG ACTAAGGAAG ACCTTCTTAA	1800
GATTGTAGAT TTGATGTTGG CTGAAGTTAA CCAAACCTTG GCTAAGAAAG ACATTGACTT	1860
GGTAGTCAGT CAAGCGGCTA AAGATTATAT CACAGAAGAA GGTTACGACG AAGTCATGGG	1920
GGTTCGTCTT CTCCGTCGCG TGGTTGAACA AGAAATTCGT GATAAGGTGA CAGACTTCCA	1980
CTTGGATCAT TTAGATGCTA AACATCTGGA AGCAGATATG GAAGATGGCG TTTTGGTTAT	2040
TCGTGAGAAA GTCTAAGACA GAATTTTGAG GATAAAAAAG AAGGAGCCAG CTGAAAAAAA	2100
CTGGTTCCTT TTTAGGTACG ACAGGCATGT CGTATAGTAG AAGTGATTA TTCTAGTTTC	2160
AATATACTAT AGTAGCTCAG AAGTCGGTAC TTAAACGTGC TATATCAAAA CCAGTCCTGG	2220
AAAAACGTGG ACTGGTTTCG TGTTTGGATT ATTACCTTGA ACGACATGCG TTTAAAGTTA	2280
GTTGAACCGC CGTAGCCGA ATGGTACGTA CGGTGGTGTG AGAGGGGCTA GAGATTATCC	2340
CCTACTCGAT TTTAAATCAC ATGACGTTCA AAGGCATCAT CTGAAATCCC TTGTTCCAAG	2400
ATGAGTTTGG CCCATTCTTT AGCAGAGAAG AGGCTGTGGT CCTTGTAGTT TCCGCAAGAT	2460
TCGATGGTTG TCCCTGGGAC ATCTTCCCAA GTAGTAGTTT CAGCGATTTC CTTGAGCGAA	2520
TCCTTGATAA CAGCTGCGAT TTTAGCACTG GTGTGACGTC CCCACATAAT CATGTGGAAG	2580
CCTGTGCGGC AACCAAATGG TGAACAGTCA ATCATGCCGT CAATGCGGGT ACGGATGAGT	2640
TTGGCTAAGA GGTGCTCGAT AGTGTGAAGG CCGGCAGTAG GGATAGAGTC TTCGTTTGGT	2700
TGCACCAAGC GAATATCATA ATTGGAGATG ATGTCTCCTT TTGGTCCTGT TTCTTCCCCA	2760
ATCAAGCGAA CATAGGGTGC TTTGACAATG GTGTGGTCAA GTTCAAACT TTCGACAATA	2820
ACTTCTTTTG ACATGGTAAA TCCTTTTCACT TTTCTTCTCT CATTATATCA TAAAGGTTGC	2880
TCCTGAGACA GAGAGAAAAC CTCTCCGAGG CTGGAGAGGT TGAAATCTTT ACTTACGATA	2940
TAAGCGGTCG TATTGGTAGT ATGGGTCAA GGTACGTTG ATACCCAGTT TACGAAGGAC	3000
ATTCTTGTCT TCATCAGTCA AGATGATGGT TGAGTGGGCT TCGCTTCCTT TGAGGTTGCC	3060

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GAGTCTCTCC ATAGCGCGGG CAGCATCAGG ATTTCTGTGA GCTGTGATAG CAAGTGCAAT	3120
CAGGATTTCA TTTGAATGAA GCGGTGGATT GCGGCTACCG AGATGATCGA TTTAAGACC	3180
TTGGATTGGC TTAACAACTT CAGGCTCGAT TAGTTTTACT TCTTTAGCGA TGTCAGCTGA	3240
TTTTTTGATG GCGTTGATCA AGGCAGCGGC TGTAGGACCA AAGAGTTCTG AGTTCTTACC	3300
AGTGATGATT TCCCCATTGG GCAATTCAAA GGCTAGGGCT GGTCCACCAG TTTCTTCTGC	3360
TTTTTGGCGC GCAACGACAG CAACCTTACG GTCTGCAGGT GTGATACCGA GGTCGTTTAT	3420
GAGCAACTCA ATTTCTTGA CGGCAGCTTC GCCAACTTTT TCAGCTTTGA AGTCAAGAAC	3480
TGTTTGATAG TAACGGCGGA TGATTTCTTG TTTAGAAGCT TCGACAGCGG CCTCGTCATC	3540
TGTAATAGCG AAACCAACCA TGTTGACACC CATATCTGTC GGTGAAGCGT ATGGTGATTT	3600
TCCGAGAATA CGTTCCAACA TGCCTTTGAG CACTGGGAAG ATTTGATAT CACGGTTGTA	3660
GTTGACAGTG GTTTCTCCAT AGGTTTGAAG ATGGAAGGGG TCAATCATGT TGACATCATC	3720
AAGGTCAGCT GTGGCAGCTT CATAAGCCAA GTTAACTGGA TGATGAAGGG GAAGATTCCA	3780
AACAGGGAAG GTTTCAAATT TAGCGTAGCC AGATTGATG CCATTGATTT GGTCGTGGTA	3840
CATATTGGAG ATACACGTTG CCAATTTTCC AGAACCAGGT CCAGGAGCGG TTACGACAAT	3900
CAAGTTGCGA CTGGTTTTGA TGTAGTCGTT TTTGCCCATG CCTTCTGGGG AAATGATGTG	3960
ATCCATATCC GTCGGATATC CTTTGATTGG ATAATGAAGA TAAGAATCAA TTCCGTTTTT	4020
CTCAAGTTGA TTGCGGAAGG CATCTGCAGC GGGTTGGCCA GCGTATTGTG TAATGACAAC	4080
GGAACCAACA AAAATCCCTA ATTCATTGAA TTTATCAATC AAACGAAGAA CTTCTTGGTC	4140
ATAAGAAATG CCTAAGTCGC CACGTGCTTT GGAATGTTCA ATGTTGCTAG CATTAATGGC	4200
AATCACAACC TCAACCTGCT CTTTCAATTC TTGCAAGAGC TTGATTTTGT TGTCAGGTTT	4260
ATAACCAGGA AGGACACGAG CAGCGTGGAA ATCTTCTAAC ATTTTACCGC CAAACTCTAA	4320
GTAGAGCTTG CCGTCAAATT GGTAAATGCG CTCCAAAATA TGGTCGCGTT GTAAATTCAA	4380
ATATTGTTCA GAACTAAAAG CTTGTTTTTT CATTTTTTTA CCTCTGGACT CTATTATAAT	4440
AAAAAATTGG AAGTTAGGAA ACTACGGAGC TAAAAAGAA ATTAAAAAGA TTAAGCAAAC	4500
GCTTGACAA AATTTTAAAA AGTGCTATCA TAGACTATAG ATTATGAAAA TAATGAGGTA	4560
AACAGATGCA AGAAAAATGG TGGCACAATG CCGTAGTCTA TCAAGTCTAT CCAAAGAGTT	4620
TTATGGATAG TAATGGAGAT GGAGTTGGTG ATTTGCCAGG TATTACCAGT AAGTTGGACT	4680
ATCTAGCTAA GCTAGGAATC ACAGCAATTT GGCTTTCTCC CGTTTATGAC AGCCCTATGG	4740
ATGATAATGG CTATGATATT GCTGATTATC AAGCGATTGC GGCTATTTTT GGAACCATGG	4800

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AGGACATGGA TCAGCTGATT GCAGAAGCTA AGAAGCGTGA CATTTCGTATC ATCATGGACT	4860
TGGTGGTCAA TCATACCTCA GATGAACATG CTTGGTTTGT CGAAGCCTGT GAAAATACTG	4920
ACAGCCCTGA GCGAGACTAC TATATCTGGC GCGATGAACC CAATGACCTA GATTCTATCT	4980
TTAGTGGGTC TGCTTGGGAA TACGATGAAA AGTCAGGTCA ATACTATCTC CACTTTTTC	5040
GCAAGAAACA GCCCGATCTC AACTGGGAAA ATGAAAAACT TCGCCAGAAA ATTTATGAGA	5100
TGATGAACTT CTGGATTGAT AAAGGTATTG GTGGTTTCCG TATGGATGTT ATTGACATGA	5160
TTGGCAAAAT TCCTGACGAG AAGGTAGTCA ATAATGGTCC TATGCTCCAT CCCTATCTCA	5220
AGGAAATGAA TCAGGCGACC TTTGGAGATA AGGATCTCTT GACAGTAGGG GAGACTTGGG	5280
GAGCAACTCC AGAGATTGCC AAGTTCTACT CTGATCCAAA GGGGCAAGAA TTGTCTATGG	5340
TCTTCCAGTT TGAACATATC GGTCTTCAGT ATCAGGAAGG TCAGCCTAAA TGGCACTATC	5400
AAAAAGAGCT GAATATCGCT AAGTTAAAAG AAATCTTCAA CAAATGGCAG ACAGAGTTAG	5460
GAGTTGAGGA CGGCTGGAAT TCCCTCTTCT GGAACAACCA TGACCTCCCT CGTATTGTCT	5520
CAATCTGGGG AAATGACCAA GAATACCGCG AAAAATCTGC CAAAGCCTTT GCAATCTTAC	5580
TTCATCTCAT GAGAGGAACT CCTTATATCT ACCAAGGTGA GGAGATTGGG ATGACCAACT	5640
ATCCGTTTGA AACACTGGAT CAAGTAGAAG ATATTGAATC TCTCAACTAT GCGCGTGAGG	5700
CTCTTGAAAA AGGTGTTCCG ATTGAAGAAA TCATGGACAG TATCCGTGTT ATTGGACGTG	5760
ACAATGCCCG TACCCCTATG CAATGGGACG AGAGCAAAAA CGCTGGTTTC TCAACAGGTC	5820
AACCTTGGTT GCGCGTTAAT CCAAATTACG AGATGATCAA TGTCCAAGAA GCGCTGGCAA	5880
ATCCAGATTC TATTTTCTAT ACCTATCAGA AACTGGTCCA AATTCGCAAG GAGAATAGCT	5940
GGCTAGTTCG AGCTGACTTT GAATGCTTG ATACGGCTGA TAAGGTCTTT GCTTATATAC	6000
GTAAGGATGG CGACCGTCGC TTCCTAGTTG TGGCTAACTT GTCCAATGAA GAGCAAGACT	6060
TGACAGTAGA AGGAAAAGTC AAATCTGTCT TGATTGAAAA CACTGCGGCT AAAGAAGTAC	6120
TTGAAAAACA GGTCTTGGCT CCATGGGATG CTTTCTGTGT GGAATTACTA TAAATATTTT	6180
TTGCAGAAAA ATTTAAAATT GAAATCGTAT AAAACAAGG GAGGACTGTA TAAAAGACAG	6240
AAATCCTTTG TTTTATATAA CCAAAGTTTA TAAACTTTCA TTCTTGAAAT TCAATTAACT	6300
TTACAAATTC CCACTATTAA GGAGAAAGAA GATGAACATA AAGAAGCGTG TCCTTAGTGC	6360
AGGCCTGACT TTTGCATCTG CTTTGCTTTT ACCCAAATCA TTCATACCTC TCTCAACTAG	6420
ATGTAACTTA CAAAACCCCT GACCTCATGA GCCACTTTCT TCCTCCTCAT GAGGTCAGTT	6480
TTACTTTCTG CTGTTCCAGT ATCGTTTTC CTCGCTAGAT TTCCTCAAAA GGGCAGACTC	6540
CTCCCTTGGT GCGTCACAG ATTTTTCAT CTCGACTGTT CTTTAATGCA TCATTAACGA	6600

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CGCTTTTCTT CTAGGTGGTT CATAAGGAAC AGGAAGATTC AGGTTGACTT TTCTAATCCT 6660  
AGAATAAAGT GCTGAAAACA ATTCGGAATA GGCATAGAGA CTAGACAATT TGAGGAGCTG 6720  
CTTGCGTCCT GTTCGAACAC ATTTTCCGG 6749

(2) INFORMATION FOR SEQ ID NO: 85:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 1842 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 85:

TCTACCCATG GACTTTGAGG CATTCAATTGT TCCATCTTCT AGTGGCGAAT CTTTGTATAC 60  
AAACGATTCA ATTCACTTGG ATAGTGAAAC TCTCCCGCAA ACATTTTCTT GTTTAACTCA 120  
ATCCAGCTGA TATTTCCTTC AGCCAAAATA ATGGACAAGT TCTCCCAAAA TCGTTCAGCC 180  
ATATTGCTTC TCCTTTAGTT AGATAAATAA TGTGTTTGGC CCATGTAAAT CAATTGTTTC 240  
GTATCTCTTG GCAATAGAGC TCTAGCCTCT TCCAAATTCA GACTTGGATA AACTCGCTTA 300  
TTTGAACCG CAAGAGGAAG TCTGATGGTT AGTTCAGGAT TTTTAAAAAT TATCTCAACG 360  
AAATCCGTTA ATCTTAGATT GTCACGGTTC TTAAATCGTA ATAAATTGGG AGATAAAAAC 420  
TCAAAACAAT CTGAAGAATA GCTCATCATC TCAATTAATT TGTCTTTGT CATTTAGAA 480  
ACTGAATGAC AAGATACCTC TATGCCATAG TTTTGAAGA AATCTAAAAG AAGTTGATTT 540  
CTTTGTCTAT TTTTACTTAG ATAGAGATCA ATCATGGGAG ACCTCCCAAA GATTCGGTTC 600  
CATTTGATAT TCTGACACGA TTAAGGAATC TAATAAATTA AGGAATCTAA TAAATTGCGG 660  
AAGTTAATCG GTTTCTTGTC TTCATCATAA GCTTTTACAG TTACTTGGGT TGTAAGTATT 720  
CCCTCTTTTC CCTCGGCTCG ATAGCCTTGT CCATATAAAA CAAAACGAG ATTTTGATGA 780  
TCATCTACAA AGGCATCAAC CCCATTCTTT ATGTCTTGAC TTTCAAGGAA TTCCATAACG 840  
TTTTGAAGAT AGGATTCGTA AAATAGTGGG TAGTTATGTT TTTTATGGTA ATCATCTAAA 900  
AATGTCACTT CAAACTCACA TGGAGAGTAA TTTTGACTTT GAACAGCCTA AAAGTGCCAT 960  
CAAAATTGAA TTGGAATAAA TCAAATAAAT AGCCCCATCC TCATCAATCC AACCTTGTCT 1020  
CAAAGACAAC TCCAACCGAT CTTTAAAAAC TGAGTAAACC ACCTTAACCT CCAGTTTCAT 1080  
ATTCTTATAC CGTTCCTCT CAAATAAAAG TTTGGGGAGC TTATAATAAC GCTCTGATGT 1140  
CTGATATTGA TTAGCGGTAA TACGCTTCAT TATTGTCCCT CCAAGACTAA AATCCAACA 1200

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TTTCCAAATT CATCAAATCG GATTAAACCT ACTTGTTCCTA TTTCATCAAC TAACTGAGTT	1260
GCTTTTACCC AAATCATTCA TACCTCTCTC AACTAGATGT AACTTACAAA ACCCCTGACC	1320
TCATGAGCCA CTTTCTTCCT CCTCATGAGG TCAGTTTAC TTTCTGCTGT TCCAGTATCG	1380
TTTTTCCTCG CTAGATTTC TCAAAAGGGC AGACTCCTCC CTTGGTGCGT CACACGATTT	1440
TTTCATCTCG ACTGTTCTTT AATGCATCAT TAACGACGCT TTTCTTCTAG GTGGTTCATA	1500
AGGAACAGGA AGATTTCAGG TGACTTTTCT AATCCTAGAA TAAAGTGCTG AAAACAATTC	1560
GGAATAGCCA TAGAGACTAG ACAATTTGAG GAGCTGCTTG CGTCCTGTTC GAACACATTT	1620
TCCCACCACG TGAAGAAAAA GATGGCGGAA GCGTTTGATT GTTAAAGTTT GGAAGTCACC	1680
TCCAGCTAGA TGTTTGAGAA AAAGATAGAG ATTGTAGGCG ATACAGCTCA TCATCATACG	1740
AACTTCGTTT TTGATTAAGG TTGAACTATC CGTTTATCG CAAAAAATC CCTCCTTCAT	1800
CTCCTTGATG AAATTCTCGG CTTGACCACG TCCACGATAA AG	1842

## (2) INFORMATION FOR SEQ ID NO: 86:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 19390 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 86:

TCATCTTTAT CTCCTCGAAA TTTTCTAATA TAGCCATTAT AACAGAATTT TGTGAAAATT	60
CCTATTATAG TAAATCACTA TTTCAGTATA AAAAGAAAAA ACGAATCAGA CGATTGCTC	120
TTCTTAAAT CTGAAAATAG CTTTCCAGAA AGGATTAGCC GATTTTTTGC AGATTGAGCA	180
CTGCATCGTG ACTCATCAAG ACTTGACCAT ACTCTTGTA GACTGAGCGA CTGATATCAC	240
TATCGTCTGC AAACCTCGCG ATACGGGCCA ACAGCCAAGC TGGATATGGG CTTGGATGAT	300
TTTCAATATC CACTAAAATG GTCAAATAAT AGCGCTCGTT CATTTTGTAG AGTTCAGAAG	360
TTTCCATTTT AAAAGTCACT GTCTTGGCAA AAGCTACCAA GTCAGCCAAC TTAGCAAAAG	420
AAAGGATGTA GTAGATGTAA GGTTCCTTCT TACTCTCAGC TTCTTGTTCA GCCTGCTCTT	480
GCTCTTCTTC CTTGACTTCA ACTTGCTCAA GAGATTGAAT GGCTTCGATA TCATCCTTGG	540
TTTTGTCTGC GATGCTTTTT TCCAGGGTTT TGATAAATTC ATCTGGAGAC ATTTGAGCCA	600
ATTCTTCCAT ATCTGGCAA TCCGATAAGT CTTCAAAATC TAGATTTTGG TCAATCTTTG	660
ACTTGGTCAC AAAGACATCT ACCTTATCAG GTTTTGGAGT CACACGGAAG CTCAACATGC	720
CTGTATCCAG AAAGCTATCA GGCATCTCTA GCTCATCCAA GATAGCATAA AAGAACTCTT	780



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CTGTTTTTTC TTGAGGAACG AGAAAGTCAG CAATCTCCAT TCCACGATCC ATCAATCCT	840
CTAAAGATAT CGTGATTTTT AAAGTTGTAT CACTAATTG TTTCATTTTC ATTGCTAGTA	900
ACCTCATACT TTCAGTTCTA TCTATTATAC TAGATTTTTA CGATTTTATC AAAAGAAGGC	960
TCCTCTATAC GGATAGATT TCCCTAGGGT CTTTCTATAG GAGACTCCAA AAGAAAATT	1020
CTGCAGACAG ATAGAAAAAG CCTTCAAAAT CGGCTAAGAG CCGACTTTGA AGACCTTATA	1080
CATCAGAATA CTTATAATT AAAGTTGCT ACACCGAGGA TAGAACGATT TAAGTTTCTG	1140
AGAATTGAA GACTTTGCTC AAATTTCTTA TAACGAGTCA CTCCGTACTC TTCAACAAGA	1200
AGGACTGTAT CTCTTTCCAA AAGAGATGAT ACATCTGTA AATCTACAAA ATGCATTCCT	1260
TTTAAAGCTT CTTGACTCTG TTTCAATTTA TCTAAGATAG CTTTATTTGA GCTAACGATG	1320
GTCAATTCTT GTCCAGTATT TTTGTATGAC AAAACATCTG CTAGGTTAGC AATTGTTGTA	1380
ATCTCTGTTA CAAAATCAAT TTGATACTGA GAAAAATCAC CTACTCTATT GATTGTTGGA	1440
TTAAAGAGAT AAATAACAC ATTTCCCATC ACAACCAAAA TCACACAAAC CACTCCAATA	1500
ACAATAAAC GAAGAATCAG ATTTTTCACA TTAAAGCCAA GCGCTGTTTC ACCATTTGCG	1560
TTCAATTCTT TAGAGTTGAT GGTTCAGT TTTTCAATT TCACATTTGC ATAGGCATGT	1620
TTAAATTCTT CAATCAACCC ATCAATTTTT TTCTCTAACA AGTTATTGGC ATCTTTACTT	1680
GATGTCAAAA TTTTCACACC AACCCCTGCA TCGTCAATCA TATAGTAGAC GGTCAATTTT	1740
TTCCACCAAT AGTCATTCTG TGAATTTTTC AAGGTTGTTT CTGTCGTGTC TAATTCACTG	1800
GCAATTTTTT TCAACTCACT GGGTCTACA TCATTGAAAA GATAAGCTCC ATTCAAATTA	1860
CCATCAATCA ATTTCCCATA AAAATCACTA TAACCACCAA TTTGATGATT CAAAATCGTT	1920
TTGTCCGACT CTTTGGAGG AGTGATTTTA TAGATAAGAT AAGTTGAATA ACTTGTGTA	1980
TCTTTGACAG TGTTTTTATT CCTAACTGCT TTAATTGTAA ATGGTACAGC AATGAGAGCA	2040
AATAAAGCGA TGAGAGCTAA AATATTTGCT TTTCGCTTTT TATAAAGATT TGCAAACAAA	2100
TCAGCTACTG AATAATGTTT AACATGATT TTTTCTCCT TTGTTTAGTA GATACTAGTT	2160
TTCCTTTGTA AGCATTTTGT CTACAAATAT AATCACAAGA ACAATCCCC AGAATTGCAT	2220
TGTAAATAAA TTGAAGAAAC TTTCTGAAAA GCTGCTTCTT GGCATAAAGA ATAGATTATT	2280
CAAGATGAGT AGGGATAAAG CAAATAGGAT TGTCTTGAG CGATAGGCTA CTTGCAGCAT	2340
GGCTATAAAT AATACGCCGA GTAAGAACT AAGCAGAAAG ACTCCAATCA TACCATAGTC	2400
GGTATACAAC TCCATGATAT AACTACTTCC GATACCATGC CCTTCAAGT ATTCCTTGTT	2460
CAAGACAAGA TAGGATAGAT TGTGGGCATA ACTATTACTA TCAATAGCTA GTTCCACACT	2520

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ATTGGTTGTA TGTTCAAAGG CTTTTCCTCC GAAAATGGCT CCCAAACTCC CCCTTGCAAA	2580
ATAATCAAGA ACAGGACCAA AAGTAAATTT ACGGAAATCT CGGTAAGGGA GGCTACTGTT	2640
AAATAGAAAA CCTCGAGCCA GAACACCAA ACTAGTCCCT TGTATTAGA TAAAGTCAAG	2700
TAAGATATCC CAGAAACCTG TATGGGAAAC TTGGACATTA TCCCGTACAT AATTGAGTAC	2760
TCCCATCGCT AACATGAGAA TAGGAGAACC TACAAAAATC GCTAACTTTT CTTTAAACCC	2820
AATCCATTTT CCTTTTTCAG TTTGCTCCCG CATAAAGTAA TAAACAAAAG CAAATMAAAT	2880
ACTTAAATA AAGGGATTTC GTGTCCCAAT TGCCAAATGA ATAGTATTAG CTGCAATAAA	2940
GGAGACAAGC ACTGCTGTGG CCTGCAATTT CTTTGGCTTG GTTGCCAGAT ACATACACAT	3000
TGCATAGACC GTAAAGGTAG ACAAATGTA GGTAAATATA GGCAGTTTAC TTTCAAATTT	3060
TGCATAGTAG GCATAGTAGG AAGTCTGCAA ACGATACAAG AGCCGTTCAA ATAACCGAAT	3120
GAAATAGAAA GGATAAGTTA GAAGAAAAAC TCCTAGTGAT ACAAAGCGTA ACCGCTTGAT	3180
ATAAACCTCT TTTAGAGAAT TTCCTATATT TGCTACTTTT ATTTCTTCC TAGCTATGAA	3240
GTAACGAGCC AGAATGCCTC CTGTGGTCAA GCCCAGAATC GAAATCATGA CAACTATAAA	3300
GGCAAAACGA TAGGCTATTG GATGATAGGT ATCCAAAGCA CCATCCCTAA AATAATCAAT	3360
GGTCGGTCTT GATACCAGAA ATACAAAAAT GGTAAATAG AAAATAAAT GGATTAAGTA	3420
ATACTTGATA TCATTCCAAC AAGCAATTAA GCTACTAACC AACAAGAACA ATAAAGTAGA	3480
AAGTAAGCTA ACATTATTAT TATTAAACAG ATACACAATT CCACTTACTA GCGTCAAGGC	3540
ATAACTGACT ATGGTCAAAAC TAAATAATAA TCGTTTCCCA TCAATCACTT GGTCAACCCC	3600
GTTCTAATGT AATTTTTTAG ATTTTTCAAT ATTTTTCAGT AATAAGAATC GATATAAGGA	3660
AATATTTATG AATAGGGCCA AAGCACTAAT TCTTCTCCCC TTACGGAAAA TTGGATTCCT	3720
AGAAATAGCA AAGGCATGGC CTTTAAAAA ACGATGAATC TGAGAATAGG CTTCAAACCTG	3780
TTTATACTGA TCATCTAGCA ACATCTTATC CAGAATAAAG AAGTGGGCAT AGGCCAATCT	3840
GAAAAAAGCG ACCTCTTTCA AGTCAGGATA GTTTTTCACA ACTTCATTAT AAAACTTTTG	3900
GTAGATATCA ATATAGGCTA AATCCTTCTC TGCATAGGGT TTGGTCGTAA TACTATCCCC	3960
TCTATGGAAA TAGTAATAAT AGGGTTTAGT ATTAACCACA TACTTCTTGG CCAACTTGAT	4020
TAAATCAAAA TGGTAATAGG CATCTTCGTA AATCAACCCC TTAGGAAAGG ATAGGGCAGT	4080
TGCAATCTGT CTCTTGATTA GCTTATTGCA AATCGTCCCA GGTATTTTTT CACCTATGAG	4140
GTATTCCTTT AGAAATGTTT GAGAATCACA GACAAAATAG TCATCCTGAT TGGCTGACTG	4200
TGGGCTTTCA TCATTAGCAT AGACATTCAT GACACCACAG CTCGAAACAT CCGCATCTTC	4260
TTGAACTAAT TGCTCATATA AGCTCTGAAT CATTTCTGGA TGGATATAAT CATCTGAGTC	4320

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AATAAAATC AGATAATCCC CGTGAGCCTG CTTTCATCCA TCATTTCGTG CTGCGACAA	4380
TCCTTCGTTT TTTTATGAA GCACTGACAC CCTGTCATCT TGTTCAGCGA TTGAATCACA	4440
CAAGCGACCA CTTTCATCTG TTGCACCATC ATCAACAAGA ATAATTTCCA GATTTTGATA	4500
GGTCTGCTTC TGAATGGAAG CTATCGATTT TTCTAGGTAC TGCGCCACAT TATAGACTGG	4560
CACAATCACA CTAATTAATG CAGTTTCCAT GCTACTCCTC TAATAGTTT TCTACTTGT	4620
CGATTGTGTT TGTAATTGTA AATTGTTGAA TGAATTGGCT AGCCTCATCG ACATCAAAGT	4680
TTGAGGCAGA AGTCATGTAA TTAGTAATCG CCTGAGCTGC CTCTTGATTG CTCTCAATGA	4740
TTTGTCAAA TCGTCCTTCT TGGGATAATT CCTCAGCCCC TCCAACGTCC GTAGAGATAA	4800
AAGGGAGTCC CAGACTCAAG GCCTCCACAT AACTCCAGG AAAACCTTCT TGTTTAGACA	4860
TAGACAAAAG AACTTTCGTC TGAGATAGAT ACTGATAAGG ATTTTTTTGA TAACCAAGGA	4920
AATGTACATA GTCCTCAATC CCATACTCTT TGACTCGTTT TTTCAAGTCC TCTTCCATAT	4980
CACCAGCCCC GATAAAATAG AGATGATAGT TTTTCCCTC TTGGTGTAAT AATCGTATCA	5040
CTTCCACTAC ACGGTCAGAA CCCTTATTTT CCTCAATCCG TCCGATAGTA CAGATACTTT	5100
GAGGAGCAAT CTCGATATCG ATCTTCTCTT GAGATTTTTC TAGAATAGTC TGAAAATCAT	5160
ATCCATTGTA GATTGTCTGT AATTTAGAAG TATAATCTGG ATAACTTCC TTGATAGAAT	5220
TGCTGGTCTT TTTTGAAATC CCTACAATTG TATTCGCAGC ATCCAAGTGG CTTCTATGTG	5280
ATTCTCTTTT AGAGCTATCC TTAAGAAGTT CTTCAATACT TCCATGAATC CAAGATATCT	5340
TCTTGACTTC TCTTCTTTTA GAGAACAACA GTGGTGGATT CATAATGGTA AAAGAACTT	5400
CAACATCATA ATCATCTTTT ACAAGCAAAC GACGAGTCAG TCTTGAAAA TAAATTCTCA	5460
TTCTCCACAA AAAAGCTCGT AACCATCTGG TTTGGCGATA ATCTTGAAGG GATTTTAAAA	5520
TGCGTACATG CTTTGAACA GATTTCATATC CCTTGTCAAA GTGCTCCATT TCAAGAATAT	5580
CAATATCATA CTTTCTGGA TCCAGATTG AAACAATGGT TGATAGAATC TTCTCTGCAC	5640
CACCTCCAAG AGAAAAAGAC CACATAAAAA ATAAGATTTT TTTCTTAGCC ACCATATTCT	5700
CCCTTGATT CTGTATAAGA CTTATCCATA TCAGCGATGA CAGCATCATG ATGCGGTACC	5760
TGCTTGCTG CTGGTGGAGG CGTCATATAA TCCCCAAAAG CAGTTCTGAG ATAGACATCA	5820
TAGCCGATTG GAATAGGCAT CTCTGTTCTT TCAAATGGCA AGAAAAGATT GTCTTCAAAA	5880
GATGTGATTG GGTACTGTT TCTCATGTAG CCAGGACCTG AGCATAATTC TGTAATGCCA	5940
TCACAATCAG CCAAATCATA CTTAGTCATT TCTTCTCAG CTTTTTCCA GATGCGATAA	6000
CGGAGAGATT TTGGAGTCAA ACCCAGTAAA ATGCGACTTC CCCATTTTAT GAGATCACCA	6060

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TGCTTTTCTG GAATAGTTTG CGCACAAAAG AGTGAATAAA TCAAGGCCCA ACGAACCTGT	6120
TTTTTCCGCT CAGCTGGATT TTTCGGATAA TAATCCAAAAG GCAAAACATC CAAGGCCAGA	6180
CCATGTGGCA AATCCAAATC CTGCTGATAA GGCTTGATAC AGGTGGTTTT CTTGTCACGA	6240
ATGGTAATAA AAAGATTACG ATCAACAAA TCCTTGTCAC TCTTTGACAA GAAATAACGT	6300
TCATCTGCAT AACGAGGCCA TAATTCCTGCT AATTTCTCAT AATCTTTACG AGGCATAAAA	6360
AAGTCTAGGT CGTCGTCCCA AGGAATAAAT CCCTTGTTTC GAAGGGCACC AATAGCGCCT	6420
CCGCCACAGA GATAACAGAG CAAATCATGT TCTTTACAAA AGGCCACAAA ATATTACGCC	6480
ATCTCCAGAC TACGAGCCTG AATTGCTTTT AAATCAGTCA TATGTTCAT TATCTTTCT	6540
ATCGTATCGT TTCATTATAC CACAAACAAG GGGTGAAAAT CTATTCGAGA CTGTAAAAA	6600
TCAAAGCCTG ACTGCTATCC AAATAGCTAT CAAACTTTGA TTTTCTGTG TATATACTCTT	6660
CGAAAATCTC TTCAAACCAC GTCAGCTTCA CCTTGCCGTA GGTATAGGTA ACTGACTTCG	6720
TCAGTCTTAT CTACAACCTC AAAACTGTGT TTTTAGCAGC CTGCGGCTAG CTTCCCTAGTT	6780
TGCACCTTGA TTTTCATTGA GTATTATCTT ATCTTAAGCC CATTTGAGCG AGCTTGGTTT	6840
GATATTTGTT TTGATCAACC AGCAGGCCCA AGCCCCATA AACATCATAG GCATCTACCC	6900
AGTCACCCAG TTCTGGAATC GTCAATTTTT CAATACCATT TTTTGCTCCA TCCAAAACAG	6960
ATAAACCGTT TGTAGGAGG AAAGTATAGG GTACGTTGGT TGAGGTCATA GCAAAAACCT	7020
TTCCAAGAGC TTCAGAACCA GTGAAAAGTT TAGTGGGATC TTTAATTGC TCTAAAATTG	7080
CTGTTAAAC TTGTTGCTGT CTTTTGTAC GGCCGTAATC TGCCTCATCA TCATCAGGA	7140
AACGAGCATA ATTGAGCAGG GTCGAGCCAT TCATCTGCTG TTTTCCGACT TTAATGGTTT	7200
GGGTGGAGA CTCAGTCTCG GTAGCGTATA AATCATCTCC GACTGTAGCT TCTGTTAGGG	7260
GACGCCCATT CAATGTTGAA AATTGAGCAT CAATCGTCAC CCCATCAGGG AAAAGCGTGT	7320
CAATCGCTGT GGCAAAGGCC TGGAAATCAA CCAAGCGTA GACTTAAATG TCCAAGTCAA	7380
AATTATCTTT CAAGACTTGG CGAACCATTT CTGCCCCCTT TTGCCCCCTT TGTCTCCTA	7440
ACTCGTAGGC TACGTTTAACT TTGTTATCTG TCTGTTTTCT ACCATTAAATC ACTTGACTAT	7500
AACCATCTAT ATAGACCAAA TTATCAGCA TGAAACTGAC TAGCTTCATT TTCTTATCTG	7560
AGCCCCGAC ATTTAATACC ATAATAGAGT CAGTTCGTGT CTCAACACTG TTCTGGCCGA	7620
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CACGCAAAAA CATGAATACC ATGGCCAAAG CCACACAGAC CAAAAGTGAA AAAATCACCA	7800
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TAATTCCTTT TGGGCAAAGT GGACCAAGTC CTTATCGGTA TAATCCACAT CGATAATGAA	8220
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CAATCCATAT TCTTCAGCAG AACTTCTAGG TGCAACTGCT GCAAAGGGCT GGTCTGGATG	8520
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GACCGATCAT CATGAGATAA GGAAGGAAAG CACTTGTAAG AAGCACTGTA ATCAGGCCAG	18540
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AACAGATGAT CATCAAGAGA CTGGAAAAAA TGTAAGAACT TAAGACTCTA GCGGAAACAT	19380
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## (2) INFORMATION FOR SEQ ID NO: 87:

- (1) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 18436 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 87:

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CCTACTCTGG TTCTGCCATG CAATTTGGCG ATAACCTATT CCTATTTTAT ACAGGAAATG	360
TTGCGGATAA AAATGGATC CGTCACCCAT ACCAGATCGG TGCTTTGATG GACAAGGAGG	420

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TCCGCGATCC ACAAATTTT AACTTTTCAGG GTCAATATTA TGCCATTGTC GGCGGACAAG	540
ACTTGGAGAA AAAAGGTTTC GTTCGTCTCT ACAAGGCTGT CAATAACGAC TACACAACT	600
GGCAAGCAGT TGGCGACCTT GACTTTGCTA ACGACCGTAC TGCCCTACATG ATGGAATGTC	660
CTAATTTGGT CTTTGTAGAG GAACAACCTG TCCTTCTCTA CTGTCCACAA GGATTGGATA	720
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CTAGGAATCG AAGACTACAA TCGTGTGACA GCGCCGATTA TTTCTTTGA CCGAAACCTA	1860
TCGCCAGACA TCCCTGTCTG CTCCTCTGAC AACTATGCTG GTGGGGTTCT TGCTGCCCAA	1920
ACCTTGGTCA AGACAGGTGC CCAGTCTATC ATCATGATTA CAGGGAATGA CAATTCTAAT	1980
TCGCCAACCG GACTGCGCCA CGCTGGTTTT GCATCCGTAC TCCCAAAGC TCCTATTATC	2040
AATGTTTCCA GTGACTTTTC TCCCGTCAGA AAAGAAATGG AAATCAAGAA TATCTTGACC	2100
CGGGAAAAAC CAGATGCCAT TTTGCTTCG GATGATTGA CAGCTATTCT GGTCAATTAA	2160
ATCGCTCAAG AATTGGGCAT TTCTGTCCCA AAAGAGCTCA AGGTCATCGG CTATGATGGG	2220